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OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 03:18:40 ; Search time 157.96 Seconds  
(without alignments)  
1240.873 Million cell updates/sec

Title: US-08-484-274-17  
Perfect score: 1296  
Sequence: 1 ATGCTGAGAACACAGAA.....AAACTGGTCTGTCATCTTAA 1296

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 262060 seqs, 75620496 residues

Total number of hits satisfying chosen parameters: 524120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_NA.\*

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2: /cgn2\_6/ptodata/2/ina/5B-COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/5C-COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/5D-COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/6-COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/6CTUS-COMB.seq.\*  
7: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1296	100.0	1296	1	US-08-391-339-17
2	1296	100.0	1296	2	US-08-484-274A-17
3	1288	99.4	1296	1	US-08-391-339-8
4	1288	99.4	1296	2	US-08-484-274A-8
5	1006.4	77.7	1296	1	US-08-391-339-7
6	1006.4	77.7	1296	2	US-08-484-274A-7
7	958.4	74.0	1296	1	US-08-391-339-6
8	958.4	74.0	1296	2	US-08-484-274A-6
9	956.8	73.8	1692	2	US-08-484-274A-3
10	925.6	71.4	1293	1	US-08-391-339-4
11	925.6	71.4	1293	2	US-08-484-274A-4
12	925.6	71.4	1689	1	US-08-391-339-3
13	58.8	4.5	62	1	US-08-391-339-27
14	58.8	4.5	62	2	US-08-484-274A-27
15	58.4	4.5	69	1	US-08-391-339-30
16	58.4	4.5	69	2	US-08-484-274A-30
17	56.2	4.3	69	1	US-08-391-339-33
18	56.2	4.3	69	2	US-08-484-274A-33
19	53.6	4.1	68	1	US-08-391-339-32
20	53.6	4.1	68	2	US-08-484-274A-32
21	53	4.1	61	1	US-08-391-339-31
22	53	4.1	61	2	US-08-484-274A-31
23	52.8	4.1	65	1	US-08-391-339-28
24	52.8	4.1	65	2	US-08-484-274A-28
25	49.8	3.8	7218	1	US-08-232-463-14
26	39.8	3.1	3489	4	US-08-728-323A-1

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27 39.8 3.1 32207 3 US-08-770-379-20 Sequence 20, Appl  
c 28 34.6 2.7 543 7 5273901-6 Patent No. 5273901  
29 34.4 2.7 1291 5 US-08-997-897-1 Sequence 1, Appl  
c 30 34.2 2.6 9551 1 US-08-056-200-93 Sequence 93, Appl  
c 31 34.2 2.6 9551 4 US-08-800-644-93 Sequence 93, Appl  
c 32 34 2.6 1447 2 US-08-403-378B-14 Sequence 14, Appl  
c 33 33.6 2.6 3292 1 US-07-814-964-12 Sequence 12, Appl  
c 34 33.6 2.6 3292 1 US-08-258-442-12 Sequence 12, Appl  
c 35 33.6 2.6 3292 6 PCT-US92-11107-12 Sequence 7, Appl  
c 36 33.6 2.6 3292 2 US-08-328-809-7 Sequence 12, Appl  
c 37 33.4 2.6 2004 2 US-08-471-033-18 Sequence 12, Appl  
c 38 33.4 2.6 2004 3 US-08-471-044-18 Sequence 18, Appl  
c 39 33.4 2.6 2004 3 US-08-463-483A-18 Sequence 18, Appl  
c 40 33.4 2.6 2004 3 US-08-471-046A-18 Sequence 18, Appl  
c 41 33.4 2.6 2004 3 US-08-470-566B-18 Sequence 18, Appl  
c 42 33.4 2.6 2004 4 US-08-469-334-18 Sequence 18, Appl  
c 43 33.4 2.6 2004 5 US-09-300-529-18 Sequence 18, Appl  
c 44 33.4 2.6 2576 2 US-08-471-033-35 Sequence 35, Appl  
c 45 33.4 2.6 2576 5 US-09-300-529-35 Sequence 35, Appl

#### ALIGNMENTS

RESULT<sup>1</sup>  
US-08-391-339-17  
; Sequence 17, Application US/08391339  
; Patent No. 5463175  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dennis R. Hoerner, Jr.,  
; ADDRESSEE: Monsanto Co. B44F,  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391,339  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/156,968  
; FILING DATE:  
; APPLICATION NUMBER: US/07/717,370  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner, Dennis R., Jr.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10533)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1296 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (recombinant)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1296  
US-08-391-339-17

Query Match		100.0%;	Score 1296;	DB 1;	Length 1296;	
Best Local Similarity		100.0%;	Pred. No. 0;			
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Qy	61	GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTGAATGATCCAAACCCACAGGT	120			
Db	61	GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTGAATGATCCAAACCCACAGGT	120			
Qy	121	GAAGTGCTCTTTTCGGTAAACGCTGGTTGCTTCAACGGTTCTCCGGTTGTTCCAAATGTCC	180			
Db	121	GAAGTGCTCTCTTTTCGGTAAACGCTGGTTGCTTCAACGGTTCTCCGGTTGTTCCAAATGTCC	180			
Qy	181	ATGCCAGCAAACTTACATAGCTTCCAAAGTGGCTTCTTGACCCCAATGGTGCCATGTGCC	240			
Db	181	ATGCCAGCAAACTTACATAGCTTCCAAAGTGGCTTCTTGACCCCAATGGTGCCATGTGCC	240			
Qy	241	ATCCGTTTCGGCTACTTCCAAACCATCATGCTTGGTTGATTGCTTCTTGTGCTGGA	300			
Db	241	ATCCGTTTCGGCTACTTCCAAACCATCATGCTTGGTTGATTGCTTCTTGTGCTGGA	300			
Qy	301	AGACCAAAAGGTTGAAGGAGCAAGCTAAGGCACATCCGTAACCTCATCAAGTCCACTGTG	360			
Db	301	AGACCAAAAGGTTGAAGGAGCAAGCTAAGGCACATCCGTAACCTCATCAAGTCCACTGTG	360			
Qy	361	CCTTTGATCAAGTCTTCCGCTGAGGAGCTGATGCTAGCCACCTTATCCGTCACCAAGT	420			
Db	361	CCTTTGATCAAGTCTTCCGCTGAGGAGCTGATGCTAGCCACCTTATCCGTCACCAAGT	420			
Qy	421	CACCTTACCGTGTACCGTGGAGAACAGACTTCGCCAGGACCGTGGAGTTGGGAACAT	480			
Db	421	CACCTTACCGTGTACCGTGGAGAACAGACTTCGCCAGGACCGTGGAGTTGGGAACAT	480			
Qy	481	CGTGTCTCAACGGTGTTCGTAACCTCAAACTCCGTCAGCGTGATGCTGATTTCCGAT	540			
Db	481	CGTGTCTCAACGGTGTTCGTAACCTCAAACTCCGTCAGCGTGATGCTGATTTCCGAT	540			
Qy	541	CCTAACTTGTCTCAGCGCTTTACCAAGGAACTCCATTATCGAAGAGACGGTCACACCAC	600			
Db	541	CCTAACTTGTCTCAGCGCTTTACCAAGGAACTCCATTATCGAAGAGACGGTCACACCAC	600			
Qy	601	AACCCACAAGTCTCGTACTCTCTTGTTCGTCGTTTCATCGCTAACGGTGGAGATTC	660			
Db	601	AACCCACAAGTCTCGTACTCTCTTGTTCGTCGTTTCATCGCTAACGGTGGAGATTC	660			
Qy	661	GTGTCGTCTGTTATCGGATTCGAGACTGAAGTCTGTCGTCCTCAAGGTTATCACCACC	720			
Db	661	GTGTCGTCTGTTATCGGATTCGAGACTGAAGTCTGTCGTCCTCAAGGTTATCACCACC	720			
Qy	721	ACCAACGGTGTCTTGTCTGTGATGACACTCCATTCGATACCGAAGTGGATACCATCTC	780			
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Qy	961	GCTGCTCTTAAGTGAAGCGTGTCTACACTCGCGCTCGCTGCTGCTTCTTCCCA	1020			
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Qy	1021	GCNCTCGCTCCCTGCCAGTTCCTGAAGAACGTTACTTCCAAAGTGGATGGGTTTCCGTC	1080			
Db	1021	GCNCTCGCTCCCTGCCAGTTCCTGAAGAACGTTACTTCCAAAGTGGATGGGTTTCCGTC	1080			
Qy	1081	ATCCCGGATTCCTTCCAGTGATTGGTCTGCTACCGTACTCCAGACGTTATCTACGCT	1140			
Db	1081	ATCCCGGATTCCTTCCAGTGATTGGTCTGCTACCGTACTCCAGACGTTATCTACGCT	1140			
Qy	1141	TTCCGCTCAGGCTCACCTCGGTATGACTTGGTCTCCAAATGACCGCAACCCCTGTTCTG	1200			
Db	1141	TTCCGCTCAGGCTCACCTCGGTATGACTTGGTCTCCAAATGACCGCAACCCCTGTTCTG	1200			
Qy	1201	CTCCTCGCAGGTGAGAACCTCTATCGACATCTCTTCCATTCGCACCAACCCGTTTCGGT	1260			
Db	1201	CTCCTCGCAGGTGAGAACCTCTATCGACATCTCTTCCATTCGCACCAACCCGTTTCGGT	1260			
Qy	1261	ATTGGTAACTCCAAAGCAAACTGGTCTGCATCCTAA	1296			
Db	1261	ATTGGTAACTCCAAAGCAAACTGGTCTGCATCCTAA	1296			

RESULT 2  
US-08-484-274A-17  
; Sequence 17, Application US/08484274A  
; Patent No. 5776760  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,274A  
; FILING DATE: 07 June 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Patterson, Melinda L.  
; REGISTRATION NUMBER: 33,062  
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (713)789-2679  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1296 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (recombinant)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1296  
US-08-484-274A-17

Query Match		100.0%;	Score 1296;	DB 2;	Length 1296;	
Best Local Similarity		100.0%;	Pred. No. 0;			
Matches 1296;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
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Qy 541 CTTAACTTGTCTCAGCGCTTTTACCAAGGGAATCCTTATCGAAGAGCAAGCGTCAACCATC 600  
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Db 601 AACCACAAAGTCTCGTCACTCTCTTGTTCGTCTGCTTTCATCGCTAAGCGTGGAGATT 660  
Qy 661 GTGTCGCTCGTGTATCGGATTCGAGACTGAAGTCTGCTCTCAAGGCTATCACACC 720  
Db 661 GTGTCGCTCGTGTATCGGATTCGAGACTGAAGTCTGCTCTCAAGGCTATCACACC 720  
Qy 721 ACCAAGGCTGTTCTGCTGTTGATGACAGTGTGTTGAGCTGTTGACACATCCAAAGTCT 780  
Db 721 ACCAAGGCTGTTCTGCTGTTGATGACAGTGTGTTGAGCTGTTGACACATCCAAAGTCT 780  
Qy 781 CTTGCTAACTCCCTTGGTGATGACATCCCATGATACCGAAGCTGGATACCATCTGT 840  
Db 781 CTTGCTAACTCCCTTGGTGATGACATCCCATGATACCGAAGCTGGATACCATCTGT 840  
Qy 841 ATGCCAACCCAGAGCTGCTCCAGTATTCACACTACCGATGCTTCTGGAAGTTCAATC 900  
Db 841 ATGCCAACCCAGAGCTGCTCCAGTATTCACACTACCGATGCTTCTGGAAGTTCAATC 900  
Qy 901 GCTACTCTCTATGAGATGGGTCTTGGTGTGCTGGAACCGTTGAGTTCGCTGGTCTCACT 960  
Db 901 GCTACTCTCTATGAGATGGGTCTTGGTGTGCTGGAACCGTTGAGTTCGCTGGTCTCACT 960  
Qy 961 GCTGCTCTCTAACTGGAAGCGTCTCACGTTCTCTACACTCGCGTCTGAAGTTCCTTCCA 1020  
Db 961 GCTGCTCTCTAACTGGAAGCGTCTCACGTTCTCTACACTCGCGTCTGAAGTTCCTTCCA 1020  
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Db 1201 CTCCTCGCAGGTGAGAAGACCTCTATCCGACATCTCTCCATTTCGACCAACCGTTTCGGT 1260  
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Db 1261 ATTGGTAGTCCAAGCAAACTGGTCTGCATCCTAA 1296  
RESULT 3  
US-08-391-339-8  
; Sequence 8, Application US/08391339  
; Patent No. 5463175  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dennis R. Hoerner, Jr.,  
; ADDRESS: Monsanto Co. B4F,  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391,339  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/156,968  
; FILING DATE:  
; APPLICATION NUMBER: US/07/717,370  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner, Dennis R., Jr.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10533)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1296 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (synthetic)  
us-08-391-339-8  
Query Match 99.4%; Score 1288; DB 1; Length 1296;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1291; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 ATGGCTGAGAACCACCAAGGTTGCTATCGCTGGAGCTGGAATCGTTGGTCTTTTGCACCT 60  
Db 1 ATGGCTGAGAACCACCAAGGTTGCTATCGCTGGAGCTGGATCGTTGGTGTTCGACT 60  
Qy 61 GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTGATTGATTCACCAACCCACCAGGT 120  
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Qy 181 ATGCCAGAAACTTGTACTAGGCTTCCAAAGTGGCTTCTTGACCCCAATGGGTCCCAATGTCC 240  
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Qy 241 ATCCGTTTCGGCTACTTTTCCAAACCATCATGCTTGGTTGATTGCTTCTTCTGCTGGA 300  
Db 241 ATCCGTTTCGGCTACTTTTCCAAACCATCATGCTTGGTTGATTGCTTCTTCTGCTGGA 300  
Qy 301 AGACAAACAAAGGTGAAGGAGCAAGCTAAGGCACTCCCTTAACCTCATCAAGTCCACTGTG 360  
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Qy 361 CCTTTGATCAAGTCCCTTGGCTGAGAGGCTGATGCTAGCCACCTTATCCGTCAAGAGGT 420  
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Qy 421 CACCTTACCGTGTACCGTGGAGAGCACTTCCGACGGACCGTGGAGGTGGGAACCTT 480  
Db 421 CACCTTACCGTGTACCGTGGAGAGCACTTCCGACGGACCGTGGAGGTGGGAACCTT 480  
Qy 481 CGTCTCTCAACGGTGTTCGTACTCAAACTCCTCAGCGCTGATGCAATTCGTGATTCGAT 540  
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Db 301 AGACCAACAAAGGTGAGGAGCAAGCTAAGGCACCTCCGTAACCTCATCAAGTCCACTGTG 360  
Qy 361 CCTTTGATCAAGTCTTGGCTGAGAGGCTGATGTAGCCACCTTATCCGTCACGAAGT 420  
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Qy 421 CACCTTACCGGTGACCGTGGAGAGCACACTTCGCCAGGACCGTGGAGGTGGGAATTT 480  
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Db 721 ACCAAGCGTGTCTTGTCTGATCGACGCTGTGTGAGCGTGTGTCACACATCCAAAGTCT 780  
Qy 781 CTTCGTAACCTCCCTGGTGATGACATCCATTTGGATACCGACGTGGATACCAATCGTG 840  
Db 781 CTTCGTAACCTCCCTGGTGATGACATCCATTTGGATACCGACGTGGATACCAATCGTG 840  
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RESULT 5

US-08-391-339-7  
; Sequence 7, Application US/08391339  
; Patent No. 5463175  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.

; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dennis R. Hoerner, Jr.,  
; ADDRESSEE: Monsanto Co. B44P  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391,339  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/156,968  
; FILING DATE:  
; APPLICATION NUMBER: US/07/717,370  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner, Dennis R., Jr.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10533)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1296 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (recombinant)  
US-08-391-339-7

Query Match 77.7%; Score 1006.4; DB 1; Length 1296;  
Best Local Similarity 86.0%; Pred. No. 0;  
Matches 1115; Conservative 0; Mismatches 181; Indels 0; Gaps 0;  
Qy 1 ATGGCTGAGAACCAAGAGGTGGTATCGCTGAGCTGGAATCGTTGGTCTTTGCACT 60  
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QY 1261 ATTGGTAAGTCCCAAGCAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1296
Db 1261 ATTGGTAAGTCCCAAGCAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1296
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## RESULT 6

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US-08-484-274A-7
: Sequence 7, Application US/08484274A
: Patent No. 5776760
: GENERAL INFORMATION:
: APPLICANT: Kishore, Ganesh M.
: APPLICANT: Barry, Gerard F.
: TITLE OF INVENTION: Glyphosate Tolerant Plants
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 4433
```

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: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/484,274A
: FILING DATE: 07 June 1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Patterson, Melinda L.
: REGISTRATION NUMBER: 33,062
: REFERENCE/DOCKET NUMBER: MOST130 38-21(13560)A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (713)789-2679
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1296 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (recombinant)
US-08-484-274A-7
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Query Match 77.7%; Score 1006.4; DB 2; Length 1296;
Best Local Similarity 86.0%; Pred. No. 0;
Matches 1115; Conservative 0; Mismatches 181; Indels 0; Gaps 0;
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Db 1 ATGGCTGAGAACCCACAAAGAGTTGGTATCGCTGGAGCTGGAATCGTGTGTTGCACT 60
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Db 1201 CTCTCCGAGGTGAGAACCTCTATCGACATCTCTCCATTCGCAACCAACCGTTTCGCT 1260  
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Db 1261 ATTTGCAAAATCCAAAGCAAAAGGTCGCGCAAGTTAA 1296

RESULT 7

US-08-391-339-6  
: Sequence 6, Application US/08391339  
: Patent No. 5463175  
: GENERAL INFORMATION:  
: APPLICANT: Kishore, Ganesh M.  
: APPLICANT: Barry, Gerard F.  
: TITLE OF INVENTION: Glyphosate Tolerant Plants  
: NUMBER OF SEQUENCES: 33  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Dennis R. Hoerner, Jr.,  
: ADDRESSEE: Monsanto CO. B4F,  
: STREET: 700 Chesterfield Village Parkway  
: CITY: St. Louis  
: STATE: Missouri  
: COUNTRY: USA  
: ZIP: 63198  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patent in Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/391,339

; FILLING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/156.968  
; FILLING DATE:  
; APPLICATION NUMBER: US/07/17.370  
; FILLING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner, Dennis R., Jr.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10533)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1296 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (recombinant)  
US-08-391-339-6

Query Match 74.0%; Score 958.4; DB 1; Length 1296;  
Best Local Similarity 83.7%; Pred. No. 0;  
Matches 1085; Conservative 0; Mismatches 211; Indels 0; Gaps 0;  
QY 1 ATGGCTGAGAACCAAGAGGTTCGCTGAGCTGGAGTTCGTAATCTGTTGCTGTTTGCAC 60  
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Db 541 CCTAACTTGTCTCAGCGCTTTTACCAAGGGAATCTTATCGAAGAGAACGCTCACACCATC 600  
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QY 721 ACCAACGGTGTCTTCTGTTGATGACAGCTGTCTTGCAGCTGGTGACACACTCCAACTCT 780  
Db 721 ACNACGGCGTCTTGGCGTGTGATGACAGCGTGTCTCCAGCGCGCACACTCGAATCA 780  
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RESULT 8  
US-08-484-274A-6  
; Sequence 6, Application US/08484274A  
; Patent No. 5776760  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,274A  
; FILING DATE: 07 June 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Patterson, Melinda L.  
; REGISTRATION NUMBER: 33,062  
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (713)789-2679  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1296 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (recombinant)  
US-08-484-274A-6  
  
Query Match 74.0%; Score 958.4; DB 2; Length 1296;  
Best Local Similarity 83.7%; Pred. No. 0;  
Matches 1085; Conservative 0; Mismatches 211; Indels 0; Gaps 0;  
  
QY 1 ATGCGTCTGAGAACCAAGAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTGGACT 60  
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Db 361 CTTTGTATCAAGTCTTGGTGTGAGGAGCTCATGCTAGCCACTTATCCGTCAGCAAGT 420  
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Db 421 CATCTGACCGGTATATCTGTTGAGAGAGCAAGCTTCCGCAAGGAGCGCGGAGTTGGAACTG 480  
QY 481 CGTCTCTCAACGCTGTTCTGCTACTCAATCTCAGCGCTGATGATTCGCTGATTTGAT 540  
Db 481 CGGCTCTCAACGCTGTTCTGCTACTCAATCTCAGCGCTGATGATTCGCTGATTTGAT 540  
QY 541 CCAACTTGTCTCAGCGCTTTTACCAAGGAATCTTATCGAAGAGAGAGCGGTACACCAATC 600  
Db 541 CCGAAGTGTGCGATGCGTTTACCAAGGAGCTTCTTATAGAGAGAGAGCGGTACACCAATC 600  
QY 601 AACCCACAAGGCTCTGCTGACTCTCTTGTTCGTCGTTTCATCGCTTAAGGTTGAGAGTTTC 660  
Db 601 AATCCGCAAGGCTCTGCTGACTCTCTTGTTCGTCGTTTCATCGCTTAAGGTTGAGAGTTTC 660  
QY 661 GTGCTGCTGCTGTTATCGGATTCGAGACTGAAGGCTGCTCTCAAGGGTATCACCACT 720  
Db 661 GTATCTCGCGTGTCTGCGCTTTGAGACTGAAGGTTGAGGCGCTTAAAGGCAATACAACT 720  
QY 721 ACCAAGCGTGTCTGCTGTTGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
Db 721 ACNACGGCGTCTTGGCGTGTGATGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
QY 781 CTGCTAACTCCCTTGTGTATGATACATCCCATTTGGATACCGAAGCTGGATACCAATCGTG 840  
Db 781 CTGCTAACTCCCTTGTGTATGATACATCCCGCTCGATCCGAACTGGATATCATATCGTC 840  
QY 841 ATCGCCAAACCCAGAGCTGCTCCACGTAATTCACAACTACCCGATGCTTCTGGAAGTTTCATC 900  
Db 841 ATCGCGAATCCGGAAGCGCTCCACGATATCCGACGACCGCTCAGGAAATTCATC 900

Db 841 ATCCGAATCCGAAGCCCTCCAGCATTCGACACCGATTCGTCAGGAAAAATTCATC 900  
Qy 901 GCTACTCTATGAGATGGGTCTTCGTGTGCTGGAACGTTGAGTTTCGCTGGTCTCACT 960  
Db 901 GCGACACCTATGAAATGGGCTTCGCGTGGGGGTACGGTTGAGTTTCGCTGGGCTCACA 960  
Qy 961 GCTGCTCTTAAGTGAAGCGTCTCAGTTCTCTACATCGCGGCTCGTAAGTTGCTTCCA 1020  
Db 961 GCGGCTCTTAAGTGAAGCGTCTCAGTTCTCTACATCGCGGCTCGTAAGTTGCTTCCA 1020  
Qy 1021 GCTCTCGCTGCTGCCAGTCTCAAGAACGTTACTCCAGTGATGGTTTCGGTCCCAAGC 1080  
Db 1021 GCGCTCGCGCTCGAGTTCTCAAGAACGATATTCAAATGATGGGTTCCGGCGGAGC 1080  
Qy 1081 ATCCGGGATTCCTTCCTCCAGTATGGTGTCTACCCGCTACTCCAGACGTTATCTACGCT 1140  
Db 1081 ATCCGGGATTCCTTCCTCCAGTATGGTGTCTACCCGCTACTCCAGACGTTATCTACGCT 1140  
Qy 1141 TTCGGTCAAGGTCACCTCGGTATGACTGGTGTCTCAATGACCGCAACCCCTCGTTTCGAG 1200  
Db 1141 TTCGGTCAAGGTCACCTCGGTATGACTGGTGTCTCAATGACCGCAACCCCTCGTTTCGAG 1200  
Qy 1201 CTCCTCGCAGGTGAGAAGACCTCTATGACATCTCTCCATTCGACCAACCGTTTCGCT 1260  
Db 1201 CTCCTCGCAGGTGAGAAGACCTCTATGACATCTCTCCATTCGACCAACCGTTTCGCT 1260  
Qy 1261 ATTTGTAAGTCCCAAGCAACTGGTCTGTCATCTAA 1296  
Db 1261 ATTTGCAATCCCAAGCAAGGGTCCGCAAGTTAA 1296

RESULT 9

US-08-484-274A-3  
; Sequence 3, Application US/08484274A  
; Patent No. 576760  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: US/08/484,274A  
; FILING DATE: 07 June 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Patterson, Melinda L.  
; REGISTRATION NUMBER: 33,062  
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (713)789-2679  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1692 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-484-274A-3

Query Match

73.8%; Score 956.8; DB 2; Length 1692;

Best Local Similarity 83.6%; Pred. No. 0;  
Matches 1084; Conservative 0; Mismatches 212; Indels 0; Gaps 0;  
Qy 1 ATGGGCTGAGAACCAAGAGGTGGTATCGCTGGAGCTGGAATCGTTCGTTGCTGCACT 60  
Db 120 ATGCTGAGAACCAAGAGGTAGGCATCGCTGGAGCCGGAATCGTCGGCGTATGACAG 179  
Qy 61 GCTTGTATGATCTCAACGTCGTGGATTCAGAGTTACGTTGATTCATCAACACCCACAGGT 120  
Db 180 GCGCTGATGCTTCAGCGCGCGGATTCAGAGTTACGTTGATTCAGCGACCCCTCTCGC 239  
Qy 121 GAAGGTGCTCTTCGCTTAACCGTTGGTTCGTTCAACCGGTTCCCTCGGTTGTTCAATGTCC 180  
Db 240 GAAGGTGCTCTTCGCTTAACCGTTGGTTCGTTCAACCGGTTCCCTCGGTTGTTCAATGTCC 299  
Qy 181 ATGCCAGGAAACTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCCAATGCGTCATTTGTC 240  
Db 300 ATGCCAGGAAACTTGACTAGCGTTGGCGAAGTGGCTTCTTGACCCCAATGCGGCGTTGTC 359  
Qy 241 ATCCGTTTCGGCTACTTTCACCACTCATCGCTGGTGGTTCGTTTCGTTTCGTTGCTGA 300  
Db 360 ATCCGTTTCAGCTATTTTCCAACTCATCGCTGGTGGTTCGTTTCGTTTCGTTGCTGA 419  
Qy 301 AGACCAACAAAGGTGAAGAGCAAGCTAAGGCACCTCCGTTAACTCATCAAGTCCACTGTG 360  
Db 420 AGACCAACAAAGGTGAAGAGCAAGCTAAGGCACCTCCGTTAACTCATCAAGTCCACTGTG 479  
Qy 361 CCTTGTATCAAGTCTTGCTGAGGAGGCTGATGCTAGCCACTTATCCGTCACGAGCT 420  
Db 480 CCTGATCAAGTCTTGCTGAGGAGGCTGATGCTAGCCACTTATCCGTCACGAGCT 539  
Qy 421 CACCTTACCGTTACCGTGGAGAGCAGACTTTCGCCAGGAGCGCTGGAGCTTCGGAACCT 480  
Db 540 CATCTGACCGTATATCGTGGAGAGCAGACTTTCGCCAGGAGCGCGGAGGTTGGGAACCT 599  
Qy 481 CGTCTGCTCAACGGTTCGTTCTACTCAATCTCAGCGCTGATGCTATGCGGTTCGATTCGAT 540  
Db 600 CGCGCTCTCAACGGTTCGTTCTACTCAATCTCAGCGCTGATGCTATGCGGTTCGATTCGAT 659  
Qy 541 CCTAACTTGTCTCAGCGCTTTCACCAAGGAACTCTTATCGAAGAGAACGCTCACACCT 600  
Db 660 CCGAATCTGCTCAGCGCTTTCACCAAGGAACTCTTATCGAAGAGAACGCTCACACCT 719  
Qy 601 AACCCACAAAGTCTCGTACTCTCTGTTTCGTTTCGTTTCATCGCTAACCGTGGAGAGTTTC 660  
Db 720 AATCCGAAGGCTCGTACCCTCTGTTTCGCGCTTTTATCGCGAAGCGTGGCGAATTC 779  
Qy 661 GTGCTGCTCGTCTGTTATCGGATTCGAGACTGAAGGTCGCTCTCAAGGTTATCACCACC 720  
Db 780 GTATCTGCGCGTGTCTATCGGCTTTGAGACTGAAGGTAGGGCGCTTAAAGGCAATACACC 839  
Qy 721 ACCAAGGCTTCTGCTGTTGATGACATCCCATTTGGATACCGAAGCTGGATACCACTCGTG 780  
Db 840 ACGAAGGCTTCTGCGCGTTCGAGCGGTTGTCGAGCGCGGCGGCGCACACTCGAATCA 899  
Qy 781 CTTGCTAACTCCCTTTGGTATGACATCCCATTTGGATACCGAAGCTGGATACCACTCGTG 840  
Db 900 CTTGCTAACTCCCTTAGGCGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC 959  
Qy 841 ATCGGCAACCCAGACGCTGCTCCAGCTATTTCCAACTACCGATGCTTCGTTGAAAGTTTCATC 900  
Db 960 ATCGGCAATCCGGAAGCGCTCCAGCTATTCGAGCGCGGCGGCGCACACTCGAATCA 1019  
Qy 901 GCTACTCTCTATGAGATGGTCTCTGTTGCTGGAAACGTTGAGTTTCGCTGCTCACT 960  
Db 1020 GCGACACCTATGAAATGGGCTTCGCTGGCGGTTACGGTTTCGCTGCGCTCACA 1079  
Qy 961 GCTGCTCTTAAGTGAAGCGTCTCACGTTCTCTACACTCGCGCTCGTAAGTTGCTTCCA 1020  
Db 1080 GCGGCTCTTAAGTGAAGCGTGGCATGTGCTCTATACGACGCTCGAANAATCTCTTCCA 1139  
Qy 1021 GCTCTCGCTTCGCGAGTTCTGAAGAACGTTTACTCAAGTGGATGGGTTTCGCTGCCAAC 1080





Db 1198 CTCTTCGAGCGGAAAGACCTCAATFCGACATTTTCGCCCTTCGGCACCAAAACCGCTTTGGT 1257  
 Qy 1261 ATTTGGTAAGTCCAAGCAAACTGCTCCTCGCATCCTAA 1296  
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 Db 1258 ATTGGCAAAATCCAAGCAAAACGGTCCGGCAAGTTAA 1293  
 RESULT 12  
 US-08-391-339-3  
 : Sequence 3, Application US/08391339  
 : Patent No. 5463175  
 : GENERAL INFORMATION:  
 : APPLICANT: Kishore, Ganesh M.  
 : APPLICANT: Barry, Gerard F.  
 : TITLE OF INVENTION: Glyphosate Tolerant Plants  
 : NUMBER OF SEQUENCES: 33  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Dennis R. Hoerner, Jr.,  
 : ADDRESSEE: Monsanto Co. BB4F  
 : STREET: 700 Chesterfield Village Parkway  
 : CITY: St. Louis  
 : STATE: Missouri  
 : COUNTRY: USA  
 : ZIP: 63198  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/391.339  
 : FILING DATE:  
 : CLASSIFICATION: 800  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/156.968  
 : FILING DATE:  
 : APPLICATION NUMBER: US/07/717.370  
 : FILING DATE:  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Hoerner, Dennis R., Jr.  
 : REGISTRATION NUMBER: 30,914  
 : REFERENCE/DOCKET NUMBER: 38-21(10533)  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (314)537-6099  
 : INFORMATION FOR SEQ ID NO: 3:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 1689 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: double  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: DNA (genomic)  
 US-08-391-339-3  
 Query Match 71.4%; Score 925.6; DB 1; Length 1689;  
 Best Local Similarity 83.6%; Pred. No. 1.7e-298;  
 Matches 1084; Conservative 0; Mismatches 209; Indels 3; Gaps  
 Qy 1 ATGCTGTGAGAACCAAGAGGTTGGTATCGTGGAGTGGAAATCGTTGGTGTTCACCT 60  
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 Db 120 ATGCTGTGAGAACCAAAAAAAGTAGGCATCGCTGGAGCGGGAATCGTGGCGGTATGCACG 179  
 Qy 61 GCPTTTCATGCTTCAAGCTCGTCGATTCAAGGTTACCTTTCATTGATTCAAAACCCACCAAGT 120  
 || ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 180 GCCTGATGCTTCAGGCGCCGGATTCAAAATGACCTTGATTGACCGAAGCCCTTCCTGGC 239  
 Qy 121 GAAGGTGCCTCTTTTCGGTAAACGCTGGTGTTCACAGGTTCTCCTCGGTGTTCCAATGTCC 180  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 240 GAAGGTGCATCGTTTGGGAATCCCGGATCCTTCAACGGCTCATCCGTCGTCCTATGTCC 299  
 Qy 181 ATGCCAGGAAACTTGACTAGCTGCTTCCAAAGTGGCTTCTTTGACCAAAATGGGTTCATTGTCC 240  
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 Db 300 ATCCCGGAAACTTGACGAGCTGCGGAAGTGGTCTTTCAGCCGATGGG-CCGCTTGTCA 358  
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ATTORNEY/AGENT INFORMATION:  
NAME: Hoerner, Dennis R., Jr.  
REGISTRATION NUMBER: 30,914  
REFERENCE/DOCKET NUMBER: 38-21(10533)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)537-6099  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 69 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (synthetic)  
US-08-391-339-30

Query Match 4.5%; Score 58.4; DB 1; Length 69;  
Best Local Similarity 91.2%; Pred. No. 2.8e-10;  
Matches 62; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 715 ACCACCACCAACGGTCTTCTGCTGTTGATGCAGCTGTTGTCAGCTGTCGTCACACTCC 774  
DB 2 ACAACCACTAACGGTCTTCTGCTGTTGATGCAGCTGTTGTCAGCTGTCGTCACACTCT 61  
QY 775 AGCTCTCT 782  
DB 62 AAATCACT 69

Search completed: January 1, 2001, 03:19:01  
Job time: 29365 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 03:16:17 ; Search time 7299.04 Seconds  
(without alignments)  
775.497 Million cell updates/sec

Title: US-08-484-274-17  
Perfect score: 1296  
Sequence: 1 ATGCGTGAGACCAAGAA.....AAACTGGTTCCTGCATCCTAA 1296

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues 2067340

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba1: \*  
2: gb\_ba2: \*  
3: gb\_om: \*  
4: gb\_ov: \*  
5: gb\_pat: \*  
6: gb\_ph: \*  
7: gb\_pl1: \*  
8: gb\_pl2: \*  
9: gb\_pl3: \*  
10: gb\_pr2: \*  
11: gb\_pr3: \*  
12: em\_fun: \*  
13: em\_hum1: \*  
14: em\_hum2: \*  
15: em\_in: \*  
16: em\_om: \*  
17: em\_ov: \*  
18: em\_or: \*  
19: em\_pat: \*  
20: em\_ph: \*  
21: em\_pl: \*  
22: em\_ro: \*  
23: em\_sts: \*  
24: em\_sy: \*  
25: em\_un: \*  
26: em\_vi: \*  
27: gb\_htg1: \*  
28: gb\_htg2: \*  
29: gb\_in1: \*  
30: gb\_in2: \*  
31: em\_ba1: \*  
32: em\_ba2: \*  
33: em\_hum3: \*  
34: em\_hum4: \*  
35: gb\_pr4: \*  
36: gb\_htg3: \*  
37: gb\_htg4: \*  
38: gb\_htg5: \*  
39: gb\_htg6: \*  
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49: gb\_htg10: \*  
50: gb\_htg11: \*  
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53: gb\_htg14: \*  
54: gb\_in3: \*  
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62: em\_hum6: \*  
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65: gb\_ba3: \*  
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89: gb\_sts1: \*  
90: gb\_sts2: \*  
91: gb\_sy: \*  
92: gb\_un: \*  
93: gb\_v11: \*  
94: gb\_v12: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1296	100.0	1296	5 AR016604	AR016604 Sequence
2	1296	100.0	1296	5 I15337	I15337 Sequence 17
3	1288	99.4	1296	5 AR016595	AR016595 Sequence
4	1288	99.4	1296	5 I15328	I15328 Sequence 8
5	1200.4	92.6	1631	5 A59869	A59869 Sequence 1
6	1006.4	77.7	1296	5 AR016594	AR016594 Sequence 1
7	1006.4	77.7	1296	5 I15327	I15327 Sequence 7
8	958.4	74.0	1296	5 AR016593	AR016593 Sequence
9	958.4	74.0	1296	5 I15326	I15326 Sequence 6
10	956.8	73.8	1692	5 AR016591	AR016591 Sequence
11	925.6	71.4	1293	5 AR016592	AR016592 Sequence
12	925.6	71.4	1293	5 I15325	I15325 Sequence 4



Qy 1261 ATTGGTAAGTCCAGCAAACTGGCTCCTCCATCCCTAA 1296  
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Db 1261 ATTGGTAAGTCCAGCAAACTGGCTCCTGCATCCCTAA 1296

RESULT 2  
115337  
LOCUS I15337 1296 bp DNA PAT 02-APR-1996  
DEFINITION Sequence 17 from patent US 5463175.  
ACCESSION I15337  
VERSION I15337.1 GI:1250245  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1296)  
AUTHORS Barry.G.F. and Kishore.G.M.  
TITLE Glyphosate tolerant plants  
JOURNAL Patent: US 5463175-A 17 31-OCT-1995;  
FEATURES Location/Qualifiers  
source 1..1296  
BASE COUNT 267 a 360 c 309 g 360 t  
ORIGIN

Query Match 100.0%; Score 1296; DB 5; Length 1296;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCTGAGAACCAAGAGTTGGTATCGCTGGAGCTGGAATGTTGGTGCAT 60  
Db 1 ATGGCTGAGAACCAAGAGTTGGTATCGCTGGAGCTGGAATGTTGGTGCAT 60

Qy 61 GCTTTGATGCTTCAACGTCGTTCAAGTTACCTTGATGATCCAAACCCACAGGT 120  
Db 61 GCTTTGATGCTTCAACGTCGTTCAAGTTACCTTGATGATCCAAACCCACAGGT 120

Qy 121 GAAGTGCTCTTTGGGTAAAGCTGGTTGCTTCAACGGTTCCCTGGTTGTTCCCAATGTCC 180  
Db 121 GAAGTGCTCTTTGGGTAAAGCTGGTTGCTTCAACGGTTCCCTGGTTGTTCCCAATGTCC 180

Qy 181 ATGGCAGAAACTTGACTAGGCTTCCAAAGTGGCTTTCTTGACCCCAATGGGTCCATGTCC 240  
Db 181 ATGGCAGAAACTTGACTAGGCTTCCAAAGTGGCTTTCTTGACCCCAATGGGTCCATGTCC 240

Qy 241 ATCCGTTTCGGCTACTTTTCCAAACCATCATGCTTGGTTGATTCGTTTCTGCTGCTGA 300  
Db 241 ATCCGTTTCGGCTACTTTTCCAAACCATCATGCTTGGTTGATTCGTTTCTGCTGCTGA 300

Qy 301 AGACCAAAACAAAGGTGAAGGAGCAAGCTAAGGCACCTCCCGTAACCTCATCAAGTCCACTGTG 360  
Db 301 AGACCAAAACAAAGGTGAAGGAGCAAGCTAAGGCACCTCCCGTAACCTCATCAAGTCCACTGTG 360

Qy 361 CTTTGTATCAAGTCTTGGCTGAGAGGCTGATGCTAGCCACCTTATCCGTCACCAAGGT 420  
Db 361 CTTTGTATCAAGTCTTGGCTGAGAGGCTGATGCTAGCCACCTTATCCGTCACCAAGGT 420

Qy 421 CACCTTACCGTGTACCGTGGAGAGCACATTCGCCAGGACCGTGGAGGTGGGAACCTT 480  
Db 421 CACCTTACCGTGTACCGTGGAGAGCACATTCGCCAGGACCGTGGAGGTGGGAACCTT 480

Qy 481 GGTGCTCTCAACGGTGTTCGTACTCAAAATCCTCAGCGCTGATGCTATTCGCTGATTTCCAT 540  
Db 481 GGTGCTCTCAACGGTGTTCGTACTCAAAATCCTCAGCGCTGATGCTATTCGCTGATTTCCAT 540

Qy 541 CCTAACTTGTCTCAGCCCTTTTACCAAGGGAATTCCTTATCGAAGAGAACGGTGCACACCATC 600  
Db 541 CCTAACTTGTCTCAGCCCTTTTACCAAGGGAATTCCTTATCGAAGAGAACGGTGCACACCATC 600

Qy 601 AACCCACAAAGTCTCGTCACTCTCTTGTTCGTTCATCGCTTAAAGTTCGTTTGCAT 660  
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Db 601 AACCCACAAAGTCTCGTCACTCTCTTGTTCGTTCATCGCTTAAAGTTCGAGAGTTC 660  
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Qy 721 ACCAAGCGTTCCTGCTGTGATGTCAGCTGTTCGTTGAGCTGGTGCACACTTCCAAAGTCT 780  
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Db 721 ACCAAGCGTTCCTGCTGTGATGTCAGCTGTTCGTTGAGCTGGTGCACACTTCCAAAGTCT 780  
Qy 781 CTTGCTAACTCCCTTGGTGATGACATCCATTCGATTCGAGCTGGTGCACACTTCCAAAGTCT 840  
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Db 781 CTTGCTAACTCCCTTGGTGATGACATCCATTCGATTCGAGCTGGTGCACACTTCCAAAGTCT 840  
Qy 841 ATCGCAACCCAGAGCTGCTCCAGTATTCACAACTACCGATGCTTCTGGAAAGTTCATC 900  
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Db 841 ATCGCAACCCAGAGCTGCTCCAGTATTCACAACTACCGATGCTTCTGGAAAGTTCATC 900  
Qy 901 GCTACTCTATGAGAGATGGTCTTCGTTGCTTGAACCGTTGAGTTCGCTGCTCACT 960  
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Db 901 GCTACTCTATGAGAGATGGTCTTCGTTGCTTGAACCGTTGAGTTCGCTGCTCACT 960  
Qy 961 GCTGCTCTAACTGGAAGCGTCTCACGTTCTCTACACTCGCGCTCGTAAGTTCGTTCCA 1020  
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Db 961 GCTGCTCTAACTGGAAGCGTCTCACGTTCTCTACACTCGCGCTCGTAAGTTCGTTCCA 1020  
Qy 1021 GCTCTCGCTCCTGCCAGTTCCTGAAGAGCTTACTCCAAGTGGATGGTTCGCTCCAAAGC 1080  
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Db 1021 GCTCTCGCTCCTGCCAGTTCCTGAAGAGCTTACTCCAAGTGGATGGTTCGCTCCAAAGC 1080  
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Db 1081 ATCCGGATTCCTTCCAGTGAATGGTCTGCTTACCCGCTACTCCAGAGCTTATCTACGGT 1140  
Qy 1141 TTGCTGTCAGGTCACCTCGGTATGACTGCTGCTCAATGACGCAACCTCGTTTCTGAG 1200  
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Db 1141 TTGCTGTCAGGTCACCTCGGTATGACTGCTGCTCAATGACGCAACCTCGTTTCTGAG 1200  
Qy 1201 CTCCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTGCGCAACACCGTTTCGGT 1260  
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Db 1201 CTCCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTGCGCAACACCGTTTCGGT 1260  
Qy 1261 ATTGTTAAGTCCAAAGCAAACTGGTCTGCATCCCTAA 1296  
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RESULT 3  
AR016595  
LOCUS AR016595 1296 bp DNA PAT 05-DEC-1998  
DEFINITION Sequence 8 from patent US 5776760.  
ACCESSION AR016595  
VERSION AR016595.1 GI:3972872  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1296)  
AUTHORS Barry.G.Francis and Kishore.G.Murthy.  
TITLE Glyphosate tolerant plants  
JOURNAL Patent: US 5776760-A 8 07-JUL-1998;  
FEATURES Location/Qualifiers  
source 1..1296  
BASE COUNT 271 a 359 c 305 g 361 t  
ORIGIN

Query Match 99.4%; Score 1288; DB 5; Length 1296;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1291; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGGCTGAGAACCAAGAGTTCGTTATCGCTGGAGCTGGAATCGTTGGTTCAT 60  
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Db 1 ATGGCTGAGAACCAACAGAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTTGCACCT 60  
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QY 781 CTTTGTAACTCCCTTGGTGATGACATCCCATTTGGATACCGAACTGGATACCAATCGTG 840  
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Db 1141 TTCCGCTCAGGTCACCTCGGTTATGACTGGTGTCTCCAATGACCGCAACCTCGTTTCTGAG 1200  
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LOCUS I15328 1296 bp DNA PAT 02-APR-1996  
DEFINITION Sequence 8 from patent US 5463175.  
ACCESSION I15328  
VERSION I15328.1 GI:1250236  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1296)  
AUTHORS Barry,G.P. and Kishore,G.M.  
TITLE Glyphosate tolerant plants  
JOURNAL Patent: US 5463175-A 8 31-OCT-1995;  
FEATURES Location/Qualifiers  
source 1. 1296  
BASE COUNT 271 a 359 c 305 g 361 t  
ORIGIN  
Query Match 99.4%; Score 1288; DB 5; Length 1296;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1291; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
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Db 1261 ATGGTAAGTCCAAAGCAACTGGTCTGCTGCATCTTAA 1296

RESULT 5
A59869
LOCUS A59869 1631 bp DNA PAT 06-MAR-1998
DEFINITION Sequence 1 from Patent WO9706269.
ACCESSION A59869
VERSION A59869.1 GI:3715060
KEYWORDS
SOURCE
ORGANISM Arabidopsis sp.
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
Rosidae; Capparales; Brassicaceae; Arabidopsis.
Jepson, I.
TITLE INDUCIBLE HERBICIDE RESISTANCE
JOURNAL Patent: WO 9706269-A 1 20-FEB-1997;
ZENECA LTD (GB)
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BASE COUNT            342 a 454 c 381 g 454 t
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Query Match          92.6%; Score 1200.4; DB 5; Length 1631;
Best Local Similarity 95.1%; Pred. No. 0;
Matches 1280; Conservative 0; Mismatches 16; Indels 50; Gaps 2;

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Db 394 GAAGTGTCTCTTTTCGGTAACGCTGTTCGCTTCAACGGTTCCTCCGTTGTTCCAAATGTCC 453
Qy 181 ATGCCAGAAACTTGTACTAGCGTTCCTCAAGTGGCTTCTTGACC----- 223
Db 454 ATGCCAGAAACTTGTACTAGCGTTCCTCAAGTGGCTTCTTGATTCGAAATTCAAAGC 513
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Db 514 TTACGGATCCAAATGGGTCCATGTCATCCGTTTCAGCTACTTTCCAACCATCATCGCTTG 573
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Db 574 GTTGATTGCTTTCGCTTGGTAAGACCAACAAAGTGAAGGAGCAAGCTTAAGGCACCT 633
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RESULT 7
LOCUS I15327 115327 1296 bp DNA PAT 02-APR-1996
DEFINITION Sequence 7 from patent US 5463175.
ACCESSION I15327
VERSION I15327.1 GI:1250235
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1296)
AUTHORS Barry G.F. and Kishore, G.M.
TITLE Glyphosate tolerant plants
JOURNAL Patent: US 5463175-A 7 31-OCT-1995;
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BASE COUNT 287 a 344 c 332 g 333 t
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Query Match 77.7%; Score 1006.4; DB 5; Length 1296;
Best Local Similarity 86.0%; Pred. No. 1e-273;
Matches 1115; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

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Qy 61 GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTGATTGATCCAAACCCACCAGGT 120
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Qy 121 GAAGGTGCTCTTTTCGGTAACGCTGGTTGCTTCAACGGTTCCCTCGTTGTTCCCAATGTCC 180
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Qy 661 GTGCTGCTGCTGTTATCGGATTCGAGACTGAAGGTCGTGCTCTCAAGGGTATCACCAACC 720
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AR016593 LOCUS AR016593 1296 bp DNA PAT 05-DEC-1998
DEFINITION Sequence 6 from patent US 5776760.
ACCESSION AR016593
VERSION AR016593.1 GI:3972870
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1296)
AUTHORS Barry G.Francis and Kishore, G.Murthy.
TITLE Glyphosate tolerant plants
JOURNAL Patent: US 5776760-A 6 07-JUL-1998;
FEATURES
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BASE COUNT 286 a 368 c 361 g 281 t
ORIGIN

Query Match 74.0%; Score 958.4; DB 5; Length 1296;
Best Local Similarity 83.7%; Pred. No. 4e-260;
Matches 1085; Conservative 0; Mismatches 211; Indels 0; Gaps 0;

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QY 481 CGTCTCTCAACGGTGTTCGTACTCAAACTCTCAGCGCTGATGCATTTCCGTGATTTTCGAT 540  
DB 481 CGGCGTCTCAACGGTGTTCGCACGCGAGTCTCAGCGCGGATCGTTTGGCGGATTTTCGAT 540  
QY 541 CCTAACTTGTCTCAGCGCTTTTACCAAGGGAATCCTTATCAAGAGAACGGTTCACACATC 600  
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DEFINITION Sequence 6 from patent US 5463175.  
ACCESSION L15326  
VERSION L15326.1 GI:1250234  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1296)  
AUTHORS Barry,G.F. and Kishore,G.M.  
TITLE Glyphosate tolerant plants.  
JOURNAL Patent: US 5463175-A 6 31-OCT-1995;  
FEATURES Location/Qualifiers  
source  
1..1296  
BASE COUNT 286 a 368 c 361 g 281 t  
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Query Match 74.0%; Score 958.4; DB 5; Length 1296;  
Best Local Similarity 83.7%; Pred. No. 4e-260;  
Matches 1085; Conservative 0; Mismatches 211; Indels 0; Gaps 0;  
QY 1 ATGGCTGAGAACACACAGAAGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTTCGACT 60  
DB 1 ATGGCTGAGAACACACAAAAGTAGGCATCGCTGGAGCCGGAATCGTCGGCGTATGACG 60  
QY 61 GCTTTGATGCTTCAACGCTCGTGATTCAGGTTACCTTTGATTCATCCAAACCCACCAAGT 120  
DB 61 GCGCTGATGCTTCAGCGCCGCGGATTCAGATCACCATTGATTGACCCGAAACCCCTCTGGC 120  
QY 121 GAAGTGCCCTCTTTTCGGTAACGGTGTGGTTGCTTCAACGGTTTCCCTCCGTTGTTTCCAATGTC 180  
DB 121 GAAGTGCCATCGTTTGGGAATGCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTC 180  
QY 181 ATGCCAGAACTTGACTACGGTTCCTCAAGTGGCTTCTTACCCCAANTGGTTCATTCCTC 240  
DB 181 ATGCCGGAAACTTGAAGAGCGTGGCGGCTTCCGCAAGTGGCTCTTACCGCGATGGGCGGTTGTCA 240  
QY 241 ATCGGTTTCGGCTACTTTCCAACCATCATGCCCTTGGTTGATTCGTTTCTTCTTGGTGTGGA 300  
DB 241 ATCGGTTTACGCTATTTTCCAAACCATCATGCCCTGTTGATTCGTTTCTTGTAGCCGGA 300  
QY 301 AGACCAAAACAGGTGAAGGAGCAAGCTTAAGCCACTCCGTAACTTCAATCAAGTCCACTGTG 360  
DB 301 AGACCAAAACAGGTGAAGGAGCAAGCTTCCGCAATCTCATCAAGTCCACGGTG 360  
QY 361 CTTTGTATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACTTATCCGTCAGGAAGT 420  
DB 361 CTTTGTATCAAGTCAATTTGGCGGAGGAGGCTGATGCGGACCATCTGATCCGCCATGAAGT 420  
QY 421 CACTTACCGTGTACCGTGAGAGCAAGCTTCCGCAAGGACCGTGAGGCTTGGAACTT 480  
DB 421 CATCTGACCGTATATCGTGAGAGCAAGCTTCCGCAAGGACCGCGAGGTTGGAACTG 480  
QY 481 CGTCTCTCAACGGTGTTCGTACTCAAACTCTCAGCGCTGATGCATTCGCTGATTTTCGAT 540  
DB 481 CGGCGTCTCAACGGTGTTCGCACGCGAGTCTCAGCGCGGATCGTTTGGCGGATTTTCGAT 540  
QY 541 CTTAACTTGTCTCAGCGCTTTTACCAAGGGAATCCTTATCAAGAGAACGGTTCACACATC 600  
DB 541 CCGAACTTGTTCGATCGCTTTTACCAAGGGAATCTTATAGAAGAGAACGGTTCACACAT 600

Qy	601	ACCACACAGGTCGTCGACTCTCTGTGTTCTGTCGTTTCATCGCTAACGGTGGAGAGTTC	660
Db	601	ATCCGCAAGGGCTCGTACCCCTCTGTGTTGCGCGCTTTATCCGAAACGGTGGCGAAATTT	660
Qy	661	GTGTCGTCGTTATCGGATTTCGAGACTGAAGGTCGTCCTCAAGGGTATCACACC	720
Db	661	GTATCTGCGCGTCTCATCGGCTTTGAGACTGAAGGTAGGGCGCTTAAAGGCATTCACACC	720
Qy	721	ACCAACGGTGTCTCTGTTGATGACAGCTGTGTTGACGTCGTGTCACACTCCCAAGTCT	780
Db	721	ACGAACGGGCTCTGCGCGTTGATGCAGCGGTTGTGCGAGCGCGCACACTCGAATCA	780
Qy	781	CTTGCTAACTCCCTTGGTGATGACATCCGATTGGATACGGAACGTGGATACACATCGTG	840
Db	781	CTTGCTAAATTCGCTAGGCGATGACATCCGCTCGATACGGAACGTGGATATCATATCGTCT	840
Qy	841	ATCGCAACCCAGAGCTGCTCCACGTATTCCAACTACCGATGCTTCTGGAAAGTTTCATC	900
Db	841	ATCGGGAATCCGGAAGCGCTCCACGCATTCGAGACCGATGCGGTGAGTTCAGGAATTCATC	900
Qy	901	GCTACTCTTATGAGATGGGCTTCGCTGTGCTGGAACCGTTGAGTTCGCTGCTCACT	960
Db	901	GCGACACCTATGGAATGGGGCTTCGCGTGGCGGTTACGGTTGAGTTCGCTGGGCTACA	960
Qy	961	GCTGCTCTAACTGGAAGGGTCTCAGGTTCTCTACACTCGCGCTCGTAAAGTTGCTTCCA	1020
Db	961	GCGCGTCTCTAACTGGAACGTGCGATGCTCTATACGCAACGCTCGAAAACCTTCTTCCA	1020
Qy	1021	GCTCTCGCTCGCGCAGTTCTGAAGACGTTACTCCAACTACCGATGCTTCTGGAAAGTTTCATC	1080
Db	1021	GCCCTCGCGCTCGAGTTCTGAGAACGATATCCAAATGGATGGGTTTCGCGCCGAGC	1080
Qy	1081	ATCCCGGATTCCTTCCTCCAGTATGGTTCGTACCCGCTACTCCAGACGTTATCTACGCT	1140
Db	1081	ATCCCGGATTCGCTCCCGTGATTGGCGGCAACCCGACACCGAGCTAATCTATGCT	1140
Qy	1141	TTGCGTCAAGGTCACCTCGGTATGACTGGTCTCAATGACCGCAACCGCTTCTCTGAG	1200
Db	1141	TTGCGGCCACGGTCATCTCGGATACAGGGCGCGGATGACCGCAACGCTCGTCTCAGAG	1200
Qy	1201	CTCCTCGCAGGTGAGAACCTCTATCGACATCTCTCCATTCGCAACCAACCGTTTCGGT	1260
Db	1201	CTCCTCGCAGGCAAGAACCTCAATCGACATTCGCAATTCGCGCTTCGCAACCAACCGTTTGGT	1260
Qy	1261	ATTGTAAGTCCAAAGCAAACTGGTCTCGATCTTAA	1296
Db	1261	ATTGGCAATCCAAAGCAAAAGGGTCCGGCAAGTTAA	1296
RESULT 10			
AR016591			
LOCUS	AR016591	1692 bp	DNA
DEFINITION	Sequence 3 from patent US 5776760.		
ACCESSION	AR016591		PAT 05-DEC-1998
VERSION	AR016591.1	GI:3972868	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1692)		
AUTHORS	Barry,G.Francis and Kishore,G. Murthy.		
TITLE	Glyphosate tolerant plants		
JOURNAL	Patent: US 5776760-A 3 07-JUL-1998;		
FEATURES	Location/Qualifiers		
source	1..1692		
BASE COUNT	381 a	480 c	469 g
ORIGIN	/organism="unknown"		
		361 t	1 others

Query Match 73.8%; Score 956.8; DB 5; Length 1692;  
Best Local Similarity 83.6%; Pred. No. 1.1e-259;

Matches 1084; Conservative 0; Mismatches 212; Indels 0; Gaps 0;	
Qy	1 ATGGCTGACAAACACAAAGGTTGGTATCGCTGGAGCTTGGAAATCGTTGGTCTTTTGCATC 60 

RESULT	12
I15325	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	

FEATURES		source		Location/Qualifiers	
		1..1293		/organism="unknown"	
BASE COUNT	286 a	367 c	359 g	281 t	
ORIGIN					
Query Match 71.4%; Score 925.6; DB 5; Length 1293;					
Best Local Similarity 83.6%; Pred. No. 7.6e-251;					
Matches 1084; Conservative 0; Mismatches 209; Indels 3; Gaps					
Qy	1	ATGGCTCAGAACACACAGAAGGTTGGTATCCCTGGAGCTTGGAAATCGTTGGTTGGTTTGCACCT	60		
Db	1	ATGTCTCAGAACACACAAAAAAGTAGGCATCGCTCGAGCCGGAATCGTCGGCTATGTCAGG	60		
Qy	61	GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTGATTGATCCAAACCCACACAGGT	120		
Db	61	CGCTGATGCTTCAGCGCCCGGATTCAAAGTACCTTGATTGATGACCCGAACCCCTCCTGGC	120		
Qy	121	GAAGGTGCCCTTTTTCGGTAAACGCTGGTTGCTTCAACGGTTTCCTTCGTTTCCAAATGTCC	180		
Db	121	GAAGGTGCATCGTTTGGGAATCGCGGATGCTTCAACGGCTCATCCGTCCTCGCTATGTCC	180		
Qy	181	ATGCCACGAACTTTGACTACGCTTCCAAAGTGGCTTCTTTGACCCAAATGGGTCCATTTGCC	240		
Db	181	ATGCCGGGAACTTGACGAGCGTGGCCGAAGTGGCTCTCTTGACCCGATGGG-CCGTTGTCA	239		
Qy	241	ATCCGTTTTCGGCTACTTTTCCAAACCATCATGSCCTTGGTTGATTGCTTTCCTTGGTTCCTG	300		
Db	240	ATCCGTTTCAGCTA-TTTTCCAAACCATCATGCC-TGGTTGATTGGCTTTCCTGTTAGCCGGA	297		
Qy	301	AGACCAACAAAGGTGAAGGAGCAAGCTTAAGGCACCTCCGTAAACCTCATCAAGTCCACACTGTG	360		
Db	298	AGACCAACAAAGGTGAAGGAGCAGCGGAAGCACTCCGCAATCTCATCAAGTCCACGGTG	357		
Qy	361	CTTTTGATCAAGTCTTTGGCTGAGGAGGTGATGCTTAGCCACTTATTCGTCACGAAGGT	420		
Db	358	CTCTGATCAAGTCATTTGGCGGAGGAGGCTGATGCGAGGCCATCTGATCGCCCATGAAGGT	417		
Qy	421	CACCTTACCCTGTACCGTCGAGAAAGCAGACTTCGCCAGGAGCCGTCGGAGGTTGGGAACCTT	480		
Db	418	CATCTGACCGTATATCGTGGAGAAAGCAGACTTCGCCAAGACCGCGGAGGTTGGGAACGTG	477		
Qy	481	CGTGTCTCAACGGTGTTCGTACTCAATCTTCAGCGCTGATGCAATTCGCTGATTTTCGAT	540		
Db	478	CGGCGTCTCAACGGTGTTCGCACGCAGATCCCTCAGCGCCGATCGGTTGCGGGATTTCCGAT	537		
Qy	541	CCTAACTTTGCTCAGCGCTTTTACCAAGGGAATCCTTTATCGAAGAGAACCGGTACACACATC	600		
Db	538	CCGAACTTGTTCGATCGCTTTTACCAAGGGCATTTCTTTATAGAAGAGAACCGGTACACAGATT	597		
Qy	601	AACCCACAAGTCTCGTGTACTCTTTGTTTTCGTCGTTTTCATCGCTAACCGGTGGAGAGTTC	660		
Db	598	ATCCGGAAGGGTCTGTGACCCCTCTTTTTCGGCGTTTTTATCGCGAACCGGTGGCGAAATTT	657		
Qy	661	GTGTCTCTCGTGTATTCGGATTCGAGACTGAAGGTCGTCTCTCAAGGCTATCACCACTG	720		
Db	658	GTATCTCGCGGTGTATCGGCTTTGAGACTGAAGGTAGGGCGCTTAAGGCGATTAACACC	717		
Qy	721	ACCAACCGGTGTTCGTGTGTGATGCAGCTGTGTGTTTGCAGCTGGTGACACATCCCAAGTCT	780		
Db	718	ACGAACCGGCTTCTGGCCGTTGTATGACGGGTGTTGTCGACGGGTGTCGACGCGGCGCACACTCGAAATCA	777		
Qy	781	CTTGTCTAACTCCCTTGGTGATGATACATCCCATTTGGATACCGAAGTGGATACCAATCTCGT	840		
Db	778	CTTGTCTAAITTCGTAGCGGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCTGCTC	837		
Qy	841	ATGCCCAACCCAGAAGTGTCTCACCGTATTTCCAACTACCGCATGCTTCTTCTGCAAGTTTCATC	900		
Db	838	ATCGGGAATCCGNAAGCCGCTCCACGCATTTCCGACGACCGGATGCGTCAGGAANAATTCATC	897		
Qy	901	CCTACTCTCTTATGGAGATGGGTCTTCGTGTGCTTGGAAACCGCTTTCAGTTTCGCTGGTCTCACT	960		

Db	998	GCACACACTTATGAAATGGGGCTTCGCCGTGGCGGGTACGGTTAGTTCGTCTGGCTCACAC	957
Qy	961	GCTGCTCCTAACTGGAAGCGTGCTCAGCTTCTCTACACTCGCGCTCGTAAGTTGCTTCACA	1020
Db	958	GCCGCTCCTAACTGGAACGCGGGCATGTGCTCTATACCGAGCTCGAAAACCTTCTTCACA	1017
Qy	1021	GCCTCGCTCCTGCCAGTTCGTAAGAAGCGTTCCTCAAGTGGATGGATGGTTCGTCACAAGC	1080
Db	1018	GCCCTCGCGCTCGGAGTTCTGAAGAACGATATTCGAATGGATGGGTTCGCGCGGAGC	1077
Qy	1081	ATCCCGATTCCTTCAGTGATGGTCTGCTACCCGTACTCCAGACGTTATCTACGCT	1140
Db	1078	ATCCCGATTCGCTTCGCCGTGATGGCCGGGCAACCCGACACCCGACGTAATCTATGCT	1137
Qy	1141	TTCCGTCACGGTCACCTCGGTATGACTGGTGTGCATGACCGCAACCTCGTTTCTGAG	1200
Db	1138	TTCCGCCATGGTCTATTCGCGCATGACAGGGGCGCGATGACCGCAACGCTGCTCTCAGAG	1197
Qy	1201	CTCCTCGCAGGTGAGAACCTCTATCGACATCTCTCCATCTCCACCAACCGTTTCGGT	1260
Db	1198	CTCCTCGCAGGCGAAGACCTCAATCGACATTTTCGCCCTTCGCAACCAACCGTTTGGT	1257
Qy	1261	ATTGGTAACTCCAAAGCAAACTGGTCTGCTGATCCTTA	1296
Db	1258	ATTGGCAAAATCCAAAGCAAAAGGGTCGGCAAGTTAA	1293
RESULT 13			
I15324			
LOCUS	I15324	1689 bp	DNA
DEFINITION	Sequence 3 from patent US 5463175.		
ACCESSION	I15324		
VERSION	I15324.1 GI:1250232		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1689)		
AUTHORS	Barry, G.F. and Kishore, G.M.		
TITLE	Glyphosate tolerant plants		
JOURNAL	Patent: US 5463175-A 31-Oct-1995;		
FEATURES	Location/Qualifiers		
source	1..1689		
BASE COUNT	381 a	479 c	468 g
ORIGIN	/organism="unknown"		
	360 t 1 others		
Query Match 71.4%; Score 925.6; DB 5; Length 1689;			
Best Local Similarity 83.6%; Pred. No. 7, 6e-251;			
Matches 1084; Conservative 0; Mismatches 209; Indels 3; Gaps			
Qy	1	ATGGCTGAGAACCAAGAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTTCGACT	60
Db	120	ATGCTCTGAGAACCAAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGGTATGCAAG	179
Qy	61	GCCTTGATGCTTCAAGCTCGTGATTCAGGTTACCTTGATGTATGATCCAAACCCACGAGT	120
Db	180	GCGCTGATGCTTCAGGCGCGGATTCGAAGTACCTTGATGTACCCGACCCCTCTGGC	239
Qy	121	GAAGTGCCTTCCTTCGGTAAACGCTGGTTCGTTCAACGGTTCCTCGGTTGTTCCAAATGTC	180
Db	240	GAAGTGCATCGTTTGGGAATCGCGATGCTTCAAGGCTATCGCTGCTCTATGTC	299
Qy	181	ATGCCAGAAACTTGACTAGCGTTCCAAAGTGGCTTCCTTGACCCCAATGGGTCCATGTGCC	240
Db	300	ATGCCGGGAAACTTGACGAGCGTGCAGAGTGGCTTCCTTGACCCCAATGGG-CCGTTGTCA	358
Qy	241	ATCGTTTCGGCTACTTTCCAACCATCATCGCTTGGTGTGATTCGTTCTGCTTGTCTGGA	300
Db	359	ATCGGTTTACGCTA-TTTCACCAACCATCATGCTCC-TGGTGTGATTCGCTTCTGTGACCCGA	416
Qy	301	AGACCAACCAAGGTGAAGGAGCAAGCTAAGGCATCCGTTAACCTCATCAAGTCCACTGTG	360

Db	417		AGACAAACAAAGCTGAAGGAGCAGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG	476
Qy	361		CTTTGATCAAGTCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTACGAAGGT	420
Db	477		CTCTCATCAAGTCATTTGGCGAGGAGGCTGATGCCAGCCATCTGATCCGCCATGAAGGT	536
Qy	421		CACCTTACCGTGTACCGTGGAGAGCAGACTTCCGCCAGGACCGTGGAGTGGGAACTT	480
Db	537		CATCTGACCGTATATCGTGAGAGACGAGACTTCGCCAAGGACCGCGAGGTTGGGAAC TG	596
Qy	481		CGTCGCTCAACGGTGTTCGTACTCAATCTCAGCGCTGATGCATTTGGTGTTCGAT	540
Db	597		CGCGCTCAACCGGTCTCCACGACGATCTCTCAGGCGCGATCGTTGCGGGATTTTCGAT	656
Qy	541		CTTAACCTTGTCTCACGCCCTTACCAAGGGAATCTTATCGAAGAGAACGGTTCACACATC	600
Db	657		CGAAGCTTGTCCGATCGCTTACCAAGGCGATCTTATAGAAGAGAACGGTTCACAGATT	716
Qy	601		AACCCACAAGGTCGCTGACTCTCTTTGTTGCTGCTTATCATCGCTAACCGTGGAGAGTTC	660
Db	717		NATCCGAAGGGCTCGTGACCTCTTGTGTTGCGCGTTTTATCCGAACGGTGGCGAATTC	776
Qy	661		GTCTCTGCTGCTGTTATCGGATTCGAGACTGAAGTCTGCTCTCAAGGGTATCACCAAC	720
Db	777		GTATCTCGCGCTGTCTATCGGCTTTGAGACTGAAGGTAGGCGGCTTAAAGCGCATTAACAAC	836
Qy	721		ACCAACGGTGTCTTCTGCTGTGATGAGCTGTTGTTGCGAGCTGGTGACACATCTCAAGTCT	780
Db	837		ACGAACGGCTTCTGCGGCTTGATGACAGGGTGTGTCGACGCCGGCGCACTCGCAATCA	896
Qy	781		CTTGTAACTCCCTTGGTGATGACATCCCATGATGATACCGAAGCTGGATACCAATCGTG	840
Db	897		CTTGCTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC	956
Qy	841		ATCGCCCAACCCAGAGCTGCTCCAGTATTCCAACTACCGATGCTTCTGGAAAGTTTCATC	900
Db	957		ATCGGGAATCCGGAAGCCGCTCCACGATTTCCGACGACCGCATCGTCAGGAAATTCATC	1016
Qy	901		GTACTCTCTATGAGATGGCTTCTGCTGTGCTGGAACCGCTTGAGTTGCGTGGCTCACT	960
Db	1017		GCACACCTATGGAATGGGCTTCCGCTGGCGGTTACGGTTGAGTTGCTGGGCTCAC	1076
Qy	961		GCTGCTCCTAACTGGAAGCGTCTCAGTCTCTACACTCGCGCTCGTAAGTTGCTTTCCA	1020
Db	1077		GCGGCTCCTAACTGGAAGCGTCTCAGTCTCTATACGACGCTCGAATACTTCTTCCA	1136
Qy	1021		GCTCTCGCTCCTCCAGTCTCTGAAGAACGTTACTCCAAGTGGATGGTTCCTGCCAAGC	1080
Db	1137		GCCCTCGCGCTTCGAGTTCTGAAGAACGATATTCCAATGGATGGGTTCCGGCCGAGC	1196
Qy	1081		ATCCCGGATTCCTTCCAGTGATTTGGTCTGCTACCGCTACTCCAGACGTTATCTACGCT	1140
Db	1197		ATCCCGGATTCGCTCCCGTGATTTGCGCGGCAACCCGACACCCGACGTAATCTATGCT	1256
Qy	1141		TTGGGTACAGGTCACCTCGGTATGATGTGCTTCCAAATACCCCAACCCCTGTTCTGAG	1200
Db	1257		TTCCGCGATGTTCTATCGGCATGACAGGGGCGCGCGATGACCGCAACGCTCGTCTCAGAG	1316
Qy	1201		CTCTCCGAGGTGAGAAGACCTCTATCGACATCTCTCCATTCGCAACCAACCGTTTCGGT	1260
Db	1317		CTCTCCGAGGGGAAAGACCTCAATCGACATTTCCGCCCTTCGCAACCAACCCGCTTGGT	1376
Qy	1261		ATTGGTAAGTCCAAAGCAACTGCTGCTGATCCCTAA	1296
Db	1377		ATTGGCAAAATCCAAGCAACGGGTCGCGCAAGTTAA	1412

RESULT 14  
PSEAKSD 3430 bp DNA BCT 26-APR-1993  
LOCUS Pseudomonas putida alpha-ketoglutarate semialdehyde dehydrogenase  
DEFINITION gene, complete cds.

ACCESSION	M69158	
VERSION	M69158.1	GI:150981
KEYWORDS	ketoglutarate semialdehyde dehydrogenase.	
SOURCE	Pseudomonas putida DNA.	
ORGANISM	Pseudomonas putida	
	Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group; Pseudomonas.	
REFERENCE	1 (bases 1 to 3430)	
AUTHORS	Burlingame, R.P., Maruya, A., Ally, A.H., Ally, D. and Backman, K.C.	
TITLE	Nucleotide sequences of hydroxyproline-specific alpha-ketoglutarate semialdehyde dehydrogenase genes from two strains of pseudomonas putida	
JOURNAL	Unpublished (1991)	
FEATURES	Location/Qualifiers	
source	1..3430	
gene	/organism="Pseudomonas putida"	
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CDS	/gene="ketoglutarate semialdehyde dehydrogenase"	
	603..2180	
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	/protein_id="AA25698.1"	
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	/translation="MTLTGYMLIGQTPVTGSREAIRAIDPATGQLEPAVLGGTGEIIV	
	AQCALAAAFDGYRETTLEORAOFLTIATQIEALGDALIDRAVAESGLPKARIOGE	
	RRTCTQLRTFARVVRAGELDVRVDNAQPERQPLRADLRQVALGPVAVFGASNF	
	PLAFSVAGGDTASALAAAGCPVVKHSAHPGTSSELVQAVAKVLCGLPAGVFSLLY	
	GSGREVGIALVSDPRIKAYFTGSRSGGIALCOATQARPEIPVYAEMSSINPVLFLE	
	AALQARAELAQGFVASTQAGQFCTNPGLVIAPOGPALQRFIDAAESBHVQAAQT	
	MLTPGFSAYQAGVGLAGNANAAGAGQGNQCAQLFVTOAEAPLADPALQA	
	EYFGAASLVACASDQVHOVAEHLQGLTATLDLDDADIDRALLPTLERKAGRIL	
	VNGWPTGVEVCDAMVHGPPATSDARTTSVGTAAILRLFLRPVCYQDFNALLPQALQ	
	HGNPLQLRLDLGKREG"	
BASE COUNT	562 a	1140 c 1157 g 571 t
ORIGIN		

Query Match	5.0%;	Score	64.6;	DB	2;	Length	3430;		
Best Local Similarity	47.4%;	Pred. No.	3.1e-07;						
Matches	193;	Conservative	0;	Mismatches	214;	Indels	0;	Gaps	0;
QY	29	TCGCTGAGCTGGAATCGTTGGTGTGTTGCACCTGTTTGATGCTTCAACGCTGTTGGATTCA	88						
Db	2214	TGTTGGGCGCGGGATTGTTCGGCGTTGCCTGTGCCCTGCAACTGGCCCGCCAGGCGCTCC	2273						
QY	89	AGGTTACCTTGATTGATCCAAACCCACCAGGTGAAGTGCTCTTTTCGGTAACGCTGGTT	148						
Db	2274	GGGTGCTATTGTCGACCGCCAGCAGCCCGCCATGCGGGGCTCTATGGCAACGCCGGGC	2333						
QY	149	GCATTCAACGGTTCTCCGTTGTTCCCAATGTCATGCCAGGAACTTACTAGCTAGCTTCCAA	208						
Db	2334	ACCTGGCCACCGAGCAGGTGTTCCCGATTGCCGACCTGTCGATCTCAACGCTTGGCCG	2393						
QY	209	AGTGGCTTCTTGACCCCAATGGGTCCATTGTCCATCCGCTTTTCGGCTACTTTTCCAAACCATCA	268						
Db	2394	GCATGCTGCTGGACCCGATGGGCCCACTGCGCCTGGACTGGAAGTACTGCCACAGGCCA	2453						
QY	269	TGCTTGGTTGATTGCTTTTCTTGTGCTGGAAGACCAACAAGGTGAAGAGCAAGCTA	328						
Db	2454	TGCGCTGGTTTACCGCGCTGCTGCTCAACCTGGCGCGCGCGCTTTCAGCGCAGTGTGG	2513						
QY	329	AGGCATCTCCGTAACTCATCAAGTCCACTGTGCTTGTGATCAAGTCTTGGCTGAGAGG	388						
Db	2514	CCGGCATCCGCAACGCTGAACGAAGGAGCGCTGGTGCATGGCAGCGCTGCTGGGCTCGA	2573						
QY	389	CTGATGCTAGCCACCTTATCCGTCACGAAGGTCACTTACCGTGTAC	435						
Db	2574	TCGGGCGCAGCGACCTGTTCCAGGAGGATGTTGTTGCTGGTGGTTC	2620						



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OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 03:45:17 ; Search time 263.11 Seconds  
(without alignments)  
1850.400 Million cell updates/sec

Title: us-08-484-274-17  
Perfect score: 1296  
Sequence: 1 ATGCTGAGAACACAGAA.....AACTGCTCTGCATCTTAA 1296

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues  
Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :	N_Geneseq_36.*
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21:	/SID56/gcgdata/geneseq/geneseqn/NA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1288	99.4	1296	13	Q20835 Synthetic glyphosa
2	1288	99.4	8418	20	X57309 Sugar beet T-DNA c
3	1200.4	92.6	1631	18	T85664 CPT1-GOX gene fusi
4	1004.8	77.5	1321	13	Q20834 Modified glyphosat
5	956.8	73.8	1321	13	Q20833 Manipulated glypho
6	953.6	73.6	1692	13	Q22705 Glyphosate oxidore
7	922.4	71.2	1689	13	Q20832 Glyphosate oxidore
8	892.2	68.8	8012	20	X57305 Sugar beet T-DNA c
9	892.2	68.8	8798	20	X57308 Sugar beet T-DNA c
10	39.8	3.1	32207	20	V73805 KSHV LUR DNA (nucl
11	39.8	3.1	137507	19	V19941 KSHV long unique c
12	37.4	2.9	397	20	X89891 Spinoecerebellar at

C 13	35.6	2.7	6558	21	245602	cDNA sequence of a
C 14	35.2	2.7	6794	21	245597	cDNA sequence of h
C 15	35	2.7	10266	17	T33007	Mouse SRV-related
C 16	34.6	2.7	543	13	Q23092	Antigen tc-7a gene
C 17	34.4	2.7	1291	20	X87940	Mycobacterium tube
C 18	34.4	2.7	2852	19	V64558	M. tuberculosis im
C 19	34.4	2.7	2852	19	V44449	Mycobacterium tube
C 20	34.4	2.7	2852	20	Z19359	M. tuberculosis an
C 21	34.4	2.7	2852	20	Z19147	M. tuberculosis re
C 22	34.4	2.7	4888	20	X13244	Enterococcus faeca
C 23	34.2	2.6	5059	20	X84332	Stealth virus nucl
C 24	34.2	2.6	9551	20	Z22301	cDNA encoding a hu
C 25	34.2	2.6	54548	21	Z45596	cDNA sequence of th
C 26	34.2	2.6	138169	21	A34791	Human adenosine re
C 27	34.2	2.6	141589	21	A35005	Human adenosine re
C 28	34.2	2.6	141589	21	A35030	Human adenosine re
C 29	34	2.6	1001	16	O80734	Phosphatidylethano
C 30	34	2.6	1447	13	Q30002	HCNP precursor gen
C 31	34	2.6	1447	15	O58686	Human hippocampal
C 32	33.8	2.6	567	21	A29550	HIV codon altered
C 33	33.6	2.6	3292	14	Q46544	Yeast SSRP DNA seq
C 34	33.6	2.6	3292	19	V09625	S. cerevisiae SSRP
C 35	33.4	2.6	2004	17	T13952	Maize-optimized VI
C 36	33.4	2.6	2004	18	T73997	Maize optimised-B.
C 37	33.4	2.6	2004	19	V16170	DNA encoding an 80
C 38	33.4	2.6	2010	15	Q74683	Bacillus cereus ve
C 39	33.4	2.6	2576	17	T13945	Maize-Optimized VI
C 40	33.4	2.6	2576	18	T74006	Maize optimised-B.
C 41	33.4	2.6	2576	19	V16181	Maize optimised DN
C 42	33.4	2.6	2655	15	Q74682	Bacillus cereus ve
C 43	33.4	2.6	2655	17	T13951	Maize-Optimized VI
C 44	33.4	2.6	2655	17	T13954	Maize-Optimized VI
C 45	33.4	2.6	2655	18	T73996	Maize optimised-B.

ALIGNMENTS

RESULT 1	
Q20835	
ID	Q20835 standard; DNA; 1296 BP.
AC	Q20835;
DT	01-MAY-1992 (first entry)
DE	Synthetic glyphosate oxldoreductase gene.
KW	Recombinant; GOR; resistance; ss.
OS	Synthetic.
FT	Key Location/Qualifiers
FT	CDS 1..1296
FT	/*tag= a
XX	
XX	WO9200377-A.
XX	
XX	09-JAN-1992.
XX	
XX	24-JUN-1991; 91WO-US04514.
XX	
XX	24-JUN-1991; 91US-0717370.
XX	25-JUN-1990; 90US-0543236.
XX	
XX	(MONS ) MONSANTO CO.
XX	
XX	Kishore GM, Barry GF;
XX	
XX	WPI; 1992-041559/05.
XX	P-PSDB; R20642.
XX	
XX	Gene encoding glyphosate oxido-reductase enzyme - used to

PT transform plants to produce plants tolerant to glyphosate  
PT herbicide

PS Claim 1: Page 1032; 142pp; English.

XX The sequence is that of the gene encoding a glyphosate oxidoreductase  
CC (GOR) enzyme, the gene sequence was synthesised so that it could be  
CC redesigned to eliminate as much as possible the following sequences or  
CC sequence features (while avoiding the introduction of unnecessary  
CC restriction sites), stretches of G's and C's of 5 or more; A + T rich  
CC regions (predominantly) that could function as polyadenylation sites  
CC or potential RNA destabilisation regions, and codons not frequently  
CC found in plant genes. The G + C% for the synthetic gene is 51% and  
CC the potential to form short, high energy, hair-pin structures is  
CC reduced. However it still encodes the wild type GOR enzyme. It is  
CC used to transform plants such that they express the enzyme  
CC sufficiently to enhance the glyphosate tolerance of the plant.  
CC Transformed plants resistant to glyphosate can be obt'd. so that  
CC weeds can be selectively controlled in fields contg. crops.  
CC See also Q20832-Q20841 and Q22705.  
XX  
SQ Sequence 1296 BP; 271 A; 359 C; 305 G; 361 T; 0 other;

Query Match 99.4%; Score 1288; DB 13; Length 1296;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1291; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGGCTGAGAACCAACAGAGGTTGGTATCCCTGGAGCTGGAATCGTTGTGCACT 60  
DB 1 atdggctgagaaacacaaagaggttggtatcgctgagctggaaatcggttggtgcaat 60  
QY 61 GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTGATTGATCCAAACCCACCAAGT 120  
DB 61 gctttgatgttcaacgtcgtggattcaaggttaccttgattgatgataccaaacccaaggt 120  
QY 121 GAAGTGCCCTCTTTCCGTTACGCTGGTTGCTTCAACGGTTCCCTCCGTTGTTCCAAATGTC 180  
DB 121 gaagtgctctcttcggttaacgcgtggttgcttcaacggttctcctcggtttccaaatgtcc 180  
QY 181 ATGCCAGCAACCTTACTAGCTTCCAAAGTGCGTCTTGACCCAAATGGGTCATTTGCC 240  
DB 181 atgccaggaacttgactagcgttccaaagtggctcttgaccctaaatgggtccatgtcc 240  
QY 241 ATCCGTTTCGGCTACTTTTCCAAACCATCATGCTCTTGGTTGATTTCGTTTCTGCTGGA 300  
DB 241 atccgttttcgactactttccaaacatcatgccttggttgattcgtttcttctgctgga 300  
QY 301 AGACCAACCAAGGTGAGGAGCAAGCTAAGGCACATCCGTAACCTCATCAAGTCCACTGTG 360  
DB 301 agaccaacaaggtgaaggagaaagctaaaggcactccgttaacctcatcaagtccactgtg 360  
QY 361 CCTTTGATCAAGTCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTACCAAGGT 420  
DB 361 cctttgataagtccttggttgagagagctgagtgcagccacttatccgtcaagaaaggt 420  
QY 421 CACCTTACCCTGTACCTGGAGAGACGACACTTCCCGAGGGACCGTGGAGGTTGGGAACTT 480  
DB 421 caacttaccgtgtaccgtggagaaagcagacttcgcaaggaccgtggaggttgggaaactt 480  
QY 481 CGTCGCTCAACGGTGTTCGTACTCAAACTCCTCAGCGCTGATGATTCGGTATTCGAT 540  
DB 481 cgtcgtcaacggtgttcgtactcaaatcctcagcgtgagtcgattgctgtatcgat 540  
QY 541 CCTAACCTTGTCTACCGCTTTTACCAAGGAATCCTTATCGAAGAGAACGGTTCACACCATC 600  
DB 541 cctaaactgtctcaacgctttaccaaagggaaatccttatcgaaagagaacggttcacaccatc 600  
QY 601 AACCCACAAGGCTTCGTACTCTCTTGTGCTTTCATTCGCTAACGGTGGAGAGTTC 660  
DB 601 aacccacaaggtctcgtactctcttgttctcgtctgttctcgtctcgtcaacggtggagagttc 660  
QY 661 GTGCTCTCGTGTATTCGGATTTCGACATCAAGGTCGTGCTCTCAAGGGTATCACCACC 720

DB 661 gtgtctgctcgtgttatcggaattcgagactgaaggtcgctgctcctcaagggtatcaccacc 720  
QY 721 ACCAACGGTGTTCCTTCTGCTTGTATGCAGCTGTGTGTTCGACGTCGACACTCCAAGTCT 780  
DB 721 accaacgggtgttctctgctgtgtgatgcagctgtgtgtgagcgtggtgacactccaggtct 780  
QY 781 CTTGTACTCCTCTTGGTGATGACATFCCCATTTGGATACCGAAGCTGGATACCAATCGTG 840  
DB 781 cttgtaactcctctggtgatgacatcccatcctgataccgaaacgttgataccacatcgtg 840  
QY 841 ATCGGCAACCCAGAGAGCTGCTCCACGTATTCCAACTACCGATGCTTCTTGAAAGTTCATC 900  
DB 841 atcgcaaacccagagagctgctccacgtatttcaactaccgatgcttctgaaagattcctc 900  
QY 901 GCTACTCCTTATGGAGATGGCTTTCGTGTGTGTGGAACCGTTTCAGTTTCGGTGGTCTCAT 960  
DB 901 gctactcctcatggagatgggttcttctggtgtgtggaacggttgagctcgtggtcctact 960  
QY 961 GCTGCTCTTAAGTGAAGCGTGTCTACGTTCTCTACACTCGCGCTCGTAAGTTGCTTCCA 1020  
DB 961 gctgctcttaactgaagcgtgtgctcaagttctctacactcaacgctcgttaagttgctcca 1020  
QY 1021 GCTCTCGCTCTGCCAGTTCTTGAAGAACGTTTACTCCAAGTGGATGGTTCCTGCTCCNAGC 1080  
DB 1021 gctctcgtcctctgaggttctgaaagacgttactccaagtggaatgggttttcgttccaagc 1080  
QY 1081 ATCCCGGATTCCTTCCAGTGATGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140  
DB 1081 atcccagatgtcctctccagtgatggctggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1140  
QY 1141 TTCGGTTCACGGTCACCTCGGTATGACTGGTGTCTTCCAAATGACCCCAACCTCTGTTCTGAG 1200  
DB 1141 ttcggttcacggtcactcgtgtatgactggtgtccaatgacgcgaacccctcgtttctgag 1200  
QY 1201 CTCCTCGAGGTGAGAACCTCTATTCGACATCTCTCATTCGCACCAACCGGTTTCGGT 1260  
DB 1201 ctccctcgaggtgagaagacctctatcgacatctctccattctccattcgacaaaacgggtt 1260  
QY 1261 ATTGTTAAGTCAAGCAAACTGGTCTCTGATCCCTAA 1296  
DB 1261 attggttaagtcacaagaaactgggtcctgcatcctaa 1296

RESULT 2  
X57309  
ID X57309 standard; DNA; 8418 BP.

XX AC X57309;  
XX DT 26-JUL-1999 (first entry)  
XX DE Sugar beet T-DNA containing cp4/epsps #2.  
XX KW Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plant;  
KW 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide;  
XX tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.  
XX OS Beta vulgaris.  
XX PN WO9923232-A1.  
XX PD 14-MAY-1999.  
XX PF 29-OCT-1998; 98WO-EP06859.  
XX PR 31-OCT-1997; 97US-0112003.  
XX PA (NOVS ) NOVARTIS AG.  
XX PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
XX PI Mannerloef M, Steen P, Tenning PP;



glyphosate, avoids constitutive expression and minimises development of herbicide tolerant weeds

Example 3; Flq 7; 59pp; English.

A chemically inducible plant gene expression cassette which comprises an inducible promoter linked to a gene (1) that confers resistance to a herbicide, is claimed. (1) imparts resistance to N-phosphonomethylglycine (glyphosate) or its salts, but may also be a gene for resistance to, e.g. chloroacetanilides, glufosinate, sulphonyl ureas, imidazolinones, etc. The inducible promoter (e.g. alcA, alcR, aldA or other alcR-induced gene promoter) is operatively linked to an alcR regulator sequence. Induced expression of (1) avoids the risk that constitutive expression may interfere with plant development; allows volunteer plants to be controlled by herbicide applied without inducer and minimises the chance that herbicide-resistant strains of weeds will arise. The expression cassette is strictly controlled and suitable for general use in plants (both mono- and dicotyledons). The alcA/alcR gene switch was exemplified with genes conferring resistance to glyphosate. The switch was used to drive inducible expression of glyphosate oxidase (GOX) in plants. Switchable GOX was expressed alone or in conjunction with constitutive expression of 5-enol-pyruvylshikimate 3-phosphate (EPSPS) CP4. Constructs were optimised for expression in mono- and dicotyledonous crop species. The present sequence comprises a fusion of the GOX gene fused to the chloroplast transit sequence 1 from *Arabidopsis* RUBISCO (CPT1). This sequence was ligated into pWJB1 (see T85666) and used in construction of dicot vectors.

Sequence 1631 BP: 342 A: 454 C: 381 G: 454 T: 0 other:

```
Query Match          92.6%; Score 1200.4; DB 18; Length 1631;
Best Local Similarity 95.1%; Pred. No. 0;
Matches 1280: Conservative 0; Mismatches 16; Indels 50; Gaps 2;
```

QY	1	ATGGCTCAGAACCAACACAGAAGTTGGTATCCGTGGAGCTGGAAATCGTTGGTGTTCACAT	60
Db	274	atggctgagaacacacaagaaggttggtatcgcgtggagctggaaatcgtgtggtcttgcacat	333
QY	61	GCATTGATGCTTCAACGCTCGTGATTCAAAGTTTACCTTGATTGATCCAAACCCACCAAGCT	120
Db	334	gcatttgatgcttcaacgctcgtggattcaagtttaccttgatgcataccaaaccaccacagct	393
QY	121	GAAAGGTGCCCTCTTTTCGGTTAACGGTTGGTTGCTTCAACGGTTTCTCCCTGTTTCCAAATGCC	180
Db	394	gaaggctcctcttcggtgaacgctggttgcttcaacggttcttccegttgttccaaigtcc	453
QY	181	ATGCCAGGAACCTTGACTACGCTTCCAAAGTGGCTTCTTCAAGC	223
Db	454	atgccaggaaacttgactcgtgcttccaaagctgcttctggatcctgttgtgaattcaagc	513
QY	224	-----CAATGGGTCCATTGTCCATCCGTTTCGGCTACTTTCCAAACATCATGCTTGG	275
Db	514	ttacggatccaaatgggtccatgtccatcctgttccagctactttccaaacctcatgccttg	573
QY	276	GTTCATTTCGTTTCTTTCGTTTGCTGGAGACCAACAAGGTGAAGGACCAAGCTTAAGCACT	335
Db	574	gttgattcgtttcttcttgcttgctggaagaccaaacaagtgtaaggacgaagctaaagcact	633
QY	336	CCGTTAACCTCATCAAGTCCACTGTGCTTTTGATCAAGTCTTTCGGCTGAGAGGCTGATGTC	395
Db	634	ccgtaaacctcaagtccactgtgctttgatccaagtcccttggctgtaggaaggtctgattgc	693
QY	396	TAGCCACCTTATCCGTACAGAAGGTCACTTACCCTGTATCCGTGGAGAGACAGACTTCGC	455
Db	694	tagccaccttatccgttcaagaaaggtcaaccttaccgttgtaacgttggaagacagacttcgc	753
QY	456	CAGGGACCGTGGAGTTGGGAACCTCGTCGCTCAACGGTGTTCGTACTCAATCCTCAG	515
Db	754	caaggaccgttggaaggttggaaggttcgcttcaacaggtgtctgtaactcaaatcctcag	813
QY	516	CGCTGATGCATTCCGCTGATTTTCGATCCTAACTTGCTTCACGCTTTTACCAGGGAACTCT	575

XX W09200377-A.  
XX 09-JAN-1992.  
XX 24-JUN-1991; 91WO-US04514.  
XX 24-JUN-1991; 91US-0717370.  
XX 25-JUN-1990; 90US-0543236.  
XX (MONS ) MONSANTO CO.  
XX Kishore GM, Barry GF;  
XX P-PSDB: R20642.  
XX WPI; 1992-041559/05.  
XX P-PSDB: R20642.  
XX Gene encoding glyphosate oxido-reductase enzyme - used to  
XX transform plants to produce plants tolerant to glyphosate  
XX herbicide  
XX  
XX Claim 1; Page 102; 142pp; English.  
XX  
XX The sequence is that of the gene encoding a glyphosate oxidoreductase  
XX (GOR) enzyme which has been modified using mutagenic primers. The  
XX gene sequence was redesigned to eliminate as much as possible the  
XX following sequences or sequence features (while avoiding the  
XX introduction of unnecessary restriction sites), stretches of G's  
XX and C's of 5 or more; A + T rich regions (predominantly) that could  
XX function as polyadenylation sites or potential RNA destabilisation  
XX regions, and codons not frequently found in plant genes. The G + C%  
XX of the GOR gene was reduced from 56% in the manipulated version  
XX (Q20833) to 52% in the modified version. However it still encodes  
XX the wild type GOR enzyme. It was obtd. from bacterial isolate LBAA.  
XX It is used to transform plants such that they express the enzyme  
XX sufficiently to enhance the glyphosate tolerance of the plant.  
XX Transformed plants resistant to glyphosate can be obtd. so that  
XX weeds can be selectively controlled in fields contg. crops.  
XX See also Q20832-Q20841 and Q22705.  
XX  
XX Sequence 1321 BP; 293 A; 349 C; 339 G; 340 T; 0 other;

Query Match 77.5%; Score 1004.8; DB 13; Length 1321;  
Best Local Similarity 86.0%; Pred. No. 0;  
Matches 1114; Conservative 0; Mismatches 182; Indels 0; Gaps 0;  
QY 1 ATGGCTGAGAACCAAGAGGTTGGTATCGCTGGAGCTGGNATCGTTGGTGGTCACT 60  
DB 9 atggctgagaaaccaaagagtaggcctgctgagctggaatcgttggtagtgcact 68  
QY 61 GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTTGATTCCAAACCCACAGGT 120  
DB 69 gctttgatgcttcaacgctcgtggattcaagtcacacttgattgacccgaacctcctggc 128  
QY 121 GAAGTGCTCTTTGGGTAAAGCTGGTGGTTCACAGGTTCTCGTGGTGTTCGAATGCC 180  
DB 129 gaagtgctctgttgggaaatgcggatgcttcaacggtcctacgtcgtcctatgtcc 188  
QY 181 ATGCAGCAAACTTCAGTACGCTTCCAAAGTGGCTTCTTGACCCCAATGGGTCCATTGCC 240  
DB 189 atgcaggaaacttgacgagcgtgcggaagtggccttgccttgaccgatgggcccgttgca 248  
QY 241 ATCCCTTTTGGCTACTTTTCCAAACATATGCTTGGTTTCTTGGTTTCTTGGTCTGGA 300  
DB 249 atccggttcagctattttcccaaccaatcagccctggttgattcgtcttctgttaaccgga 308  
QY 301 AGACCAAAACAGGTGAAGAGCAAGCTAAGGCACCTCCGCTTAACCTCATCAAGTCCACTGTG 360  
DB 309 agaccaaaacaggtgtaaggagcggcgaagcaactccgcaactcctcatcaagtcacggtg 368  
QY 361 CTTTGTATCAAGTCTTGGCTGAGAGGCTGTATCGCCACCTTATCCGTCACCAAGGT 420  
DB 361 ctttgtatcaagtcttggctgagagctgtatcgccaccttattccgtcaccaaggt 420

DB 369 cctctgatacaagtcaltggcggaggagagctgatgcagccatctgatccgcatgaaggt 428  
QY 421 CACCTTACCCTGTACCGTCGAGAACAGACTTTCGCCAGGACCGTGGAGTTCGGAACCTT 480  
DB 429 catctgacggtatatactcgtggagaagcgaactctgcgaagaccgcggaggttggcaactg 488  
QY 481 CGTCTCTCAACGGTGTTCGTACTCAAAATCTCAGCGGTGATGCATTTGGTGATTTTCGAT 540  
DB 489 cggcgtctcaacggtgttgcgacgcagatcctctctgtgactgtcttgcgtgatttcgat 548  
QY 541 CCTAACTTGTCTCACGCTTTCACCAAGGAATCCTTATCGAAGAGAACGGTCCACACCATC 600  
DB 549 cctaaacttgcgcagtgctttaccagaagggcatctctcagaagaagacgggtccacagalt 608  
QY 601 AACCCACAAGGTCGTCTGACTCTTGTTCGTTCGTCTTCATCGCTTAAGGGTGAGAGTTC 660  
DB 609 aatccgcaagggtcgtgacccctctgttttcggcggttttatcgcgaacgggtggcgaaatt 668  
QY 661 GTGTCGTCTGCTGTATTCGGATTCCGACTTCGAGACTGAAGTCTGCTCTCAAGGGTATCACACC 720  
DB 669 gtatctgcgctgtcatcggttttgagactgaaggtcgtgctctcaaaaggcattacaacc 728  
QY 721 ACCAACGGTGTCTTTCCTTTCGTTCGTTCGTTCGTTCGTTCGTTCGTTCGTTCGTTCGT 780  
DB 729 actaacgggttcttgcgctgttgcagctgttgcagctgttgcagctgttgcagctgttgcag 788  
QY 781 CTTGCTAACTCCCTTGGTTCATGACATCCCATTTGGATACCGAAGCTGGATACACATTCGCTG 840  
DB 789 cttgctaattcgtcaggcgtgacatccgcgtcgcataccgaacgtggatatacatatcgtc 848  
QY 841 ATGCCAACCCAGAGCTGCTCCAGTATTCCAACTACCGATGCTTCTGGGAAGTTTCATC 900  
DB 849 atcgcgaataccggaagcgcctccacgcattccgcagccgaatgcgtcaggaataatcctc 908  
QY 901 GCTACTCTATTCGAGATGGTCTTCTGTTGCTGTAACCGTTGAGTTCGCTGCTCTCACT 960  
DB 909 gcgacacctatggaaatgggtcttcgtgttgcgtgactgttgcgtgttgcgtgttgcgt 968  
QY 961 GCTGCTCTTACTGGAAGCGTCTCACGTTCTCTACACTTCGCGCTCGTAAGTTGGTTTCCA 1020  
DB 969 gctgctcctaactggaacgtgcgcattgctctatacgcagcgtcgaataacttcttcca 1028  
QY 1021 GCTCTGCTCTGCTGCCAGTTCGTAAGAACGTTACTCCAGTGGATGGTTCGTCGTCAGAC 1080  
DB 1029 gccctcgcgctcgcaggttcttgaagaacgatatcccaaatggatgggttttgcgtcctagc 1088  
QY 1081 ATCCCGGATTCCTTCCAGTGTGCTGCTGCTACCGTACTCCAGAGCTTATCTACGCT 1140  
DB 1089 atctcgtgattctctccagtgattgggtgcgtgcaactcgtacacccgcgtaactatgct 1148  
QY 1141 TTTCGCTCACGCTCACCTCGGTATGCTGCTGCTCCAAATGACCGCAACCCCTCGTTCTGAG 1200  
DB 1149 ttgtgcaggtcatctcgtgatgacaggtgctccaaagtgcacactcgtctcagag 1208  
QY 1201 CTCCTCGGAGGTGAGAAGACCTCTATCGACATCTCTCCATTCGCAACCAACCGTTTCGGT 1260  
DB 1209 ctctcgcagggcgaagaagacccctcaatcgacatttgcctctgcgaccacaaacgcttgg 1268  
QY 1261 ATTGTGTAAGTCCCAAGCAAACTGGTCTTCATCTTAA 1296  
DB 1269 attggcaaatcccaagcaaacgggtccggcaagttaa 1304  
RESULT 5  
Q20833  
ID Q20833 standard; DNA; 1321 BP.  
XX  
AC Q20833;  
XX  
DT 01-MAY-1992 (first entry)  
XX  
DE Manipulated glyphosate oxidoreductase gene.  
XX





Db 1380 attgccaatcccaagcaaacagggtcccggaagttaa 1415

RESULT 7

Q20832

ID Q20832 standard; DNA; 1689 BP.

XX

AC Q20832;

XX

DT 01-MAY-1992 (first entry)

XX

DE Glyphosate oxidoreductase gene.

XX

KW Recombinant; GOR; resistance; ss.

XX

OS Bacterial isolate LBMA.

XX

FH Key Location/Qualifiers

FT CDS 120..1412

FT /\*tag= a

FT /note= "glyphosate oxidoreductase coding region"

FT misc\_feature 349..350

FT /\*tag= b

FT /note= "in the alternative sequence G is present here"

FT misc\_feature 375..376

FT /\*tag= c

FT /note= "in the alternative sequence T is present here"

FT misc\_feature 389..390

FT /\*tag= d

FT /note= "in the alternative sequence C is present here"

XX

PN W09200377-A.

XX

XX

PD 09-JAN-1992.

XX

XX

PF 24-JUN-1991; 91WO-US04514.

PR 24-JUN-1991; 91US-0717370.

PR 25-JUN-1990; 90US-0543236.

XX

XX (MONS ) MONSANTO CO.

XX

XX Kishore GM, Barry GF;

PI

XX

DR WPI; 1992-041559/05.

DR P-PSDB; R20642.

XX

PT Gene encoding glyphosate oxido-reductase enzyme - used to

PT transform plants to produce plants tolerant to glyphosate

PT herbicide

XX

PS Claim 1; Page 93; 142pp; English.

XX

CC The sequence is that of a gene encoding a glyphosate oxidoreductase

CC (GOR) enzyme. It was obtd. from bacterial isolate LBMA. It is used

CC to transform plants such that they express the enzyme sufficiently

CC to enhance the glyphosate tolerance of the plant. Transformed plants

CC resistant to glyphosate can be obtd. so that weeds can be selectively

CC controlled in fields congt. crops. This sequence (SEQ ID No.3 in the

CC specification) contains apparent discrepancies (see feature table)

CC with a supposedly identical sequence (fig 2), since it is unclear

CC from the specification which of these is correct, both sequences have

CC been indexed. See also Q20833-Q20841 and Q22705 - the alternative

CC sequence for the GOR gene.

XX

XX

SQ Sequence 1689 BP; 381 A; 477 C; 470 G; 360 T; 1 other;

Query Match 71.2%; Score 922.4; DB 13; Length 1689;

Best Local Similarity 83.5%; Pred. No. 1.4e-278;

Matches 1082; Conservative 0; Mismatches 211; Indels 3; Gaps 3;

QY 1 ATGGCTGAGAACCAAGAGGTTGGTATCCCTGGAGCTGGAAATCGTTGGTTCGACT 60

Db 120 atgtctggaaccacaacaaagtaggcatacgtcggaagcggaaatcgctcggtatgcacy 179

QY 61 GCTTTGATGCTTCAAGCTCGTGATTCAAGGTTACCTGATTGATCCAAACCCACACAGGT 120

Db 180 ggcgtgatagtctcagcgccggtattcaaaagtcacactctgattgacccgagcgtccctcggc 239

QY 121 GAAGGTGCTCTTTCCGGTAACGCTGCTTCAACGGTTCCCTCCGTTGTTTCCAATGTCC 180

Db 240 gaagtgcatcgcttgggaatgcgggatgcttcaacggtcatccgtcgctccctatgtcc 299

QY 181 ATGCCAGGAACTTGACTAGCGTTCCAAAGTGGCTTCTTTCACCAATGGGTCCATTTGTC 240

Db 300 atgcgggaaacttgacgagcgtgcgaagtgtcctcttgaccgcgatggg-cggtgtca 358

QY 241 ATCCGTTTCGGCTACTTTCCAAACATCATGCTTGGTTGATTCTGTTTCTTGTGCTTGGGA 300

Db 359 atccggttcagcta-tttccaccaatcattgcc-tggttattcgtcttctctgtagccgga 416

QY 301 AGACCAACAAGGTGAAGGAGCAAGCTAAGGCACCTCCGTAACTCATCAATCAAGTCCACTGTG 360

Db 417 agaccaacaaggtagaaggcaggcgaagcaactccgcaatctcatcaagtccacggtg 476

QY 361 CCTTTGATCAAGTCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTTCAGGAAGGT 420

Db 477 cctctgatcaagtcatcttgaggaggctgatcgagccatctgatccgccatgaaggt 536

QY 421 CACCTTACCGTGTACCGTGGAGAAGCAGACTTCGCCAGGAGCGTGGAGGTTGGGAACCTT 480

Db 537 catctgaccggtatctgttggaagcagactctcgcaagaccgcgagggtcttggaactg 596

QY 481 CGTCTCTCAACGGTGTCTGCTACTCAATCTCTCAGCGCTGATGCAATTCGCTGATTTTCGAT 540

Db 597 cggcgctcaacggtgtctcgacgcagatccctcagcgcgatcgcttgaggatttcgat 656

QY 541 CCTAATCTGCTCACGCCCTTTACCAAGGAATCCTTTATCGAAGAGACGGTTCACACATC 600

Db 657 ccgaactgtcgcatgctttaccaagggtctctatagaagagaacggttcacacgatt 716

QY 601 AACCACACAGGTCTCGTGACTCTCTTGTTCGTCTTTCATCGCTAACGGTGGAGAGTTC 660

Db 717 aatccgcaagggtcgctgacctcttcttggttcggttttatcgcgcaacggtcggaattc 776

QY 661 GTGCTGCTGCTGTTATCGGATTTCGAGACTGAAGGTCTGCTCTCAAGGGTATCACACAC 720

Db 777 gtatctgcgctgcatcgctttgagactgaaggtagggcgttaaaaggcattacaacc 836

QY 721 ACCAAGGTTGTTCTTGTCTGCTGATGCTGTTGTTGCAAGCTGGTGCACACTCCAAGTCT 780

Db 837 acgaacggtcttcggttgatgagcggttctgagcggttctgagcggttcggttcggttcaca 896

QY 781 CTTGCTTAAGTCTGCTGATGATGATCCATTCGATACCGAAGCTGGTATACCACATCGTG 840

Db 897 cctgtaattcgtctaggcgatgacatcccgctcgatcaccgaaacttgatatcatcgtc 956

QY 841 ATCGCAACCCAGAGAGCTGCTCCACGATTTCCAACTATCCGATGCTTCTGGAAGTTTCATC 900

Db 957 atcggaattccggaagcgcgtccacgcatccgagacgagatcgctcaggaaaaattcatg 1016

QY 901 GCTACTCTCTGAGATGGGTCTTCGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 960

Db 1017 ggcacacctatgaaatgggtcttcgctggttcggttcggttcggttcggttcggttcggttcaca 1076

QY 961 GCTGCTCTTAAGTGGAGGCTGCTCAGTCTCTCTACACTCGCGCTGCTGATGTTGCTTCCA 1020

Db 1077 gccgctctcaactggaaacgtgcatgctctatcaccgcaactctctctccca 1136

QY 1021 GCTCTCGCTCTCCAGTTCCTGAAGAACGTTTACTCCAAGTGGATGGGTTTTCGTTCCAAGC 1080

Db 1137 gccctcgccctgcagttctgaagaacgatatctccaaatggatgggtttccggcgagc 1196

QY 1081 ATCCCGGATTCCTTCCAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1140



Db 1197 atccggattcgctcccccgtgattgcccgggcaaccccgacacccgcagcytaatatctatgct 1256

Qy 1141 TTCGGTCACGGTCACCTCGGTATGACTGGTGTCTCCAAATGACCGCAACCCCTGGTTCTGTGAG 1200

Db 1257 ttcggccatggtcatctcgtcgatgacagggcgccgatgaccgcaacgctcgctcagag 1316

Qy 1201 CTCCTCGCAGGTGAGAACACCTCTATCGACATCTCTCCATTTCGCACCAACCGTTTCGGT 1260

Db 1317 ctcctcgagcgagaaagacctcaatcgacatttcgccttcgcaccaaaccgcttggt 1376

Qy 1261 ATTGGTAAGTCCAAAGCAACTGGTCTCATCTCAATCCCTAA 1296

Db 1377 attggcaaatccaagcaaacgggtccggcaagttaa 1412

RESULT 8

X57305

ID X57305 standard; DNA; 8012 BP.

XX

AC X57305;

XX

DT 26-JUL-1999 (first entry)

XX

DE Sugar beet T-DNA containing cp4/epsps fragment.

XX

KW Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plant;

KW 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide;

KW tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.

XX

OS Beta vulgaris.

XX

PN WO9923232-A1.

XX

PD 14-MAY-1999.

XX

PF 29-OCT-1998; 98WO-EP06859.

XX

PR 31-OCT-1997; 97US-0112003.

XX

PA (NOVS ) NOVARTIS AG.

PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX

PI Mannerloef M, Steen P, Tenning PP;

XX

DR WPI; 1999-313347/26.

XX

PT Glyphosate resistant transgenic sugar beet plants

XX

PS Claim 8; Page 24-29; 55pp; English.

XX

CC This invention describes a novel sugar beet plant, including its

CC descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase

CC (cp4/epsps) enzyme activity which is obtainable by Agrobacterium

CC mediated transformation with a gene allowing expression of cp4/epsps

CC in plants, where the plant lacks both right and left T-DNA border

CC sequences. The transgenic sugar beet plants of the invention are capable

CC of tolerating herbicide treatment with glyphosate (also known as

CC N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.

XX

SQ Sequence 8012 BP; 2096 A; 1855 C; 1879 G; 2182 T; 0 other;

Query Match 68.8%; Score 892.2; DB 20; Length 8012;

Best Local Similarity 99.7%; Pred. No. 9.2e-269;

Matches 894; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGCGTCGAGACCAACAGAGTTGCTATCCCTGGAGCTGCAATCGTTGCTTGCACACT 60

Db 7116 atggctgagaaccacaagaaggttggtatcgctgagctggaatcgttggtgttgcaact 7175

Qy 61 GCTTTGATGCTTCAACGCTGCTGGATTCAAGGTTACCTTGATTGATCCAAACCCACACAGGT 120

Db 7176 gctttgatgcttcaacgctcgtggattccaaggttaccttgattgatcccaacccaccaggt 7235

Qy 121 GAAGGTGCCCTCTTCGGTTAACGCCTGGTTTCCTTCGGTTTCCTTCGAATGTCC 180

Db 7236 gaaggtgctctcttcggttaacgctggttgcctcaacggttctctcgttgcctcaatgccc 7295

Qy 181 ATGCCAGCAAGTTCACATAGCGTTCCAAAGTGGCTTCCTTGACCCCAATGGGTCCATCTGCC 240

Db 7296 atgccagaaacttgactagcgttcctcaagtgctcttgacccaatgggtccatgtgcc 7355

Qy 241 ATCCGTTTCGGCTACTTTTCCAAACCATCATGCTTGGTTGATTTCGTTTCTTGGCTGTGA 300

Db 7356 atccgtttcagctactttcccaaccaatcgtgccttggttgattcgtcttctgcttgcctgga 7415

Qy 301 AGACCAACAAGGTGAAGGAGCAACCTAAGGCACATCCGTTAACCTCATCAAGTCCACTGTG 360

Db 7416 agaccaacaagggtgaaggagcaagcctaagcactccgttaacctcatcaagtcacatgtg 7475

Qy 361 CCTTTTGATCAAGTCCCTTGGCTCAGGAGGCTGATTCGTAGCCACCTTATCCGTCACCAAGGT 420

Db 7476 cctttga tcaagtccttgctgagaggtgatgtagccacctatccgctcacgaagt 7535

Qy 421 CACCTTACCGTGTACCGTGGAGAACGACACTTCGCGCAGGACCGTGGAGGTTGGGAACCT 480

Db 7536 cacttacggtgtaccgtggagaagcagacttcgccaaggaccgtggagggttgggaactt 7595

Qy 481 CGTCTCTCAACGGTGTTCGTTACTCAATTCCTACGCGTGTATGCAATTCGCTGATTCGAT 540

Db 7596 cgtcgtctcaacggtgttgcgtactcaaatcctcagcgtcgtgcatcgctgatttcgat 7655

Qy 541 CCTTAATTTGCTCAGCGCTTTACCAAGGGAATCCTTATCGAAGAACGCGTCACACCATC 600

Db 7656 cctaacttgtctcagcctttaccagaagggaatccttatcgaagaagacggtcacaccatc 7715

Qy 601 AACCCACAAGGTCTCGTACTCTCTTGTTCGTCGTTTCATCGCTAACGGTGGAGAGTTC 660

Db 7716 aaccacaaggctcgtgactctctgttctcgttcgttcctcgtctaaagggtgagagttc 7775

Qy 661 GTGCTGCTGCTGTTCGGATTTCGAGACTGAAGTTCGCTGCTCAAGGGTATACACCACC 720

Db 7776 gtgtcgtcgtgttatcggaatcgagactgaggtcgtgctcctcaagggtatccaccac 7835

Qy 721 ACCAAGCGGTCTTCGCTGTTCGATCGACGCTGTTGTCGAGCTGGTGCACACTCCAAGTCT 780

Db 7836 accaaacggttctctgctgtgatcagctgtgtgtcagcgtggtgcacactcccaagct 7895

Qy 781 CTTCGTAATCCCTTGGTGTGATGACATCCCATTCGATACCGAAGTGCATACCATCGTG 840

Db 7896 ctgtctaactcccttgggtgatgacatcccatgtgataccgaacggtggataccacatcgtg 7955

Qy 841 ATCGCCCAACCCAGAACGCTGCTCCACGTTATTCCAACTACCGATGCTTCTGGAAAGTTC 897

Db 7956 atcgccaaccagaagctgctccacgtattcccaactaccgatgcttctcgaaagtcc 8012

RESULT 9

X57308

ID X57308 standard; DNA; 8798 BP.

XX

AC X57308;

XX

DT 26-JUL-1999 (first entry)

XX

DE Sugar beet T-DNA containing cp4/epsps.

XX

KW Sugar beet; transformation; T-DNA; Insertion; cp4/epsps; plant;

KW 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide;

KW tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.

OS Beta vulgaris.

XX

PN WO9923232-A1.

XX

PD 14-MAY-1999.

XX 29-OCT-1998; 98WO-EP06859.  
XX 31-OCT-1997; 97US-0112003.  
XX (NOVS ) NOVARTIS AG.  
XX (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
XX Mannerloef M, Steen P, Tenning PP;  
XX WPI; 1999-313347/26.  
XX  
XX Glyphosate resistant transgenic sugar beet plants  
XX  
XX Claim 11; Page 31-36; 55pp; English.  
XX  
XX This invention describes a novel sugar beet plant, including its  
XX descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase  
XX (cp4/epsps) enzyme activity which is obtainable by Agrobacterium  
XX mediated transformation with a gene allowing expression of cp4/epsps  
XX in plants, where the plant lacks both right and left T-DNA border  
XX sequences. The transgenic sugar beet plants of the invention are capable  
XX of tolerating herbicide treatment with glyphosate (also known as  
XX N-phosphonomethyl-L-glycine) as the active ingredient, e.g. Roundup.  
XX  
XX Sequence 8798 BP; 2346 A; 1999 C; 2032 G; 2421 T; 0 other;  
SQ

Query Match 68.8%; Score 892.2; DB 20; Length 8798;  
Best Local Similarity 99.7%; Pred. No. 9.6e-269;  
Matches 894; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATCGGTGAGAACACCAAGGTTGGTATCGTGGAGTGGATCGTGGTGGTCACT 60  
DB 7205 atggctgagaccacacagaggttggtatcgctggagctggaatcgtgtttgcact 7264

QY 61 GCTTTGATGCTTCAACGTCGTCGATCAAGTTACCTTGATGATCCAAACCCACGAGT 120  
DB 7265 gctttgatgcttcaacgctcgtgattcaaggttaccttgatgatccaaacccaccaggt 7324

QY 121 GAAGGTGCCCTCTTTCGGTAACCGTCGTTGCTTCAACGGTTCCTTCGCTTGTCCAATGTCC 180  
DB 7325 gaagggtcctcttcggttaacgctggttcttcaacggtctctccgctgtttccaaatgctcc 7384

QY 181 ATCCGAGGAAACTTGACTACGCTTCCAAAGTGGCTTCTTTCACCCCAATGGTCCATTTGTCC 240  
DB 7385 atgcccaggaacttgactagctgtccaaagtggcttcttgaccacaaatgggtccattgtcc 7444

QY 241 ATCCGTTTCGGGTACTTCCACACCATCATGCTTGGTTGATTCGTTCTGCTGTGGA 300  
DB 7445 atccggtttcagctactttccaaacacatcatgcttggttgattcgtttctgtgtgga 7504

QY 301 ACACCAAAACAGGTCAAGGAGCAAGCTAAGGCACATCCGTAACCTCATCAAGTCCACTGTG 360  
DB 7505 agaccaaaacaaaggtgagaggagcaagctgaagcactccgtaacctcaacgaatccactctg 7564

QY 361 CTTTTCATCAAGTCTTGGCTCAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGT 420  
DB 7565 ccttgatcaagtctcttgctgaggagctgatgctagccacttatccgtcacgaaggt 7624

QY 421 CACCTTACCGTGTACGTCGAGCAAGCAGACTTCGCCAGGACCGTGGAGTGGGAACATT 480  
DB 7625 caacctacgctgaactgtgagaagcagacttcgcaaggacgctggaggttgggaactt 7684

QY 481 COTCGTCTCAACCGTGTTCGTTACTCAAAATCCCTCAGGCTGATGCAATTCGTTGATTCGAT 540  
DB 7685 cgtcgtctcaacaggttgctcgttactcaaaacctcaagcgtctga tgcgtgattctcgal 7744

QY 541 CCTAATCTTCTCACGCCCTTTACCAAGGGAATCTTTATCGAAGAGAACCGGTACACCATC 600  
DB 7745 cctaactgtctcagccctttaccaggggaatcccttatcgaaagacagcgttcacaccatc 7804

QY 601 AACCCACANAGGTCTCGTGACTCTCTTGTTCGTGCTTTCATCGCTAACGGTGGAGAGTTC 660

DB 7805 aaccacaaaggtctcgtgactctctgttttcgctcgtttcatcgttaacggtgagaggttc 7864  
QY 661 GTGCTCGTCTGCTTATTCGGATTTCGAGACTGAAGTGTGCTCTCAAGGGTATCACCAACC 720  
DB 7865 gtgtctgctcgtcttatacggattcagagactgaaggtcgtctcctcaaggggtatcaccacc 7924  
QY 721 ACCAAGCGGTGTTCTTGTCTGTGATGCAGCTGTTGTTTCAGCTGGTGACACACTCCAAGTCT 780  
DB 7925 accaagcgtgtctctcgtctgttgatgcagctgtgtgttcagctggtgcacactccaagtct 7984  
QY 781 CTTGCTAACTCCCTTGGTGTGATGACATCCCATTTGGATTACCGAACGTGGATACCATCGTG 840  
DB 7985 ctgtctaactcccttggtgatgacatcccatgtgataccgaacgtggataccacatcgtg 8044  
QY 841 ATCGCCAAACCCAGAAGCTGCTCCACGTTATTCCAACTACCGATGCTTCTGGAAAGTTC 897  
DB 8045 atcgccaacccaagactgctccacgtattccaactaccgatgcttctgaaaagttc 8101

RESULT 10  
V73805  
ID V73805 standard; DNA; 32207 BP.  
AC V73805;  
XX  
XX 25-FEB-1999 (first entry)  
XX  
XX KSHV LUR DNA (nucleotides 105,301-137,507).  
XX  
XX Kaposi's sarcoma; acquired immune deficiency syndrome; AIDS; DHFR; Bcl-2;  
XX dihydrofolate reductase; LUR; long unique region; vaccine; prophylaxis;  
XX diagnosis; treatment; HHV8; capsid protein IV; tegument protein IV;  
XX glycoprotein; Kaposin; cyclin D; immediate early protein; IEP; OX-2;  
XX v-adi; G-protein coupled receptor; FGARAT; ds.  
XX  
XX Kaposi's sarcoma-associated herpesvirus.  
XX  
XX US5849564-A.  
XX  
XX 15-DEC-1998.  
XX  
XX 29-NOV-1996; 96US-0770379.  
XX  
XX 29-NOV-1996; 96US-0770379.  
XX  
XX (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
XX Bohenzky RA, Chang Y, Edelman IS, Moore PS, Russo JJ;  
XX WPI; 1999-069741/06.  
XX  
XX Kaposi's sarcoma-associated herpes virus nucleic acid - encodes  
XX dihydrofolate reductase and is useful for treatment, prophylaxis  
XX or diagnosis of Kaposi's sarcoma  
XX  
XX Disclosure; Column 155-182; 109pp; English.  
XX  
XX This sequence is a fragment of the Kaposi's sarcoma-associated  
XX herpesvirus (KSHV) LUR (long unique region). This fragment contains  
XX coding regions for ORF65 which encodes capsid protein IV, ORF66, ORF67  
XX which encodes tegument protein IV, ORF68 which encodes a glycoprotein,  
XX ORF69, K12 which encodes Kaposin, K13, ORF72 which encodes cyclin D,  
XX ORF73 which encodes immediate early protein (IEP), K14 which encodes  
XX OX-2 (v-adi), ORF74 which encodes G-protein coupled receptor, ORF75  
XX which encodes tegument protein/FGARAT, K15. KSHV is a new human  
XX Herpesvirus (HHV8) believed to cause Kaposi's sarcoma (KS) which is the  
XX most common form of neoplasm occurring in persons with acquired immune  
XX deficiency syndrome (AIDS). The DHFR protein is useful for vaccination,  
XX prophylaxis, diagnosis and treatment of a subject with Kaposi's sarcoma  
XX and for detecting expression of a DNA virus associated with Kaposi's  
XX sarcoma in a cell.  
XX

```
SQ Sequence 32207 BP; 7229 A; 9156 C; 8713 G; 7109 T; 0 other;

Query Match          3.1%; Score 39.8; DB 20; Length 32207;
Best Local Similarity 47.7%; Pred. No. 0.11;
Matches 116; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 727 GGTGTTCTTTGATGACATCCATTCGATACCGAAGCTGGATACACATCGTGTATCGCC 846
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 19842 gctgctcatcctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 19901

QY 787 AACTCCCTTGGTGATGACATCCATTCGATACCGAAGCTGGATACACATCGTGTATCGCC 846
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 19902 catcctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 19961

QY 847 AACCAGAGCTGCTCCACGATTTCCAACTACCGATGCTTCTGGAAAGTTTACATCGCTACT 906
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 19962 catcctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 20021

QY 907 CCTATGGAGATGGCTTTCGTTGCTCGAACCCTTGGATTCGCTGGTCTCACATCGCTGCT 966
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 20022 catcctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 20081

QY 967 CCT 969
Db 20082 cat 20084

RESULT 11
V19941
ID V19941 standard; DNA; 137507 BP.
AC V19941;
XX
XX 03-AUG-1998 (first entry)
XX
XX KSHV long unique coding region and terminal repeat.
XX
XX KSHV; HHV8; human herpes virus 8; macrophage inflammatory protein II;
KW interleukin-6; IL-6; interferon regulatory factor; rheumatoid arthritis;
KW complement-binding protein; glycoprotein; capsid protein IV; infection;
KW immediate early protein; Kaposi's sarcoma; protective vaccine; lymphoma;
KW lymphoproliferative disease; leukaemia; splenomegaly; mycosis fungoides;
KW HIV immune status; anti-inflammatory agent; therapy; ds.
XX
XX Kaposi's sarcoma-associated herpes virus.
XX
XX Key Location/Qualifiers
FH CDS 1142..2794
FT /*tag= a
FT /product= complement-binding protein
FT 8699..11236
FT /*tag= b
FT /product= glycoprotein B
FT complement (17261..17875)
FT /*tag= c
FT /product= interleukin 6
FT complement (21548..21832)
FT /*tag= d
FT /product= macrophage inflammatory protein II
FT complement (27137..27424)
FT /*tag= e
FT /product= interferon regulatory factor 1
FT 28661..29741
FT /*tag= f
FT /product= protein T1.1
FT complement (58976..60175)
FT /*tag= g
FT /product= glycoprotein M
FT complement (69412..69915)
FT /*tag= h
FT /product= glycoprotein L
FT complement (88410..88910)
```

```
FT /*tag= i
FT /product= interferon regulatory factor 2
FT 89600..90541
FT /*tag= j
FT /product= interferon regulatory factor 3
FT 90173..90643
FT /*tag= k
FT /product= glycoprotein X
FT complement (93636..94127)
FT /*tag= l
FT /product= interferon regulatory factor 4
FT complement (111931..112443)
FT /*tag= m
FT /product= capsid protein IV
FT complement (123808..127296)
FT /*tag= n
FT /product= immediate early protein
XX
PN W09804576-A1.
XX
XX 05-FEB-1998.
XX
XX 22-JUL-1997; 97WO-US13346.
XX
XX 29-NOV-1996; 96US-0757669.
XX 25-JUL-1996; 96US-0686243.
XX 25-JUL-1996; 96US-0686349.
XX 25-JUL-1996; 96US-0686350.
XX 25-JUL-1996; 96US-0687253.
XX 25-JUL-1996; 96US-0688814.
XX 05-SEP-1996; 96US-0708678.
XX 10-OCT-1996; 96US-0728323.
XX 13-NOV-1996; 96US-0747887.
XX 13-NOV-1996; 96US-0748640.
XX
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX
XX Bohenzky RA, Chang Y, Edelman IS, Moore PS, Russo JJ;
XX WPI; 1998-130615/12.
XX
XX New nucleic acid encoding Kaposi's sarcoma associated herpes virus
XX proteins - useful for, e.g. detecting levels of HHV8 in, and
XX preparation of vaccines for treatment of, HIV patients
XX
XX Example 2; Page 135-203; 230pp; English.
XX
XX This sequence represents the long unique region and terminal repeat of
XX the Kaposi's sarcoma-associated herpes virus (KSHV). KSHV is also known
XX as human herpes virus 8 (HHV8). This sequence contains the DNAs of the
XX invention which encode KSHV polypeptides selected from: (a) viral
XX macrophage inflammatory protein (MIP) II; (b) viral interleukin-6 (IL-6);
XX (c) viral IRF 1; (d) complement-binding protein; glycoproteins B, M or L;
XX (e) capsid protein IV encoded by ORF65; and (e) immediate early protein
XX encoded by ORF73. Labelled probes for the nucleic acid, proteins encoded
XX by it, and antibodies (Ab) specific for the proteins are useful for
XX detecting HHV8, specifically for diagnosis of Kaposi's sarcoma, in body
XX fluids or tissue samples. HHV8 infections can be treated with antise
XX or triplex forming molecules or agents that bind specifically to the
XX protein. Ab may be used for prophylaxis or treatment of HHV8 infection,
XX while the protein can be used in protective vaccines. Ab may also be used
XX to differentiate between lymphomas, and HHV8 may be implicated in many
XX other lymphoproliferative diseases such as lymphomas, leukaemia,
XX splenomegaly and mycosis fungoides. Cells and animals containing the
XX nucleic acid are useful for drug screening. HHV8-derived peptides can be
XX used as targets for antiviral drugs, e.g. dihydrofolate reductase gene
XX can be inhibited with methotrexate. These can also be used to determine
XX the immune status of a patient infected with HIV. HHV8 derived protein
XX viral MIP III may be used as an anti-inflammatory agent for,
XX e.g. treating rheumatoid arthritis. This sequence is stated as containing
XX 81 open reading frames.
XX
XX Sequence 137507 BP; 32579 A; 37795 C; 35758 G; 31375 T; 0 other;
```

[illegible]

CC gene. The human OPA gene is derived from the PCTG4 region of chromosome  
CC q13. Polymorphisms in this region are associated with mental  
CC retardation, autism, depression, bipolar affective disorder or  
CC hypothyroidism. One 12 bp insertion polymorphism occurs within the  
CC coding region of the human OPA gene, and introduces a 4 amino acid  
CC insertion in a putative OPA domain. This domain has been shown to be  
CC involved in tissue specific expression. Another polymorphism consists  
CC of a pentanucleotide repeat approximately 7 kb upstream of the 12 bp  
CC polymorphism. Another polymorphism consists of a dinucleotide repeat  
CC approximately 4.5 kb downstream of the 12 bp polymorphism. The  
CC specification describes a method for screening for polymorphisms in a  
CC PCTG4 nucleic acid sequence obtained from a subject. The PCTG4 related  
CC sequences within the q13 region of the X chromosome have polymorphisms  
CC associated with neuropsychiatric disorders. The methods can be used  
CC to screen for the presence of a heritably linked form of mental  
CC retardation, autism, depression, bipolar affective disorder or  
CC hypothyroidism.  
XX  
SQ Sequence 6558 BP; 1637 A; 1801 C; 1644 G; 1475 T; 1 other;

Query Match 2.7%; Score 35.6; DB 21; Length 6558;  
Best Local Similarity 45.2%; Pred. No. 1;  
Matches 131; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

QY 665 CTGCTCGTGTATCGGATCGAGACTGAAGTCTGCTCTCAAGGGTATCACCACCACA 724  
DB 6396 CTGGCGCTGGAACTGGGACTGGGCTGGGGTTGGGAGGAGCTGCTGCTG 6337

QY 725 ACGGTGTTCTTGTCTTATGATCAGCTGTTGTGACGTGGTGCACACTCCAAAGTCTCTTG 784  
DB 6336 CTGCTGGTGTGGCTGCTGCTGCTGTGCTGTGTTGTTGCTGCTGCTGCTGCTGCTG 6277

QY 785 CTAACCTCCCTTGGTGATGACATCCCATTTGGATACCGAACGTTGGATACCATTCGTCG 844  
DB 6276 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6217

QY 845 CCAACCCAGAGCTGCTCCAGTATTCACACTACCGATGCTTCTGGAAGTTTCATCGCTA 904  
DB 6216 CTGTCGGATATGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6157

QY 905 CTCTCTATGAGATGGTCTTCTGCTGCTGCTGGAACGTTGAGTTCGCTGCT 954  
DB 6156 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6107

RESULT 14  
245597/C  
ID 245597 standard; cDNA; 6794 BP.  
XX 245597;  
AC  
XX  
XX  
DT 06-APR-2000 (first entry)  
XX  
DE cDNA sequence of human OPA gene.  
XX  
KW Human; PCTG4 region; X chromosome; q13 region; polymorphism;  
KW mental retardation; autism; depression; bipolar affective disorder;  
KW hypothyroidism; OPA gene; neuropsychiatric disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO955915-A2.  
XX  
XX  
PD 04-NOV-1999.  
XX  
PF 29-APR-1999; 99WO-US09365.  
XX  
XX 29-APR-1998; 98US-0083465.  
XX  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA (IOWA ) UNIV IOWA RES FOUND.  
XX

PI Philibert RA, Glans EI;  
XX  
DR WPI; 2000-126357/11.  
XX  
PT Identification of polymorphisms in the PCTG4 region of q13 for  
PT diagnosing mental retardation or autism -  
XX  
PS Example 7; Page 68-71; 100pp; English.  
XX  
XX The present sequence represents the cDNA sequence of the human OPA  
CC gene, which is derived from the human PCTG4 region of chromosome q13.  
CC Polymorphisms in this region are associated with mental retardation,  
CC autism, depression, bipolar affective disorder or hypothyroidism.  
CC One 12 bp insertion polymorphism occurs within the coding region of  
CC the human OPA gene, and introduces a 4 amino acid insertion in a  
CC putative OPA domain. This domain has been shown to be involved in tissue  
CC specific expression. Another polymorphism consists of a pentanucleotide  
CC repeat approximately 7 kb upstream of the 12 bp polymorphism. Another  
CC polymorphism consists of a dinucleotide repeat approximately 4.5 kb  
CC downstream of the 12 bp polymorphism. The specification describes a  
CC method for screening for polymorphisms in a PCTG4 nucleic acid sequence  
CC obtained from a subject. The PCTG4 related sequences within the q13  
CC region of the X chromosome have polymorphisms associated with  
CC neuropsychiatric disorders. The methods can be used to screen for the  
CC presence of a heritably linked form of mental retardation, autism,  
CC depression, bipolar affective disorder or hypothyroidism.  
XX  
SQ Sequence 6794 BP; 1624 A; 1938 C; 1754 G; 1478 T; 0 other;

Query Match 2.7%; Score 35.2; DB 21; Length 6794;  
Best Local Similarity 54.7%; Pred. No. 1.4;  
Matches 70; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 643 GCTAACGGTGGAGAGCTTCGTGCTGCTGCTATCGGATTCGACACTCAAGTCTGCT 702  
DB 6289 GCTGCTGCCGAGGATCTGCTGCTGCTGCTGCTGCCGATGGTACTGCTGCTGCT 6230

QY 703 CTCAAGGTATCACCAACCAACCGTCTTCTTGTGTTGATGCAGCTGTTTTCAGCT 762  
DB 6229 GCTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6170

QY 763 GGTGCACA 770  
DB 6169 GCTGCTCA 6162

RESULT 15  
T33007/c  
ID T33007 standard; DNA; 10266 BP.  
XX  
XX T33007;  
AC  
XX  
DT 23-OCT-1996 (first entry)  
XX  
DE Mouse SRV-related gene.  
XX  
KW Mouse; SRV; primer; PCR; polymerase chain reaction; amplification; probe;  
KW HMG box; human; bovine; sex; animal; birth; ds.  
XX  
XX Mus musculus.  
XX  
XX  
XX Key Location/Qualifiers  
XX CDS 7148..8335  
XX FT /\*tag=a  
XX FT /product= SRV-related protein  
XX  
XX JP08154685-A.  
XX  
XX 18-JUN-1996.  
XX  
XX 30-NOV-1994; 94JP-0319525.  
XX



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OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 01:13:01 ; Search time 3327.86 Seconds  
(without alignments)  
2407.829 Million cell updates/sec

Title: US-08-484-274-17  
Perfect score: 1296  
Sequence: 1 ATGGCTGAGAACCAAGAA.....AAACTGGTCTGCATCCTAA 1296

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues  
Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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10: gb\_est10:\*  
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116: gb\_gss17:\*





LOCUS BE019568 526 bp mRNA EST 06-JUN-2000  
DEFINITION ba83f05.y1 NIH\_MGC\_21 Homo sapiens cDNA clone IMAGE:2907009 5', similar to TR:O15413 O15413 CTG7A ;, mRNA sequence.  
ACCESSION BE019568  
VERSION BE019568.1 GI:8279646  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 526)  
AUTHORS NTH-MGC http://www.ncbi.nlm.nih.gov/MGC/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml  
Seq primer: -40RP from Glbco  
High quality sequence stop: 463.  
Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2907009"  
/clone\_lib="NIH\_MGC\_21"  
/tissue\_type="choriocarcinoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: placenta; Vector: pORF7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGG(G). Size-selected for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."  
BASE COUNT 154 a 189 c 119 g 64 t  
ORIGIN  
Query Match 3.4%; Score 44.6; DB 32; Length 526;  
Best Local Similarity 49.0%; Pred. No. 0.024;  
Matches 119; Conservative 0; Mismatches 124; Indels 0; Gaps 0;  
Qy 727 GGTCTTCTTGGTGTGATGCAGCTGTTGTCAGCTGGTGCACACTCCAACTCTCTTGGCT 786  
Db 251 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 192  
Qy 787 AACTCCCTTGGTGTGATGACATCCCATTTGATACCGACGTGGATACCACATCGTATCCGC 846  
Db 191 GCACCTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 132  
Qy 847 AACCAGAACTGCTGCCAGCTATTCACCACTACCGATGCTTCTGGAAAGTTTCATCGCTACT 906  
Db 131 GCT 72  
Qy 907 CCTATGGAGATGGGTCTTTCGTTGCTGGAAACCGTTGATGTTTCGCTGGTCTCACTGCTGCT 966  
Db 71 GCT 12  
Qy 967 CCT 969  
Db 11 GCT 9  
RESULT 3  
CNS03H6V/c

LOCUS CNS03H6V 970 bp DNA GSS 17-MAY-2000  
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 026011 of library G from Tetraodon nigroviridis, genomic survey sequence.  
ACCESSION AL243904  
VERSION AL243904.1 GI:7964916  
KEYWORDS GSS; genome survey sequence.  
SOURCE Tetraodon nigroviridis.  
ORGANISM Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Eurypterygii; Ctenosquamata; Acanthomorpha; Eucanthomorpha; Holacanthopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.  
REFERENCE 1 (bases 1 to 970)  
AUTHORS Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissbach, J.  
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 970)  
AUTHORS Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissbach, J.  
TITLE Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 970)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases  
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/tetraodon.  
Location/Qualifiers  
1..970  
/organism="Tetraodon nigroviridis"  
/db\_xref="taxon:99883"  
/clone="026011"  
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BASE COUNT 311 a 298 c 194 g 152 t 15 others  
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Query Match 3.4%; Score 44.6; DB 123; Length 970;  
Best Local Similarity 45.6%; Pred. No. 0.029;  
Matches 149; Conservative 2; Mismatches 176; Indels 0; Gaps 0;  
Qy 643 GCTAACGCTGGAGAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 702  
Db 717 GTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 658  
Qy 703 CTCAGGATATCACACCAACCAACGGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 762  
Db 657 GTTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 598  
Qy 763 GGTGCACACTCAAGCTCTTGTGCTAACTCCCTTGTGCTGATGACATCCCATTTGGATACCGAA 822  
Db 597 GTTGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 538  
Qy 823 CGTGGATACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 882  
Db 537 GTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 478  
Qy 883 GCTTCTGGAAAGTTTCATCGCTACTCTATGGAGATGGGTCTTCTGCTGCTGCTGCTGCTGCT 942  
Db 477 GCTGTTGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 418  
Qy 943 GAGTTCGCTGCTCCTCCTGCTGCTCCT 969  
ORIGIN







Fax: 864 656 4293  
Email: rdean@clemons.edu  
Seq primer: T3 primer (AATTAAACCCTCACTAAAGGG)  
High quality sequence stop: 403.

FEATURES  
source

## FEATURES

## FEATURES

## FEATURES

project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

FEATURES  
SOURCE

FEATURES  
SOURCE

FEATURES  
SOURCE

FEATURES  
SOURCE









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OM nucleic - nucleic search, using sw model

Run on: December 31, 2000, 19:08:36 ; Search time 7299.04 Seconds  
(without alignments)  
773.702 Million cell updates/sec

Title: US-08-484-274-4  
Perfect score: 1293  
Sequence: 1 ATGCTGAGAACCAAAAA.....AAACGGGTCGGCAAGTTAA 1293

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues 2067340  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_ba2.\*  
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14: em\_hum2.\*  
15: em\_in.\*  
16: em\_om.\*  
17: em\_or.\*  
18: em\_ov.\*  
19: em\_pat.\*  
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90: gb\_sts2.\*  
91: gb\_sy.\*  
92: gb\_un.\*  
93: gb\_v11.\*  
94: gb\_v12.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1293	100.0	1293	5	AR016592	AR016592 Sequence
2	1293	100.0	1293	5	I15325	I15325 Sequence 4
3	1293	100.0	1689	5	I15324	I15324 Sequence 3
4	1260	97.4	1692	5	AR016591	AR016591 Sequence
5	1255.2	97.1	1296	5	AR016593	AR016593 Sequence
6	1255.2	97.1	1296	5	I15326	I15326 Sequence 6
7	1160.8	89.8	1296	5	AR016594	AR016594 Sequence
8	1160.8	89.8	1296	5	I15327	I15327 Sequence 7
9	928.8	71.8	1296	5	AR016595	AR016595 Sequence
10	928.8	71.8	1296	5	I15328	I15328 Sequence 8
11	925.6	71.6	1296	5	AR016604	AR016604 Sequence
12	925.6	71.6	1296	5	I15337	I15337 Sequence 17

13 857.6 66.3 1631 5 A59869 Sequence 1  
14 84.2 6.5 3430 2 PSEAKSD  
15 61.8 4.8 2289 2 PSEAKSDA  
16 56.2 4.3 69 5 AR016616  
17 56.2 4.3 69 5 AR016616  
18 54.6 4.2 69 5 AR016619  
19 54.6 4.2 69 5 AR016619  
20 50.6 3.9 65 5 AR016614  
21 50.6 3.9 65 5 AR016614  
22 48.2 3.7 61 5 AR016617  
23 48.2 3.7 61 5 AR016617  
24 47.6 3.7 62 5 AR016613  
25 47.6 3.7 62 5 AR016613  
26 47.4 3.7 1540 2 EH017017  
27 47.2 3.7 68 5 AR016618  
28 47.2 3.7 68 5 AR016618  
29 41.4 3.2 6175 1 AF151698  
30 40.4 3.1 12695 1 AE004164  
31 40.2 3.1 23550 2 SCE39  
32 39.8 3.1 38914 2 MSGB937CS  
33 37.8 2.9 1020 52 AC033443  
34 36.2 2.8 1579 45 ZMB2TUBR  
35 36.2 2.8 3300 1 AF208523  
36 36.2 2.8 67200 2 FTV017  
37 36 2.8 13799 1 AE002359  
38 35.4 2.7 10236 1 AE000097  
39 35.4 2.7 179381 53 AC055863  
40 35.4 2.7 236165 5 A79351  
41 35.4 2.7 236165 5 A93003  
42 35.2 2.7 3185 2 PSEPEAX  
43 35.2 2.7 75095 38 AC013676  
44 35 2.7 1600 45 TRPGK  
45 35 2.7 3286 1 AF053760

## ALIGNMENTS

RESULT 1  
LOCUS AR016592 1293 bp DNA PAT 05-DEC-1998  
DEFINITION Sequence 4 from patent US 5776760.  
ACCESSION AR016592  
VERSION AR016592.1 GI:3972869  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1293)  
AUTHORS Barry,G.Francis and Kishore,G.Murthy.  
TITLE Glyphosate tolerant plants  
JOURNAL Patent: US 5776760-A 4 07-JUL-1998;  
FEATURES Location/Qualifiers  
source 1..1293  
BASE COUNT 286 a 367 c 359 g 281 t  
ORIGIN

Query Match 100.0%; Score 1293; DB 5; Length 1293;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 61 GCGCTGATGCTTCAGCCCGCGGATTCAAAGTCACCTTGATTCACCGAACCCTTCCTGGC 120  
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Db 61 GCGCTGATGCTTCAGCCCGCGGATTCAAAGTCACCTTGATTCACCGAACCCTTCCTGGC 120  
QY 121 GAAGGTGCATCGTTTGGGAATCGCGGATCGCTTCACCGGCTCATCCGCTCGTCCCTATGTCC 180  
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Db 121 GAAGGTGCATCGTTTGGGAATCGCGGATCGCTTCACCGGCTCATCCGTCCTCCCTATGTCC 180  
QY 181 ATGCCGGGAAACTTGCACGAGCGTCCCGAAGTGGCTTCTTGACCCGATGGCGCGTGTCTCAA 240  
|||||  
Db 181 ATGCCGGGAAACTTGCACGAGCGTCCCGAAGTGGCTTCTTGACCCGATGGCGCGTGTCTCAA 240  
QY 241 TCCGTTTCAGCTATTTTCCAACCATCATGCCCTGGTGTGATTCGCTTCTCTTACCGGAAGA 300  
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Db 241 TCCGTTTCAGCTATTTTCCAACCATCATGCCCTGGTGTGATTCGCTTCTCTTACCGGAAGA 300  
QY 301 CCAACAAGGTGAAGGAGCAGCGGAAAGCATCTCCGCAATCTCATCAAGTCACCGTGGCT 360  
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Db 301 CCAACAAGGTGAAGGAGCAGCGGAAAGCATCTCCGCAATCTCATCAAGTCACCGTGGCT 360  
QY 361 CTGATCAAGTCATTTGGCGGAGGAGCTGATCGGAGCCATCTGATCCGCCATGAAGGTCTAT 420  
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Db 361 CTGATCAAGTCATTTGGCGGAGGAGCTGATCGGAGCCATCTGATCCGCCATGAAGGTCTAT 420  
QY 421 CTGACCGGTATATCGTTGGAGAAAGCAGACTTCGCCAAGGAGCCCGGAGGTTCGGAACTGGCG 480  
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Db 421 CTGACCGGTATATCGTTGGAGAAAGCAGACTTCGCCAAGGAGCCCGGAGGTTCGGAACTGGCG 480  
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|||||  
Db 481 CGTCTCAACGGTGTTCGCACGACAGATCCTCAGCCGATCGCTTCGCGGATTTCCGATCCG 540  
QY 541 AACTTTGCGCATGCTTTACCAAGGGCATCTTATAGAGAGACCGTTCACACGATTAAT 600  
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Db 541 AACTTTGCGCATGCTTTACCAAGGGCATCTTATAGAGAGACCGTTCACACGATTAAT 600  
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Db 601 CCGCAAGGGTCTGACCCCTCTTCTTTCGGCGTTCATTCGCGAAGCGTTCGGAATTCGTA 660  
QY 661 TCTCGCGGTGTCTCGGCTTTTGTAGACTGAAGGTAGGGCGCTTAAAGGCATTTACAACACG 720  
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Db 661 TCTCGCGGTGTCTCGGCTTTTGTAGACTGAAGGTAGGGCGCTTAAAGGCATTTACAACACG 720  
QY 721 AACGGCGTTCGCGCGTGTGTAGCAGCGGTTCTCGCAGCCCGCGCACACTCGAAATCAGTT 780  
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Db 721 AACGGCGTTCGCGCGTGTGTAGCAGCGGTTCTCGCAGCCCGCGCACACTCGAAATCAGTT 780  
QY 781 GCTAATTCGCTAGCGCATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTCATC 840  
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Db 781 GCTAATTCGCTAGCGCATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTCATC 840  
QY 841 GCGAATCCGGAAGCGCTCCACGCAATTCGAGCGGCGGATCGGTCAGGAAATTCATCGCG 900  
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Db 841 GCGAATCCGGAAGCGCTCCACGCAATTCGAGCGGCGGATCGGTCAGGAAATTCATCGCG 900  
QY 901 ACACCTATGGAATGGGGTTCGCGTGGCGGTACGGTTGATTTGCTGGCTCAGAGCC 960  
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Db 901 ACACCTATGGAATGGGGTTCGCGTGGCGGTACGGTTGATTTGCTGGCTCAGAGCC 960  
QY 961 GCTCCTAAGTGGAAACGTGCGCATGTCTCTATACGCAAGCTCGAAACCTTCTTCCAGCC 1020  
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Db 961 GCTCCTAAGTGGAAACGTGCGCATGTCTCTATACGCAAGCTCGAAACCTTCTTCCAGCC 1020  
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Db 1021 CTGCGGCTCGGAGTCTCTGAAGACGATATTCGCAATGGATGGGGTTCGCGCCGAGCATC 1080  
QY 1081 CCGGATTCGCTCCCGGTGATTTGGCGGCAACCGGACACCCGACGTAATCTATGCTTTC 1140  
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Db 1081 CCGGATTCGCTCCCGGTGATTTGGCGGCAACCGGACACCCGACGTAATCTATGCTTTC 1140  
QY 1141 GGCAATGGTTCATTCGCGCATGACAGGGGCGCGGATGACCGAAGCTCTGCTCAGAGCTC 1200  
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Db 1141 GGCAATGGTTCATTCGCGCATGACAGGGGCGCGGATGACCGAAGCTCTGCTCAGAGCTC 1200  
QY 1201 CTGCGAGCGGAAAGACCTCAATCGACATTTTCGCCCTTCGCAACCAACCGCTTTGGTATT 1260  
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Db 1201 CTGCGAGCGGAAAGACCTCAATCGACATTTTCGCCCTTCGCAACCAACCGCTTTGGTATT 1260

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QY 1261 GCGAATCAAGCAACGGGTCGGCAAGTTAA 1293
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Db 1261 GCGAATCAAGCAACGGGTCGGCAAGTTAA 1293

RESULT 2
I15325
LOCUS I15325 1293 bp DNA PAT 02-APR-1996
DEFINITION Sequence 4 from patent US 5463175.
ACCESSION I15325
VERSION I15325.1 GI:1250233
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 1293)
TITLE Barry, G.F. and Kishore, G.M.
JOURNAL Glyphosate tolerant plants
FEATURES Patent: US 5463175-A 4 31-OCT-1995;
source Location/Qualifiers
BASE COUNT 286 a 367 c 359 g 281 t
ORIGIN

Query Match 100.0%; Score 1293; DB 5; Length 1293;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGAGAACCAACAAAGTAGGCGATCGCTGGAGCGGAATCGTCGGCGTATGCAAG 60
Db 1 ATGCTGAGAACCAACAAAGTAGGCGATCGCTGGAGCGGAATCGTCGGCGTATGCAAG 60

QY 61 CGCGTGATGCTTCAGCGCGCGGATTCAAAGTCACCTTGATTGACCCCGAACCCCTCCTGCG 120
Db 61 CGCGTGATGCTTCAGCGCGCGGATTCAAAGTCACCTTGATTGACCCCGAACCCCTCCTGCG 120

QY 121 GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC 180
Db 121 GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC 180

QY 181 ATGCCGGGAAACTTCACGAGGTCGCCGAAGTGGCTCTTGACCCGATGGCGGTTGTCAA 240
Db 181 ATGCCGGGAAACTTCACGAGGTCGCCGAAGTGGCTCTTGACCCGATGGCGGTTGTCAA 240

QY 241 TCCGGTTTCAGCTATTTCGAACCATCATCGCTGGTTGATTTCGCTTTCAGCGGAAGA 300
Db 241 TCCGGTTTCAGCTATTTCGAACCATCATCGCTGGTTGATTTCGCTTTCAGCGGAAGA 300

QY 301 CCAACAAAGGTGAAGGAGCAGCGCAAGACACTCCGCAATCTCATCAAGTCCACACGGTGCCT 360
Db 301 CCAACAAAGGTGAAGGAGCAGCGCAAGACACTCCGCAATCTCATCAAGTCCACACGGTGCCT 360

QY 361 CTGATCAAGTCATTTGGCGGAGGAGCTGATCGGAGCCATCTGATCCGCCATGAAGGTCA 420
Db 361 CTGATCAAGTCATTTGGCGGAGGAGCTGATCGGAGCCATCTGATCCGCCATGAAGGTCA 420

QY 421 CTGACCGGTATATCTGGGAGAGCAGACTTCGCCAAGGACCGCGAGGTTGGAACTGCGG 480
Db 421 CTGACCGGTATATCTGGGAGAGCAGACTTCGCCAAGGACCGCGAGGTTGGAACTGCGG 480

QY 481 GTCCTCAACGGTGTTCGACACGACATCTCAGCGCGGATGGGTTTCGGGATTTTCGATCCG 540
Db 481 GTCCTCAACGGTGTTCGACACGACATCTCAGCGCGGATGGGTTTCGGGATTTTCGATCCG 540

QY 541 AACTTGTCCGATGGCTTTACCAAGGGCATCTTATAGAAGAGAGCGGTCACACGATTAAT 600
Db 541 AACTTGTCCGATGGCTTTACCAAGGGCATCTTATAGAAGAGAGCGGTCACACGATTAAT 600

QY 601 CCGAAGGGCTCGTACCCCTCTCTTCGGCGTTTATCGGCAACGGTGGCGAATTCGTA 660
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Db 601 CCGAAGGGCTCGTACCCCTCTTGTTCGGCGTTTATTCGCAACGGTGGCGAATTCGTA 660
QY 661 TCTGCGCGTGTTCATCGGCTTTGAGACTGAAGCTAGGGCGCTTTAAAGGCATTTCAACACGCG 720
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Db 661 TCTGCGCGTGTTCATCGGCTTTGAGACTGAAGCTAGGGCGCTTTAAAGGCATTTCAACACGCG 720
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QY 721 AACGGCGTTCTCGCGCTTGATCGAGCGGTTGTCGAGCGCGGCACACCTCGAAATCACATT 780
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Db 721 AACGGCGTTCTCGCGCTTGATCGAGCGGTTGTCGAGCGCGGCACACCTCGAAATCACATT 780
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QY 781 GCTAATTCGCTAGGCGATGACATCCGCTCGATACCGAAGCTGGATATCATATCGTCAATC 840
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Db 781 GCTAATTCGCTAGGCGATGACATCCGCTCGATACCGAAGCTGGATATCATATCGTCAATC 840
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QY 841 GCGAATCCGGAAGCGCTCCAGCATTCGAGAGCGGATCGCTCAGGAAATTCATCGCGG 900
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Db 841 GCGAATCCGGAAGCGCTCCAGCATTCGAGAGCGGATCGCTCAGGAAATTCATCGCGG 900
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QY 901 ACACCTATGGAATGGGCTTCGCGTGGCGGTACGGTTGAGTTGCTGGGCTCAGAGCC 960
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Db 901 ACACCTATGGAATGGGCTTCGCGTGGCGGTACGGTTGAGTTGCTGGGCTCAGAGCC 960
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Db 1021 CTCGCGCTTCGAGTTCTGAAGACGATATTCAAATGATGGGTTCCGGCGGAGCATC 1080
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QY 1081 CCGGATTCGCTCCCGTGATTCGGCGGGCAACCCGAGACCTCTATGCTTTTC 1140
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QY 1141 GCGCATGTCATCTCGGATGACAGGGCGCGGATGACCGCAACGCTCGCTCAGAGCTC 1200
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Db 1141 GCGCATGTCATCTCGGATGACAGGGCGCGGATGACCGCAACGCTCGCTCAGAGCTC 1200
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QY 1201 CTCGAGCGCAAAAGACCTCAATCGACATTTCCGCTTCGCAACCAACCGCTTTGGTATT 1260
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Db 1201 CTCGAGCGCAAAAGACCTCAATCGACATTTCCGCTTCGCAACCAACCGCTTTGGTATT 1260
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QY 1261 GCGAATCAAGCAACGGGTCGGCAAGTTAA 1293
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Db 1261 GCGAATCAAGCAACGGGTCGGCAAGTTAA 1293

RESULT 3
I15324
LOCUS I15324 1689 bp DNA PAT 02-APR-1996
DEFINITION Sequence 3 from patent US 5463175.
ACCESSION I15324
VERSION I15324.1 GI:1250232
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 1689)
TITLE Barry, G.F. and Kishore, G.M.
JOURNAL Glyphosate tolerant plants
FEATURES Patent: US 5463175-A 3 31-OCT-1995;
source Location/Qualifiers
BASE COUNT 381 a 479 c 468 g 360 t 1 others
ORIGIN

Query Match 100.0%; Score 1293; DB 5; Length 1689;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGAGAACCAACAAAGTAGGCGATCGCTGGAGCGGAATCGTCGGCGTATGCAAG 60
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Db 120 ATGTCTGAGAACCAAAAAAGTAGGCATCGCTGGAGCCGGAATCGTGGCGTATGCACG 179  
QY 61 GCGTGTATGCTTACAGCCCGCGGATTCAAAGTACACCTTGATTGACCCGAACCCCTCCCTGGC 120  
Db 180 GCGTGTATGCTTACAGCCCGCGGATTCAAAGTACACCTTGATTGACCCGAACCCCTCCCTGGC 239  
QY 121 GAAGGTGCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGTCCTTATGTC 180  
Db 240 GAAGGTGCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGTCCTTATGTC 299  
QY 181 ATGCCGGGAACCTTGACGAGCGTCCGAAGTGGCTCCTTGACCGGATGGCCGCTTGTC 240  
Db 300 ATGCCGGGAACCTTGACGAGCGTCCGAAGTGGCTCCTTGACCGGATGGCCGCTTGTC 359  
QY 241 TCCGGTTTCACTATTTTCCAAACCATCATGCTGCTGTTGATTGCTTTTGTAGCCGGAAGA 300  
Db 360 TCCGGTTTCACTATTTCCAAACCATCATGCTGCTGTTGATTGCTTTTGTAGCCGGAAGA 419  
QY 301 CCAAAACAGGTGAAGGAGCAGGCGAAAGCAGCTCCGCAATCTCATCAAGTCCACGGTGCCT 360  
Db 420 CCAAAACAGGTGAAGGAGCAGGCGAAAGCAGCTCCGCAATCTCATCAAGTCCACGGTGCCT 479  
QY 361 CTGATCAAGTCATTTGCCGAGGAGGCTGATCCGAGCCATCTGATCCGCCATGAAGTTCAT 420  
Db 480 CTGATCAAGTCATTTGCCGAGGAGGCTGATCCGAGCCATCTGATCCGCCATGAAGTTCAT 539  
QY 421 CTGACCTATATCTGTGAGAGCAGACTTCCCAAGGACCGCGAGGTGGGAAGTCCGG 480  
Db 540 CTGACCTATATCTGTGAGAGCAGACTTCCCAAGGACCGCGAGGTGGGAAGTCCGG 599  
QY 481 CGTCTCAACGGTGTCCGACGCGAGATCCTCAGCGCCGATCGTTGCGGGATTTTCGATCCG 540  
Db 600 CGTCTCAACGGTGTCCGACGCGAGATCCTCAGCGCCGATCGTTGCGGGATTTTCGATCCG 659  
QY 541 AACTTGTCCGATCGGTTTACCAAGGCGATTTCTATAGAAGAACGCTCAGACGATTAA 600  
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QY 601 CCGCAAGGCTTCTGACCCCTCTTGTTCGCGCTTTTATCGCAACGCTGGCGAATTCGTA 660  
Db 720 CCGCAAGGCTTCTGACCCCTCTTGTTCGCGCTTTTATCGCAACGCTGGCGAATTCGTA 779  
QY 661 TCTGCGGCTGTCTGCGCTTTGAGACTGAAGGTAGGCGGCTTAAAGGCATTACAAACACG 720  
Db 780 TCTGCGGCTGTCTGCGCTTTGAGACTGAAGGTAGGCGGCTTAAAGGCATTACAAACACG 839  
QY 721 AACGGCTTCTGCGGCTTGTATGCGCGGTTGTCGACGCGCGCACACTCGAATCACTT 780  
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Db 1080 GCTCTCAACTGGAAAGCTGCGCATGTCTCTATACGACGCTCGAAACCTTCTTCCAGCC 1139  
QY 1021 CTCGCGCTTCGAGTCTGAAGAACGATATTCCAATFGATGGGTTCCGCGCGGAGATC 1080  
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QY 1081 CCGSANTCGCTCCCGGTGATTGCGCGGCAACCGGACACCCGACCTGAATCTATGCTTTC 1140

Db 1200 CCGGATTGCTCCCGCTGATTGGCCGGGCAACCCGGACACCCGAGTAATCTATGCTTTC 1259  
QY 1141 GCCCATGCTATCTCGGCATGACAGGGCGCGGATGACCCGAAGCTCTGCTTCAGAGCTC 1200  
Db 1260 GCCCATGCTATCTCGGCATGACAGGGCGCGGATGACCCGAAGCTCTGCTTCAGAGCTC 1319  
QY 1201 CTGCGAGGCGAAAAGACTCAATCGACATTTGCGCCCTTCGACCAAAACCGCTTTGGTATT 1260  
Db 1320 CTGCGAGGCGAAAAGACTCAATCGACATTTGCGCCCTTCGACCAAAACCGCTTTGGTATT 1379  
QY 1261 GGCAAAATCCAAAGCAAAACGGGTCCGCGCAAGTTAA 1293  
Db 1380 GGCAAAATCCAAAGCAAAACGGGTCCGCGCAAGTTAA 1412  
RESULT 4  
AR016591 AR016591 1692 bp DNA PAT 05-DEC-1998  
LOCUS Sequence 3 from patent US 5776760.  
DEFINITION AR016591  
ACCESSION AR016591  
VERSION AR016591.1 GI:3972868  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1692)  
AUTHORS Barry,G.Francis and Kishore,G.Murthy.  
TITLE Glyphosate tolerant plants.  
JOURNAL Patent: US 5776760-A 3 07-JUL-1998;  
FEATURES Location/Qualifiers  
source 1.1692  
BASE COUNT 381 a 480 c 469 g 361 t 1 others  
ORIGIN  
Query Match 97.4%; Score 1260; DB 5; Length 1692;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1293; Conservative 0; Mismatches 0; Indels 3; Gaps 3;  
QY 1 ATGTCCTGAGAACCAAAAAAGTAGGCATCGCTGGAGCCGGAATCGTGGCGTATGCACG 60  
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QY 61 GCGTGTATGCTTACAGCCCGCGGATTCAAAGTACACCTTGATTGACCCGAACCCCTCCCTGGC 120  
Db 180 GCGTGTATGCTTACAGCCCGCGGATTCAAAGTACACCTTGATTGACCCGAACCCCTCCCTGGC 239  
QY 121 GAAGGTGCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGTCCTTATGTC 180  
Db 240 GAAGGTGCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGTCCTTATGTC 299  
QY 181 ATGCCGGGAACCTTGACGAGCGTCCGAAGTGGCTCCTTGACCCGAT-GGGCCGTTGTCA 239  
Db 300 ATGCCGGGAACCTTGACGAGCGTCCGAAGTGGCTCCTTGACCCGATGTGTCA 359  
QY 240 ATCCGGTTCAGCTA-TTTTCCAAACCATCATG-CTTGGTTGATTTCGCTTCTCTTACCGCGA 297  
Db 360 ATCCGGTTCAGCTATTTTCCAAACCATCATGCGCCCTGGTTGATTTCGCTTCTCTTACCGCGA 419  
QY 298 AGACCAACAAAGGTGAAGGAGCAGCGGAAAGCACTCCGCAATCTCATCAAGTCCACCGTG 357  
Db 420 AGACCAACAAAGGTGAAGGAGCAGCGGAAAGCACTCCGCAATCTCATCAAGTCCACCGTG 479  
QY 358 CCTCTGATCAAGTCATTTGGCGGAGGAGGCTCATCGGAGCCATCTGATCCGCCATGAAGGT 417  
Db 480 CCTCTGATCAAGTCATTTGGCGGAGGAGGCTCATCGGAGCCATCTGATCCGCCATGAAGGT 539  
QY 418 CATCTGACCGCTATATCTGTGGAAGACGACTTCCGCCAAGGACCGCGGAGGTTCGGAAGT 477  
Db 540 CATCTGACCGCTATATCTGTGGAAGACGACTTCCGCCAAGGACCGCGGAGGTTCGGAAGT 599  
QY 478 CGGCGTCTCAACGGTGTTCGCACGAGATCCTCAGCGCCGATGCGTTGCGGGATTTTCGAT 537

Db 600 CGGGCTCTCAACGGGTTCGACGACGAGATCTCAGCGCGGATGCGTTCGGGGATTTTCGAT 659  
Qy 538 CCGAACTTGTCCGATCCGCTTTACCAAGGCGATCTTATAGAAGAGCAACGGTCACACGATTT 597  
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Qy 598 AATCGCAAGGGCTGCTGACCCCTCTTGTTCGGGGTTTTATCGCGAAGCGGTGGGAATTC 657  
Db 720 AATCGCAAGGGCTGCTGACCCCTCTTGTTCGGGGTTTTATCGCGAAGCGGTGGGAATTC 779  
Qy 658 GTATCTCGCGCTGTATCGCGCTTTGAGACTGAAGTAGGGCGCTTAAAGGCAATTACACCC 717  
Db 780 GTATCTCGCGCTGTATCGCGCTTTGAGACTGAAGTAGGGCGCTTAAAGGCAATTACACCC 839  
Qy 718 ACGAAGCGGCTTCTGGCCGCTTGATCGACGGTTGTGCGAGCGCGGCGCACACTCGAAATCA 777  
Db 840 ACGAAGCGGCTTCTGGCCGCTTGATCGACGGTTGTGCGAGCGCGGCGCACACTCGAATCA 899  
Qy 778 CTTGCTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC 837  
Db 900 CTTGCTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC 959  
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Qy 1018 GCCCTCGCGCTCGAGTTCTGAGAACGATATCCNAATGATGGGTTCCGGCCGAGC 1077  
Db 1140 GCCCTCGCGCTCGAGTTCTGAGAACGATATCCNAATGATGGGTTCCGGCCGAGC 1199  
Qy 1078 ATCCCGGATTCGCTCCCGCTGATTGGCCGGGCAACCCGACACCGAGCTAATCTATGCT 1137  
Db 1200 ATCCCGGATTCGCTCCCGCTGATTGGCCGGGCAACCCGACACCGAGCTAATCTATGCT 1259  
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Qy 1198 CTCCTCGCAGCGGAACACCTCAATCAGATTTCCGCCCTTCGCACCAACCGCTTTGGT 1257  
Db 1320 CTCCTCGCAGCGGAACACCTCAATCAGATTTCCGCCCTTCGCACCAACCGCTTTGGT 1379  
Qy 1258 ATTGGCAATCCAAGCAACGGGTCGGCAAGTTAA 1293  
Db 1380 ATTGGCAATCCAAGCAACGGGTCGGCAAGTTAA 1415

RESULT 5  
AR016593  
LOCUS AR016593 1296 bp DNA PAT 05-DEC-1998  
DEFINITION Sequence 6 from patent US 5776760.  
ACCESSION AR016593  
VERSION AR016593.1 GI:3972870  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 1296)  
AUTHORS Barry.G.Francis and Kishore,G.Murthy.  
TITLE Glyphosate tolerant plants  
JOURNAL Patent: US 5776760-A 6 07-JUL-1998;  
FEATURES  
Location/Qualifiers  
1..1296  
source /organism="unknown"

BASE COUNT 286 a 368 c 361 g 281 t  
ORIGIN  
Query Match 97.1%; Score 1255.2; DB 5; Length 1296;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1290; Conservative 0; Mismatches 3; Indels 3; Gaps 3:  
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Db 61 GCGCTGATGCTTTCAGCGCGCGGATTCAAAGTCACTTGTATGACCCGAAACCCCTCTGGC 120  
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Db 121 GAAGTGTGATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGTCCTATGTC 180  
Qy 181 ATGCCGGGAAACTTTCAGCAGGCTGCCGAAGTGGCTTCCTTTCAGCCGAT -GGGCGGTTGTCA 239  
Db 181 ATGCCGGGAAACTTTCAGCAGGCTGCCGAAGTGGCTTCCTTTCAGCCGATGGGCGGTTGTCA 240  
Qy 240 ATCCGGTTCAGCTA -TTTCCAAACCATCATG -CCTGGTGTATTCGCTTTCTGTAGCCGA 297  
Db 241 ATCCGGTTCAGCTA TTTTCCAAACCATCATGCTTTCGCTTTCGCTTTCTGTAGCCGA 300  
Qy 298 AGACCAACAAAGGTGAAGCAGCGAGCAACGACATCCCAATCTCATCAAGTCCACGGTG 357  
Db 301 AGACCAACAAAGGTGAAGCAGCGAGCAACGACATCCCAATCTCATCAAGTCCACGGTG 360  
Qy 358 CCTCTGATCAAGTCAATTCGCGAGGAGGCTCATGCGAGCCCATCTCTGATCCGCCATCAAGGT 417  
Db 361 CCTCTGATCAAGTCAATTCGCGAGGAGGCTCATGCGAGCCCATCTCTGATCCGCCATCAAGGT 420  
Qy 418 CATCTGACCGTATATCTGCTGGAGACGACATTCGCCAAGGACCGCGGAGGTTGGGAATG 477  
Db 421 CATCTGACCGTATATCTGCTGGAGACGACATTCGCCAAGGACCGCGGAGGTTGGGAATG 480  
Qy 478 CGGCTCTCAACGGTGTTCGACGCGAGATCCCTCAGCGCGATGCGTTCGGGATTTTCGAT 537  
Db 481 CGGCTCTCAACGGTGTTCGACGCGAGATCCCTCAGCGCGATGCGTTCGGGATTTTCGAT 540  
Qy 538 CCGAACTTGTCCGATCCGCTTTACCAAGGCGATCTTATAGAAGAGCAACGGTCACACGATTT 597  
Db 541 CCGAACTTGTCCGATCCGCTTTACCAAGGCGATCTTATAGAAGAGCAACGGTCACACGATTT 600  
Qy 598 AATCGCAAGGGCTCGTGACCCCTCTTGTTCGGCGTTTTATCGCGAAGCGGTGGGAAATTC 657  
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Qy 718 ACGAAGCGGCTTCTGGCCGCTTGATCGACGCGTTGTTCGACGCGCGGCGCACACTCGAAATCA 777  
Db 721 ACGAAGCGGCTTCTGGCCGCTTGATCGAGCGGTTGTTCGACGCGCGGCGCACACTCGAAATCA 780  
Qy 778 CTTGCTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC 837  
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Qy 838 ATCGGGAATCCGGAAGCGCTCCACGCAATTCGAGACCGGATGCTCAGGAAATTCATC 897  
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Db 901 GCGACACCTATGGAATGGGGCTTCGCGTGGGGGTACGGTTGAGTTTCGCTGGGCTCACA 960  
Qy 958 GCCGCTCTAACTGGAAACGTCGCGATGTGCTCTATACGACGCTCGGAAACTTCTTCCA 1017



ORGANISM	Unknown: Unclassified.									
REFERENCE	1 (bases 1 to 1296)									
AUTHORS	Barry,G.Francis and Kishore,G.Murthy.									
TITLE	Glyphosate tolerant plants									
JOURNAL	Patent: US 576760-A 7 07-JUL-1998;									
FEATURES	Location/Qualifiers 1..1296									
BASE COUNT	287	a	344	c	332	g	333	t		
ORIGIN	/organism="unknown"									
Query Match	89.8%; Score 1160.8; DB 5; Length 1296;									
Best Local Similarity	95.0%; Pred. No. 0;									
Matches 1231; Conservative	0; Mismatches 62; Indels 3; Gaps									
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Db	1	ATGGCT	GAGAACCA	CAAAAAAGTAGGCAT	CCCTGGAGCTGGGAATCGTTGGTGATATGCAT	60				
Qy	61	CGCGT	GATGCTT	CAGCGCCGCGGATTC	AAAGTCACCTTGATTGACCCGAACCTCTCTGGC	120				
Db	61	GCTTT	GATGCTT	CAACGTCGTGGATT	CAAAAGTCACCTTGATTGACCCGAACCTCTCTGGC	120				
Qy	121	GAAGT	GCATCGTTT	GGGAATGCCGGA	TGCTTCAACGGCTCATCCCTCGTCCCTATGTCC	180				
Db	121	GAAGT	GCATCGTTT	GGGAATGCCGGA	TGCTTCAACGGCTCATCCCTCGTCCCTATGTCC	180				
Qy	181	ATCGCGG	GAACCTTG	ACGACGCGTCCGGA	AGCTGGCTCCTTTGACCCGAT	240				
Db	181	ATCGCGG	GAACCTTG	ACGACGCGTCCGGA	AGCTGGCTCCTTTGACCCGAT	240				
Qy	240	ATCGG	TTTCAGCTA	TCATATG	CTCGTGGTTCATTCGCTTTCTGTAGCGCGA	300				
Db	241	ATCGG	TTTCAGCTA	TCATATG	CTCGTGGTTCATTCGCTTTCTGTAGCGCGA	300				
Qy	298	AGACCA	AACAAAGGTGA	AGGAGCAGGCGA	AAGCACTTCGGCAATCTCATCAAGTCCACGGTG	357				
Db	301	AGACCA	AACAAAGGTGA	AGGAGCAGGCGA	AAGCACTTCGGCAATCTCATCAAGTCCACGGTG	360				
Qy	358	CCCTG	ATCAAGTCAT	TGGCGGAGGAGCGCT	GATCGCAGGCCATCTGATCGCCCATGAAGT	417				
Db	361	CCCTG	ATCAAGTCAT	TGGCGGAGGAGCGCT	GATCGCAGGCCATCTGATCGCCCATGAAGT	420				
Qy	418	CATCT	GACCGGTAT	ATCGTGAGAGCAGAC	CTTCGCCAAGGACCGCGAGGTGTGGGAAGTG	477				
Db	421	CATCT	GACCGGTAT	ATCGTGAGAGCAGAC	CTTCGCCAAGGACCGCGAGGTGTGGGAAGTG	480				
Qy	478	CGGCGT	CTCAACGGTGT	TCCGACGCAGATCCT	CAGCGCCGATCGCTTGGGGATTTTCGAT	537				
Db	481	CGGCGT	CTCAACGGTGT	TCCGACGCAGATCCT	CTCTGCTGATGCTTTGGTGTGATTTTCGAT	540				
Qy	538	CCGAAC	CTTGTTCGGATGCGT	TTTACCAAGGGCATTC	TTTATAGAAGAGAACGGTACACACAT	597				
Db	541	CCTAAC	TTTGTTCGGATGCGT	TTTACCAAGGGCATTC	TTTATAGAAGAGAACGGTACACACAT	600				
Qy	598	AATCCG	CAAGGGTCTGTG	ACCCCTCTGTTTTCGGCGT	TTTTATCCGCAACCGGTGGCGAATTC	657				
Db	601	AATCCG	CAAGGGTCTGTG	ACCCCTCTGTTTTCGGCGT	TTTTATCCGCAACCGGTGGCGAATTC	660				
Qy	658	GTATCT	CGCGCTGT	ATCTCGCT	TTTGAGACTGAAGGTAGGGCGTTTAAAGGCATTTACAACC	717				
Db	661	GTATCT	CGCGCTGT	ATCTCGCT	TTTGAGACTGAAGGTAGGGCTGCTCTCAAGAGGCATTTACAACC	720				
Qy	718	ACGAAC	CGCGCTTCT	TGGCGGTGAT	TGCAGCGCTTTTGTCCGACCCCGCGCACACTCGAAATCA	777				
Db	721	ACTA	ACCGCTGT	TTCTGGCTGT	TGATGCAGCTGTGTGTCAGCTGGTCCACACTCTAAATCA	780				
Qy	778	CTTGC	TAA	TTTCGCTAGCGGAT	AGACATCCCGCTCGATACCGAAGCTGGATATCATATCTGTC	837				
Db	781	CTTGC	TAA	TTTCGCTAGCGGAT	AGACATCCCGCTCGATACCGAAGCTGGATATCATATCTGTC	840				

Qy	838	ATCGCGAATTCGGGAAGCCGCTCCACGCAATTCGAGACACCGATGCGTTCAGGAAAAATTCATC	897
Db	841	ATCGCGAATTCGGGAAGCCGCTCCACGCAATTCGAGACACCGATGCGTTCAGGAAAAATTCATC	900
Qy	898	CGGACACCTATGGAAATGGGGCTTCGCGTGGCGGGTACGGTTGAGTTGCGTGGGCTCACA	957
Db	901	CGGACACCTATGGAAATGGGGCTTCGCGTGGCGGGTACGGTTGAGTTGCGTGGGCTCACA	960
Qy	958	GCCGCTCCTAACTGGAAACGTGGCATGTGCTCTATACGCACGCTCGAAAACTTCTTCCA	1017
Db	961	GCTGCTCCTAACTGGAAACGTGGCATGTGCTCTATACGCACGCTCGAAAACTTCTTCCA	1020
Qy	1018	GCCCTCGCGGCTCGGAGTTCTGAAGAACGATATTCCAAATGGATGGGTTCCGGCCGAGC	1077
Db	1021	GCCCTCGCGGCTCGGAGTTCTGAAGAACGATATTCCAAATGGATGGGTTTCGTCCTAGC	1080
Qy	1078	ATCCCGGATTCGCTCCCGGTATTGGCGCGGGCAACCCGACACCCGACGTAATCTATGCT	1137
Db	1081	ATTCCTGATTCTCTTCAGATGATTTGGTGTGGTAACCTGCTACACCGACGTAATCTATGCT	1140
Qy	1138	TTCCGGCATGCTATCTTCGGCATGACAGGGGGCGCGATGACCGCAACGCTGCTCTCAGAG	1197
Db	1141	TTTGGTCACGGTCATCTCGGTATGACAGGTGCTCCAATGACTGCAACTCTGCTCTCAGAG	1200
Qy	1198	CTCTCGCAGCGGAAAAAGACCTCAATTCGACATTTTCGCCCTTCGCCACCAACCGCTTTGGT	1257
Db	1201	CTCTCGCAGCGGAAAAAGACCTCAATTCGACATTTTCGCCCTTCGCCACCAACCGCTTTGGT	1260
Qy	1258	ATTGGCAAAATCCAAAGCAACGGGTCCGGCAAGTTAA	1293
Db	1261	ATTGGCAAAATCCAAAGCAACGGGTCCGGCAAGTTAA	1296
RESULT 8			
LOCUS	115327	1296 bp	DNA
DEFINITION	Sequence 7 from patent US 5463175.	PAT	02-APR-1996
ACCESSION	115327		
VERSION	115327.1	GI:1250235	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1296)		
AUTHORS	Barry,G.F. and Kishore,G.M.		
TITLE	Glyphosate tolerant plants		
JOURNAL	Patent: US 5463175-A 7 31-OCT-1995;		
FEATURES	Location/Qualifiers		
source	1..1296		
BASE COUNT	287 a 344 c 332 g	333 t	
ORIGIN			
Query Match 89.8%; Score 1160.8; DB 5; Length 1296;			
Best Local Similarity 95.0%; Pred. No. 0;			
Matches 1231; Conservative 0; Mismatches 62; Indels 3; Gaps			
Qy	1	ATGTCTGAGAACACAAAAAGTAGGCATCGCTGGAGCGCGGAATCGTGGCGGTATGCACG	60
Db	1	ATGGCTCAGAACACAAAAAGTAGGCATCGCTGGAGCTTGGGAATCGTTGGTGTATGCAC	60
Qy	61	CGCTGATGCTTACGCGCGCGGATTCAAAGTCACCTTGATTGACCCGCAACCCCTCTCGC	120
Db	61	GCTTTGATGCTTACGCTCGTGGATTCAAGATCACCTTGATTGACCCGCAACCCCTCTCGC	120
Qy	121	GAAGGTGCATCGTTTGGGAATCGCGGATGCTTCAACGGCTCATTCGCTCTGCTATGTCC	180
Db	121	GAAGGTGCATCGTTTGGGAATCGCGGATGCTTCAACGGCTCATTCGCTCTGCTATGTCC	180
Qy	181	ATGCGGGAAACTTGACGAGCGTGCCGAGTGGCTCTTTGACCCGAT-GGGCGGTTGTCA	239
Db	181	ATGCGGGAAACTTGACGAGCGTGCCGAGTGGCTCTTTGACCCGATGGGCGGTTGTCA	240





QY	718	ACGAACGGGGTTCTGGCCGTTGATGACAGGGTTGTGCGACGGCGGCACACTCGAAATCA	777
Db	721	ACCAACGGGTGTTCTTCTGCTGTTGATGACAGCTGTGTGACAGTGGTGCACACTCCAAGTCT	780
QY	778	CTTGCTAATTCCTAGGCGATGACATCCGCTCGATACCGAAGTGGATATATATCGTC	837
Db	781	CTTGCTAATTCCTAGGCGATGACATCCGCTCGATACCGAAGTGGATATATATCGTC	840
QY	838	ATCGGGAATCCGGAAGCCCTCCAGCAATTCGACAGCAGATGCCGTGAGGAAATTCATC	897
Db	841	ATCGGCAACCCAGAGTCTCCAGTATTCCAACTACCGATGCTTCTGGAAGTTTATC	900
QY	898	GGGACACCTATGGAATGGGGTTCGCGTGGGGGTACGGTTGAGTTGCTGGGTGCACA	957
Db	901	GCTACTCCTATGAGATGGGCTTCTGCTGTGCTGGAACCGTTGAGTTGCTGCTCACT	960
QY	958	GGCGCTCCTAACTGGAAAGTGGCGATGCTCTATACGACGCTCGAANAATTTCTTCA	1017
Db	961	GCTGCTCCTAACTGGAAAGTGGCGATGCTCTATACGACGCTCGAANAATTTCTTCA	1020
QY	1018	GCCCTCGCCCTCGAGTTCTGAAGAAGCATATCCAAATGGATGGGTTCCGGCGCAGC	1077
Db	1021	GCTCTCGCTCCTGCCAGTTCTGAAGACGTTACTCCNAGTGGATGGTTTCCGTCACGC	1080
QY	1078	ATCCCGGATTCGCTCCCGTGATTTGGCGGGCAACCGGACACCGACGTAATCTATGCT	1137
Db	1081	ATCCCGAGATTCCTTCCAGTGTATGGTGTGCTACCCGCTACTCCAGACGCTTATCTACGCT	1140
QY	1138	TTTCGCCATGGTCATCTGGCATGACAGGGCGCGGATGACCGACGCTCTCTCAGAG	1197
Db	1141	TTTCGCCATGGTCATCTGGCATGACAGGGCGCGGATGACCGACGCTCTCTCAGAG	1200
QY	1198	CTCCTCGCAGGCGAAAGACCTCAATTCGACATTTCCGCCCTTCGACCAAAACCGCTTGGT	1257
Db	1201	CTCCTCGCAGGTCGAGACCTCTATCGACATCTCTCCATTCGACCAAAACCGCTTGGT	1260
QY	1258	ATTTGGAATCAAGCAACGGGTCGGGCAAGTTAA	1293
Db	1261	ATTTGGAATCAAGCAACGGTCTGTCATCTAA	1296
RESULT 10			
115328			
LOCUS	115328	1296 bp	DNA
DEFINITION	Sequence 8 from patent US 5463175.	PAT	02-APR-1996
ACCESSION	115328		
VERSION	115328.1	GI:1250236	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1296)		
AUTHORS	Barry.G.F. and Kishore.G.M.		
TITLE	Glyphosate tolerant plants		
JOURNAL	Patent: US 5463175-A 8 31-OCT-1995;		
FEATURES	Location/Qualifiers		
source	1..1296		
BASE COUNT	271 a 359 c 305 g 361 t		
ORIGIN			
Query Match 71.8%; Score 928.8; DB 5; Length 1296;			
Best Local Similarity 83.8%; Pred. No. 3e-244;			
Matches 1086; Conservative 0; Mismatches 207; Indels 3; Gaps 3;			
QY	1	ATGCTGAGAACCAAAANAGTAGCATCGCTGGAGCGGAATCGTGGCGCTATGACAG	60
Db	1	ATGGCTGAGAACCAAGGATGGTATCGCTGGAGTGGAAATCGTTGGTGTGTCAC	60
QY	61	GGCTGTAGCTTCAGGCGCGCGATTCAGAGTCACCTTGATTGACCCGCAACCCCTCTGGC	120

Db	61	GCTTGTGATGCTTCAACGCTGGATTCAGAGTTTACCTTGATTGATCCAAACCCACAGGT	120
QY	121	GAAGTGTGATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCGTCTGCTCCCTATGTCC	180
Db	121	GAAGTGTGCTTCTTTCGGTAACCGTGGTTCCTTCAACGGTTCCTCCGTTGTTCCAATGTCC	180
QY	181	ATGCGGGGAAATTCGACGAGCGTCCGGAAGTGGCTCTTTGACCCGATGGG - CCGTTGTCA	239
Db	181	ATGCGGAGGAAATTCGACAGCGTCCAAAGTGGCTCTTTGACCCCAATGGGTTCATTTGTCC	240
QY	240	ATCCCGTTCAGCTA - TTTCCCAACCATCATGCC - TGGTTGATTTCCGCTTCTGTGTACCCGA	297
Db	241	ATCCCGTTCAGCTACTTTCCCAACCATCATGCCCTGGTTGATTTGCTTCTTGTGCTGA	300
QY	298	AGACAAACAAAGGTGAAGGAGCAGCGCAAGACACTTCGCAATCTCATCAAGTCCACGGTG	357
Db	301	AGACAAACAAAGGTGAAGGAGCAAGCTAAGGCACCTCCGTTAACTCATCAAGTCCACTGTG	360
QY	358	CCTCTGATCAAGTCATTTGGCGAGGAGGCTGATGGAGGCCATCTGATCCGCCCATGAAGGT	417
Db	361	CCTTTGATCAAGTCTTGGCTGAGGAGGCTGATGGTACCCACTTATCCGTCACGAAGGT	420
QY	418	CATCTGACCGTATATCGTGGAGAACGACACTTCGCAAGGACCGCGGAGGTGGGAACIG	477
Db	421	CACCTTACCGTGTACCGTGGAGAACGACACTTCGCCAAGGACCGTGGAGGTGGGAACIT	480
QY	478	CGCGCTCTCAACGGTGTTCGCACGAGATCTTCAGCGCGGATCGCTTGGGGATTTCCGAT	537
Db	481	CGTCTGCTCAACGGTGTTCGTACTCAAACTCTCAGCGCTGATGCTTGGCTGATTTCCGAT	540
QY	538	CCGAATCTGTTCGATCGGTTTACCAGGGCATCTTTATAGAAGAACGGTCAACAGATT	597
Db	541	CCTAACTTGTCTCACCGCTTTTACCAAGGGAATCTTTATCGAAGAGAACGGTCAACCAATC	600
QY	598	AATCCGCAAGGCTCGTGACCCCTCTTGTTCGGCGCTTTTATCGCAAGCGTTCGCGAATTC	657
Db	601	AACCCACAGGCTCGTGACTCTCTTGTTCGTCTTCTATCGCTAACGGTGGAGAGTTC	660
QY	658	GTATCTGCGCTGTCTATCGGCTTTTGAGACTGAAGGTAGGGCGCTTAAAGGCAATACAAAC	717
Db	661	GTGCTGCTCGTGTATTCGGATTCGAGACTGAAGGTTCGCTCTCAAGGGTATCACCAACC	720
QY	718	ACGAACGGGTTCTGGCGCTTGTGATGAGCGGTTGTGCGACGCGCGGCACACTCGAATCA	777
Db	721	ACCAACGGTGTTCCTGCTGTTGATGACAGCTGTGTTCGACGCTGGTCCACACTCCAAGTCT	780
QY	778	CTTGCTAATTCGCTAGGCGATGACATCCGCTCGATACCGAAGCTGGATATCATATCGTC	837
Db	781	CTTGCTAATTCGCTAGGCGATGACATCCCATTTGGATACCGAAGCTGGATACCAATCGTG	840
QY	838	ATCGGCAATCCGGAAGCCGCTCCAGCGATTCGAGACGCGATCGCTCAGGAAATTCATC	897
Db	841	ATCGCAACCCAGAGCTCTCCACGTATTCCAACTACCGATGCTTCTCGGAAAGTTTATC	900
QY	898	GGGACACCTATGGAATGGGGTTCGCGTGGGGGTACGGTTGAGTTGCTGGGTGCACA	957
Db	901	GCTACTCCTATGAGATGGGTTCTGCTGTGCTGGAACCGTTGAGTTGCTGCTCACT	960
QY	958	GGCGTCTCTAACTGGAACGTCGCGATGCTCTATACGACGCTCGGAAACCTCTCTTCA	1017
Db	961	GCTGCTCCTAACTGGAAAGTGGCGATGCTCTATACGACGCTCGGAAATTTCTTCA	1020
QY	1018	GCCCTCGCCCTCGAGTTCTGAAGAAGCATATTCCAATGGATGGGTTCCGGCGCAGC	1077
Db	1021	GCTCTCGCTCCTGCCAGTTCTCAAGAACGTTACTCCAAGTGGATGGGTTTCCGTCCAAC	1080
QY	1078	ATCCCGGATTCGCTCCCGTGATTTGGCGGGCAACCGGACACCGACGTAATCTATGCT	1137
Db	1081	ATCCCGAGATTCCTTCCAGTGTATGGTGTGCTGCTACCCGCTACTCCAGACGCTTATCTACGCT	1140
QY	1138	TTTCGCCATGGTCATCTGGCATGACAGGGCGCGGATGACCGACGCTCTCTCAGAG	1197
Db	1141	TTTCGCCATGGTCATCTGGCATGACAGGGCGCGGATGACCGACGCTCTCTCTGAG	1200



Best Local Similarity 83.68; Pred. No. 2.3e-243;			
Matches 1084; Conservative 0; Mismatches 209; Indels 3; Gaps 3;			
Qy	1	ATGCTGAGAACCAACAAAAATAGGCATCGCTGGAGCGGAATCGTCGGCGGTATGACAG	60
Db	1	ATGCTGAGAACCAACAAAGTTGGTATCGCTGGAGCTGGAACTGTTGGTGTTCGACT	60
Qy	61	CGCTGTATGCTTTACAGCGCGGGGATTCAAAGTTCACCTTTGATTTGACCCGAACCCCTCTGGC	120
Db	61	GCTTTGATGCTTTACAGCTCGTGATTCAAAGTTTACCTTTGATTTGATTCACCAACACCAAGT	120
Qy	121	GAAGTGCTATGTTTGGGAATCCGGATGCTTCAACGGCTCATCCGTGTCCTATGTC	180
Db	121	GAAGTGCTCTTTTCGGTAACCGTGTGCTTCAACGGTTCCTCGTTGTTCCTAATGTC	180
Qy	181	ATCGCGGAAACTTTCAGCAGGGCTGCGGAAGTGGCTTCCTGACCCGATGGG-CCGTTGTCA	239
Db	181	ATGCCAGAACTTTCAGCTAGGCTTCCAAGTGGCTTCTTGACCCCAATCGGTCCTATGTC	240
Qy	240	ATCGGTTTCAGCTA-TTTTCCAACCATCATGCG-FTGGTTGATTCGGCTTTCTGTAGCCGGA	297
Db	241	ATCGGTTTCGGCTACTTTTCCAACCATCATGCTTGGTTGATTCGTTTCTTGTCTGCTGA	300
Qy	298	AGACCAACAGCTGAAGGACGCGGCAAGCACTCCGCAATCTCATCAAGTCCACGGTG	357
Db	301	AGACCAACAGGTCAGGAGCAAGCTTAAGGCATTCGGTAACCTCATCAAGTCCACTGTG	360
Qy	358	CCTGTATCAAGTTCATTCGGCGGAGGCTGATGCGAGCCATCTGATCCGCCATCAAGGT	417
Db	361	CCTTTGATCAAGTCTTTGGCTGAGGAGCTGATGCTAGCCACTTATCCGTCACGAAGT	420
Qy	418	CATCTGACCGTATATCGTGGAGAACAGACATTCGCCAAGAGCCGCGAGTGGGAACGTG	477
Db	421	CACCTTACCCTGATACCGTGGAGAGACACTTCGCCAGGACCGGTGGAGTTGGGAACCT	480
Qy	478	CGCGCTCTCAACGGTTTCGACAGCAGATCCTCAGCGCCGATGCGTTCCGGGATTTCCAT	537
Db	481	CGTCTCTCAACGGTTTCGTACTCAAACTCTCAGCGCTGATGCAATTCGCTGATTTCCAT	540
Qy	538	CCGAACCTTTCGCTATCGCTTTTACCAAGGCAATCTTATAGAAGAACCGGTACACAGATT	597
Db	541	CCTAACTGTCTACGCGCTTTTACCAAGGAATCTTATCGAAGAACCGGTACACCAATC	600
Qy	598	AAATCCGAAGGCTCGTGACCCCTCTTGTTCGGGCTTTTATCGCGAACCGTGGCGAATTC	657
Db	601	AACCCACAAGTCTCGTGACTCTCTTGTTCGTCTTTCATCGCTTAACCGTGGAGAGTTC	660
Qy	658	GTATCTGCGCGTGTATCAGCGCTTTTGAGACTCAAGAGTAGGGCGCTTAAAGGCATTCACAC	717
Db	661	GTGTCTGCTGTGTATCGGATTCGGAATTCGAGACTCAAGGTCCTGCTCTCAAGGGATCACACC	720
Qy	718	ACGAAGCGGCTTTCGGCGGTTGATGACAGGTTGTGCGACGCGCGGCACACTTCGAANATCA	777
Db	721	ACCAAGCGGTCTTTCGTGTTGATGCAGCTGTGTTGACGCTGGTGGCACACTTCCAAGTCT	780
Qy	778	CTTGCTAAATTCGCTAGCGCATGACATCCCGCTCGATACCGAACCTGGATATCATATCGTC	837
Db	781	CTTGCTAACTCCCTTGGTGATGACATCCCATTTGGATACCGAACCTGGATACCATCTGCG	840
Qy	838	ATCGGGAATCCGGAAGCCGCTCCACGCAATCCGACGACCGATGGCTCAGGAAAAATTCATC	897
Db	841	ATCGCAACCCAGAGCTGCTCCACGATATTCCAACTACCGATGCTTCTTGGAAAGTTCATC	900
Qy	898	CGCACACCTATGGAATGGGGCTTCGCGTGGGGTACGGTTGAGTTGCTCGCTGGGCTCAC	957
Db	901	GCTACTCTCATGGAGATGGGTCTTCGTGTTGCTGGAACCGTTGAGTTGCTGGTCTCACT	960
Qy	958	CGCGCTCTTAATCGGAACGCTCGCATGTGCTCTATACGCAACGCTTCGAAAACTTCTTCCA	1017
Db	961	GCTGCTCTTAATCGGAACGCTGCTCACGTTCTCTACACTCGCGCTCGTTAAGTTGCTTCCA	1020
Qy	1018	CCCCTCGCGCTGCGAGTTCTTGAAGAACGATATTCCAAAATGGATGGGTTCCGGCCGAGC	1077

Db	634	CCGTAACCTCATCAAGTCCACCTGTGCTTTGATCAAGTCCCTGGCTGAGGAGCTGATGCG	693
Qy	393	CAGCCATCTGATCGCCATGAAGGTCACTCGACCTATATCGTGGAGAGCAGACTTCGCG	452
Db	694	TAGCCACCTTATCGGTACAGAGGTCACTTACCGTGTACCGTGGAGAGCAGACTTCGCG	753
Qy	453	CAAGGACCGGAGGTTGGGAACCTCGCGCTCAACCGGTGTTCGACGCGAGATCCTCAG	512
Db	754	CAAGACCGTGGAGTTGGGAACCTCGCTGCTCAACCGTGTTCGTAACAATCCTCAG	813
Qy	513	CGCGATCGGTTGGGGATTTTCGATCCGAACCTTGTGCGATCGGTTTACCAAGGCAATCT	572
Db	814	CGCTGATGCATTTGGTGATTTTCGATCCTTAACCTGTCTCACGCCCTTACCAAGGAAATCCT	873
Qy	573	TATGAACAGAACCGGTTCACAGATTAATCCGCAAGGGTCTGTGACCCCTCTTTGTTGGCG	632
Db	874	TATGAAGAGAACCGGTTCACACCATCAACCCACAGGTCCTGTGACTCTTGTGTCGTCG	933
Qy	633	TTTTATCGGAACCGTGGCGAATTTCGTATCTGCGGTGTCTATCGCTTGGACTTGAAGG	692
Db	934	TTTCATCGCTAACGGTGGAGAGTTCGTCTGCTGCTGTTATCGGATTCGAGACTGAAGG	993
Qy	693	TAGGCGCTTAAGGCATTACACCAACGAGCGGTTCTGCGCGTTGATG-----	742
Db	994	TCGTGCTCTCAAGGGTATCACACACCAACCGGTGTTCTGCTGTGATGCTGCAGTGTT	1053
Qy	743	-----CAGCGTGTTCGCGAGCGCGGCACACTCGAAATCACTTGTCTAAT	787
Db	1054	GTGAATTCAGCTTACTGCACTTGTTCGAGCTGGTGCACACTCCNACTCTTGTCTAAT	1113
Qy	788	CGTAGGCGATGACATCCCGTTCGATACCGAACGTGGATATCATATCGTCATCGGAATC	847
Db	1114	CCCTTGGTGATGACATCCCATTTGATACCGAACGTGGATACCACTGTCATCGCAACC	1173
Qy	848	CGGAAGCGCTCCACGCATTCGAGGACCGATCGGTACGGAATATTCATCGGACACCTA	907
Db	1174	CAGAAGCTGCTCCACGATATCCAACTACCGATGCTTCTGGAAGTTTCATCGTACTCCTA	1233
Qy	908	TGGAATGGCGTTTCGCGTGGCGGTACGGTTGAGTTGCTGGCTGAGCTCACAGCGCTCCTA	967
Db	1234	TGGAGATGGGTCTTCGTGTTGCTGGAACCGTTGAGTTGCTGGTCTACTGCTCTCCTA	1293
Qy	968	ACTGGAACGTGGCGATGCTCTATAGCACGCTCGAATACTTTCACGCCCTCGCGC	1027
Db	1294	ACTGGAACGTGGCTACCTCTCTACACTCGTCTGCTGTAAGTTGCTCCAGCTCTCGCTC	1353
Qy	1028	CTGCGAGTTCTGAGAACGATATTCGAAATGATGGGTTCGCGCGGAGCATCCCGAAT	1087
Db	1354	CTGCCAGTTCTGAGAACGTTTACTCCAAAGTGGATGGGTTCGCTCCCAAGCATCCAGAT	1413
Qy	1088	CGCTCCCGCTGATTTGGCGGGCAACCGCGACACCGAGCTAATCTATGCTTTTCGGCCATG	1147
Db	1414	CCCTTCCAGTATTTGGTGTGCTACTACCGCTACTCCAGAGTTATCTACGCTTCGCTCAG	1473
Qy	1148	GTATCTCGGCATGACAGGGCGCGATGACCGCAACGCTCGTCTCAGAGCTCTCGCAG	1207
Db	1474	GTACACTCGGTATGACTGGTGTCTCCAATGACCGCAACCCCTGTTCTGAGCTCTCGCAG	1533
Qy	1208	GCAGAAAGACCTCAATCGACATTTTCGCCCTTCGCACCAACCCGCTTTGGTATTGGCAAT	1267
Db	1534	GTGAGAAGACCTCTATCGACATCTCTCCATTCGCACCAACCCGTTTCGGTATTGGTAAGT	1593
Qy	1268	CCAAGCAACCGGTTCGCGCAAGTTAA	1293
Db	1594	CCAAGCAACCGGTTCCTGCATCTTAA	1619

RESULT 14  
PSEAKSD  
LOCUS  
DEFINITION  
Pseudomonas putida alpha-ketoglutarate semialdehyde dehydrogenase  
gene, complete cds.

ACCESSION	M69158
VERSION	M69158.1
KEYWORDS	GI:150981
SOURCE	ketoglutarate semialdehyde dehydrogenase.
ORGANISM	Pseudomonas putida DNA.
REFERENCE	Pseudomonas putida
AUTHORS	Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group; Pseudomonas.
TITLE	1 (bases 1 to 3430)
JOURNAL	Burlingame, R.P., Maruya, A., Ally, A.H., Ally, D. and Backman, K.C.
FEATURES	Nucleotide sequences of hydroxyproline-specific alpha-ketoglutarate semialdehyde dehydrogenase genes from two strains of pseudomonas putida
Location/Qualifiers	Unpublished (1991)
source	1..3430
gene	/organism="Pseudomonas putida"
CDS	/db_xref="taxon:303"
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	/db_xref="GI:150982"
	/translation="MTLTGYMLIGQTPVTGSREAIRAIDPATGQPLPAYLGGTGEHV
	AOACALAAAFADGVRRTTLEORAQFLETATQIALGDALIDRAVESGLPKARIQGE
	RGRTCTOLRTFARVVRAGENLDVVDNAQPERQPLPRADLRQROVALGVPVAFGASNF
	PLAFVAGGDTASALAAGCPVVKAAHSPGTSELVQVAQVAQVACGLGPAVFSLLY
	GSQREVGIALVSDPRIKAVGTGSRGGIALCQNTAQRPEPIPVYAAEMSHVROAAQT
	AALQARAELAQGFVASTGAGQCFCTNPGLVAPQCPALQRFIDAAEMSHVROAAQT
	MLTPGIFSAVQAGVGLAGNAAQAAAGGCGPNCQQAQLFVTOAEAFADPALQA
	EVGGAASLVACASDEOVHQAHLGQLTATLQDDADIDRALLLPTLERKAGRIL
	VNSHPTGVEVCDAMVHGGPPPTSDARTT"SVGTAAILRFLRPVCYQDFPNALLPQALQ
	HGNPLQURLLDDGRREG"
BASE COUNT	562 a 1140 c 1157 g 571 t
ORIGIN	

Query Match	6.5%	Score	84.2	DB 2	Length	3430
Best Local Similarity	46.2%	Pred. No.	2.7e-12			
Matches	537	Conservative	0	Mismatches	608	
				Indels	18	Gaps
Qy	23	TAGGCATCGCTGGAGCGGGAATCGTGGCGCTATGCACGCGCTGATGCTTCAGCGCCGCG	82			
Db	2208	TCGCGCTGGTGGCGCGCGGATTTGTCGCGCTTGCTGTGCGCTCGCACTGCCGCCGAG	2267			
Qy	83	GATTCAAAGTCACCTTGATGACCCGAACCTCTCTGGCGAAGGTGCATCGTTTGGGAATG	142			
Db	2268	CCCTCCGGGTGCTATTTGTCGACGCGCCAGGACCGCGCAATGGGCGTCTTATGCAACG	2327			
Qy	143	CCGATGCTTCAACGGCTCATCCGCTCGCTCCCTATGCTCCATCCCGGGAACCTGACGAGCG	202			
Db	2328	CCGGGACCTGGCCACCGAGGAGTGTTCGCGATGGCGACCTGTCGATCTCAAGCGCT	2387			
Qy	203	TGCGCAAGTGCCTCTTGACCCGATGGGC---CGTTGTCAATCCGGTTTCAGCTATTTC	259			
Db	2388	TGCCGCGCATCTCTGGACCCGATGGCCCACTGCCGCTGGAGTACCTTGCCCA	2447			
Qy	260	ACCATCATGCTGTTGATTCGCTTCTGTTAGCGCGAAGACCAACAAAGGTGAAGGAGC	319			
Db	2448	CGGCGATGCCCTGGTTTACCGCGCTGCTGCTCAACCTGCGCGCGCGCTTCCAGCGCA	2507			
Qy	320	AGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTGCCTCTGATCAAGTCAATTGGCGG	379			
Db	2508	GTGTGGCGGATCCGCACGCTGAACGAGCGCTGGGTGTCATGGAGCGCGCTGCTGG	2567			
Qy	380	AGGAGGCTGATGCGAGCGCATCTGATCCGCCATGAAGGTCACTCGACCTATATCGTGGAG	439			
Db	2568	GCTCGATCGGCGCGGACGACCTGTTCAGGAGGATGGTTCGTTCTGCTGTGT-TCGAGAG	2626			
Qy	440	AAGCAGACTTCGCCCAAGACCGCGGAGGTTGGGAACATGCG-GGCGTCTCAACGCGTGTTCGC	498			

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Db 2627 CCTGAGTCACCCAGCCGACTGAGCGTTGCGCCACCGCATGCAACACAGCGCGTGCCG 2686
Qy 499 ACGCAGATCCTCAGCGCGATCGCTTGGGGATTTTCGATCGAACTTGTGCGCATCGTTT 558
Db 2687 GTGGAGCTCTGTCGCGCGCAAACTGCGCGAGGAGCGCGCACTGAGCCCGTCACTG 2746
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Qy 979 GCGCATGCTCTATACCGACGCTCGAAACTTCTTCCAGGCTTCGCGCTCGCGAGTCT 1038
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RESULT 15

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PSEKSDA
LOCUS PSEKSDA 2289 bp DNA BCT 26-APR-1993
DEFINITION Pseudomonas putida alpha-ketoglutarate semialdehyde dehydrogenase
gene, complete cds.
ACCESSION M69159
VERSION M69159.1 GI:151317
KEYWORDS ketoglutarate semialdehyde dehydrogenase.
SOURCE Pseudomonas putida (strain ATCC 12633) DNA.
ORGANISM Pseudomonas putida
Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
Pseudomonas.
REFERENCE 1 (bases 1 to 2289)
AUTHORS Burlingame,R.P., Maruya,A., Ally,A.H., Ally,D. and Backman,K.C.
TITLE Nucleotide sequences of hydroxyproline-specific alpha-ketoglutarate
semialdehyde dehydrogenase genes from two strains of pseudomonas
putida
JOURNAL Unpublished (1991)
FEATURES Location/Qualifiers
source 1..2289
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BASE COUNT 378 a 766 c 734 g 411 t
ORIGIN

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Query Match 4.8%; Score 61.8; DB 2; Length 2289;
Best Local Similarity 54.7%; Pred. No. 3.9e-06;
Matches 123; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
Qy 8 AGAACCAACAAAAAGTAGGCATCGCTGGAGCGCGGAATCGTGGCGGTATGCACGCGCGCTGA 67
Db 1732 ACAATCGCCACGACATAACCCCTCATCGCGCGCGGAATCATCGCGCTCGCCGCGCTGC 1791
Qy 68 TGCCTTCAGCGCGCGGATTCAAAAGTCACCTTGATTGACCCGGAACCCCTCCTGGCGAAGGTG 127
Db 1792 AACTGGCGCGCTGGCGCTGCGGCTGACGGTCTGACGAGAGAGAGAGAGAGAGAGAGAG 1851
Qy 128 CATCGTTTGGGAATCCGGATGCTTCAACGGCTCATCGCTCGTCCCTATGTCCTATGCCCGG 187
Db 1852 CTCCTGTCGGCAATCGCGGATCTGCGGACGCGAGCAGGTGTTCCCATCGCGGATTTGT 1911
Qy 188 GAAACTTTCAGCAGCGTTCGCGAAGTGGCTTCCTTGACCCCATGGGC 232
Db 1912 CGATCTGAAACGCTTGCCCTGCCATGCTCATGACCCCATGGGC 1956

```

Search completed: January 1, 2001, 03:14:54  
Job time: 29178 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2000, 22:06:32 ; Search time 263.11 Seconds  
(without alignments)  
1846.117 Million cell updates/sec

Title: US-08-484-274-4  
Perfect score: 1293  
Sequence: 1 ATGCTGAGACCAACAAAA.....AAACGGGTCCGGCAAGTTAA 1293

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 18781343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1289.8	99.8	1689	13 Q20832	Glyphosate oxidoreductase
2	1256.8	97.2	1692	13 Q22705	Glyphosate oxidoreductase
3	1253.6	97.0	1321	13 Q20833	Manipulated glyphosate
4	1159.2	89.7	1321	13 Q20834	Modified glyphosate
5	928.8	71.8	1296	13 Q20835	Synthetic glyphosate
6	928.8	71.8	8418	20 X57309	Sugar beet T-DNA c
7	857.6	66.3	1631	18 T85664	CPT1-GOX gene fusi
8	641.8	49.6	8798	20 X57308	Sugar beet T-DNA c
9	640.2	49.5	8012	20 X57305	Sugar beet T-DNA c
c 10	35.4	2.7	534720	19 V30458	Rhizobium species
c 11	35.4	2.7	536165	19 V30459	Rhizobium species
c 12	34	2.6	405	20 X98168	Nucleotide sequenc

c 13	34	2.6	603	20 X98167	Nucleotide sequenc
c 14	34	2.6	1137	20 X98164	Nucleotide sequenc
c 15	34	2.6	42235	20 X98035	Nucleotide sequenc
c 16	33	2.6	2241	21 Z51469	Vector pVgXR-enco
c 17	33	2.6	2295	21 Z51470	Vector pVgXR-5A/5
c 18	33	2.6	2301	21 Z51471	Control vector pVg
c 19	33	2.6	2455	21 Z45836	cDNA of intestinal
c 20	33	2.6	2821	21 Z45837	cDNA of intestinal
c 21	32.8	2.5	1140	20 X36611	Pseudomonas oxidat
c 22	32.6	2.5	534720	19 V30458	Rhizobium species
c 23	32.6	2.5	536165	19 V30459	Rhizobium species
c 24	32.4	2.5	922	19 V15073	Hybrid DNA compris
c 25	31.4	2.4	1436	11 Q03319	cDNA of Elmeria te
c 26	31.4	2.4	1755	19 V03306	Bacterium OC9a pho
c 27	31.4	2.4	2241	18 V06244	Modified ecdysone
c 28	31.4	2.4	2970	14 Q37556	DHR23alpha cDNA cl
c 29	31.4	2.4	5534	12 Q13574	Eck gene, drosoph
c 30	31.2	2.4	1116	20 X81700	DNA encoding a fru
c 31	31.2	2.4	3358	20 V70229	Human receptor tyr
c 32	31.2	2.4	35099	19 V27112	Adenovirus 17. Ma
c 33	31	2.4	1531	18 T46195	Maize insecticidal
c 34	31	2.4	5059	20 X84332	Stealth virus nucl
c 35	30.8	2.4	611	21 Z80753	Human colon cancer
c 36	30.8	2.4	1800	20 X56121	HIV-1 Group M env
c 37	30.8	2.4	34094	20 Z30163	Complete nucleotid
c 38	30.6	2.4	1321	13 Q20834	Modified glyphosat
c 39	30.4	2.4	1113	21 Z58692	Pseudomonas PROC p
c 40	30.4	2.4	3747	19 V05714	Maize retinoblasto
c 41	30.4	2.4	3747	19 V17081	Maize retinoblasto
c 42	30.2	2.3	1359	21 Z53148	Neisseria gonorrhoe
c 43	30.2	2.3	1359	21 Z53150	Neisseria meningit
c 44	30.2	2.3	2880	17 T15599	Laccase-LCC2 gene.
c 45	30	2.3	624	16 T02335	Human proteasome s

ALIGNMENTS

RESULT 1	
Q20832	
ID Q20832 standard; DNA; 1689 BP.	
XX	
AC Q20832;	
XX	
DT 01-MAY-1992 (first entry)	
XX	
DE Glyphosate oxidoreductase gene.	
XX	
KW Recombinant; GOR; resistance; ss.	
XX	
OS Bacterial isolate LBAA.	
XX	
FH Key Location/Qualifiers	
FT CDS 120..1412	
FT	/tag= a
FT	/note= "glyphosate oxidoreductase coding region"
FT misc_feature 349..350	
FT	/tag= b
FT	/note= "in the alternative sequence G is present here"
FT misc_feature 375..376	
FT	/tag= c
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FT misc_feature 389..390	
FT	/tag= d
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PN W09200377-A.	
XX	
PD 09-JAN-1992.	
XX	
PD 24-JUN-1991; 91WO-US04514.	
XX	
PD 24-JUN-1991; 91US-0717370.	















```
ID T85664 standard: DNA; 1631 BP.
XX
XX T85664;
XX
XX 21-NOV-1997 (first entry)
XX
XX CPT1-GOX gene fusion.
DE
XX
XX expression cassette; inducible promoter; alca; alcR; aldA; regulator;
KW alcohol dehydrogenase; herbicide resistance gene; glyphosate;
KW N-phosphonomethyl-L-glycine; glyphosate oxidase; GOX; EPSPS;
KW 5-enol-pyruvylshikimate 3-phosphate CP4; monocotyledon; crop; ss.
KW Arabidopsis; RUBISCO; CPT1; dicotyledon; chloroplast transit sequence 1;
XX
XX Chimeric Arabidopsis.
OS Synthetic.
OS
OS W09706269-A1.
PN
PN
XX 20-FEB-1997.
XX
XX 02-AUG-1996; 96WO-GB01883.
XX
XX 03-AUG-1995; 95GB-0015941.
PR
XX (ZONE ) ZENECA LTD.
PA
XX
XX Jenson I;
PI
XX
XX WPI; 1997-154273/14.
DR
XX
XX Chemically inducible cassette for expressing herbicide resistance
PT gene in plants - and derived plants, partic. for resistance to
PT glyphosate, avoids constitutive expression and minimises development
PT of herbicide tolerant weeds
XX
XX Example 3; Fig 7; 59pp; English.
PS
XX
XX A chemically inducible plant gene expression cassette which comprises an
CC inducible promoter linked to a gene (I) that confers resistance to a
CC herbicide, is claimed. (I) imparts resistance to N-phosphonomethyl-
CC glycine (glyphosate) or its salts, but may also be a gene for resistance
CC to, e.g. chloroacetanilides, glufosinate, sulphonyl ureas, imidazolinones,
CC etc. The inducible promoter (e.g. alcA, alcR, aldA or other alcR-induced
CC gene promoter) is operatively linked to an alcR regulator sequence.
CC Induced expression of (I) avoids the risk that constitutive expression
CC may interfere with plant development; allows volunteer plants to be
CC controlled by herbicide applied without inducer and minimises the chance
CC that herbicide-resistant strains of weeds will arise. The expression
CC cassette is strictly controlled and suitable for general use in plants
CC (both mono- and dicotyledons). The alcA/alcR gene switch was exemplified
CC with genes conferring resistance to glyphosate. The switch was used to
CC drive inducible expression of glyphosate oxidase (GOX) in plants.
CC Switchable GOX was expressed alone or in conjunction with constitutive
CC expression of 5-enol-pyruvylshikimate 3-phosphate (EPSPS) CP4. Constructs
CC were optimised for expression in mono- and dicotyledonous crop species.
CC The present sequence comprises a fusion of the GOX gene fused to the
CC chloroplast transit sequence 1 from Arabidopsis RUBISCO (CPT1). This
CC sequence was ligated into pWJb1 (see T85666) and used in construction of
CC dicot vectors.
XX
XX Sequence 1631 BP; 342 A; 454 C; 381 G; 454 T; 0 other;
SQ

Query Match 66.3%; Score 857.6; DB 18; Length 1631;
Best Local Similarity 80.2%; Pred. No. 7.3e-265;
Matches 1079; Conservative 0; Mismatches 214; Indels 53; Gaps 4;

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Db 274 atggctgagaacacaagaagttggtatcgctggagctggaatcggtgtgttgacct 333
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GCCTGTATGCTTCAGCGCCCGGGATTCAAAGTCACCTTGATTGACCCGAAACCTCCTGGC 120
```

```
Db 334 gctttgatgttcaacgctcgtggattcaaggttaccttgattgatccaaacccaccaggt 393
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QY 121 GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCCTCATGTCC 180
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Db 394 gaaggtgtctctcttcgtaaacgctgggttgcttcaacggttctctcgttgttccaatgtcc 453
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Db 514 ttacgagtcctcaatgggtccatgtccatcctgttcagctactttccaaacctatgccttg 573
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 273 GTTCATTCGCTTCTGTAGCCGGAAGACCAACAAGGTGAAGAGGAGGAGCGAAGCACT 332
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Db 1414 cccctccagtgattggtcgctaccccglaclcccaagagcgtttatctacagcttccggtcaag 1473

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Db 1474 gtccctcgggtatgactggtgctccaatgacgcgcaaccctcggtttctgagctccctgcag 1533

Qy 1208 GCGNAAGACCTCAATCGACATTTCCGCCCTTCGCACCAACCGCTTTGGTATTGGCAAT 1267

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Qy 1268 CCAACCAACCGGTCGGCAAGTTAA 1293

Db 1594 ccaagcaactggtcgtcatctctaa 1619

RESULT 8

X57308

ID X57308 standard; DNA: 8798 BP.

AC X57308;

XX

DT 26-JUL-1999 (first entry)

DE Sugar beet T-DNA containing cp4/epsps.

XX

KW Sugar beet; transformation; T-DNA; Insertion; cp4/epsps; plant;

KW 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide;

KW tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.

OS Beta vulgaris.

XX

PN WO9292322-A1.

XX

PD 14-MAY-1999.

XX

PP 29-OCT-1998; 98WO-EP06859.

XX

PR 31-OCT-1997; 97US-0112003.

XX

PA (NOVS ) NOVARTIS AG.

PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.

PI Mannerloef M, Steen P, Tenning PP;

XX

DR WPI; 1999-313347/26.

XX

PT Glyphosate resistant transgenic sugar beet plants

XX

PS Claim 11; Page 31-36; 55pp; English.

XX

CC This invention describes a novel sugar beet plant, including its

CC descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase

CC (cp4/epsps) enzyme activity which is obtainable by Agrobacterium

CC mediated transformation with a gene allowing expression of cp4/epsps

CC in plants, where the plant lacks both right and left T-DNA border

CC sequences. The transgenic sugar beet plants of the invention are capable

CC of tolerating herbicide treatment with glyphosate (also known as

CC N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.

XX

SQ Sequence 8798 BP; 2346 A; 1999 C; 2032 G; 2421 T; 0 other;

Query Match 49.6%; Score 641.8; DB 20; Length 8798;

Best Local Similarity 83.2%; Pred. NO. 2.5e-195;

Matches 766; Conservative 0; Mismatches 152; Indels 3; Gaps 3;

Qy 1 ATGCTGAGAACCAAAAAGTAGGATCGCTGGAGCGGAGNATCGTCGGCGTATGCAGG 60

Db 7205 atggctgagaacacaagaagttggtatcgtcgagctggaatcgttgggtttgcact 7264

Qy 61 GCGCTGATCTACGCGCGGGATTCAAAGTCAACCTTGATTCACCGCAACCTCCTGGC 120

Db 7265 gctttgatgcttcaacgctcgtaggttcaaggttaccttgattgattccaaacccaccaggt 7324

Qy 121 GAAGGTGCATCGCTTTGGGAATCCCGGATGCTTTCAACGGCTCATCGTCCCTATGTCC 180

Db 7325 gaaggtgcttcttcggttaacgctggttgctccaacggttctcctcggttgctccaatgtcc 7384

Qy 181 ATGCGGGGAAACTTACGAGCGGTGCGGAAGTGGCTTCCTTGACCCCGATGGG-CCGTTGTCA 239

Db 7385 atgcaggaacttgactlagedttccaaagtggctcttgaaccaatgggtccattgtcc 7444

Qy 240 ATCCCGTTTCAGCTA-TTTTCCAAACCATCATGCGC-TGGTTGATTTTCGTTTTCGTAGCCGA 297

Db 7445 atccgcttcagctacttcccaaccatcatgcttgggttgattcgttcttgccttgcctgga 7504

Qy 298 AGACCAACAAAGGTGAAGAGCAGCGCAAAACACCTCCGCAATCTCATCAAGTCCACGGTG 357

Db 7505 agaccaacaaggtgaaggagcaagtaagcactcctgaactcctcaagtcacactgtg 7564

Qy 358 CCTCTGATCAAGTCAATGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAGGT 417

Db 7565 cctttgatcaagctccttgctgagggctgatgtagccaccttaccgtaacaggt 7624

Qy 418 CATCTGACCGTATATCTGTCGGAAGCAGACACTTCGCGCAAGCGCGGAGGTTGGGAACGTG 477

Db 7625 cactttaccggtgaccgtggagaagcagacttcgccaaggaccgtggaggttgggaactt 7684

Qy 478 CGGCTCTCAACGGTGTTCGCACGAGATCTCTACGCGCGGATGCGTTCGGGATTTCCGAT 537

Db 7685 cgtcgtccaacggtgttcgtactcaaatcctcagcgtgatgcttgcgtgatttcgat 7744

Qy 538 CCGAACTTGTGCGATGCGTTTACCAAGGGCATTTATAGAGAGAACGGTCACACGATT 597

Db 7745 cctaaactgtctcacgcctttaccaagggaaaccttaccgaagaaacggtcacaccatc 7804

Qy 598 AATCCGCAAGGCTCGTGACCCCTCTGTTTCGCGCTGTTTATCGCAACGGTCGCAATTC 657

Db 7805 aaccacaaggtcctcgtgactctctgttcgcttcacgctcaacggttggaggttc 7864

Qy 658 GTATCTGCGCTGTCATCGGCTTTGAGACTGAAGGTAGGCGCTTTAAAGGCATTTACAAC 717

Db 7865 gtgctcgtcgtgttatcggtatcgactgaagctgctcctcaaggttatcaccacc 7924

Qy 718 ACGAAGCGGTTCTGCGCGTTGATGACGCGGTTGTGCGAGCGCGGCACACTCGAATCA 777

Db 7925 accaacggtgttcttgcttgatgctcagctgttgtcagctggtgacacacccaagttc 7984

Qy 778 CTTGCTAATTTGCTAGGCGCATGACATCCGCTCGATACCGAACGTCGATATCATATCGTC 837

Db 7985 ctltgctaaactccttgggtgatgacatcccatcctggaacacgctggataccacacacgtg 8044

Qy 838 ATCGCGAATTCGGAAGCGGCTCCACGCAATTCGACGACCGATGCGTCAGGAAATTCATC 897

Db 8045 atcgccaacccagaagctgctccacgtattccaactaccgatgcttctcgaaagtccgg 8104

Qy 898 GCGACACCTATGGAATGGG 918

Db 8105 tccaaatttgtttacattgtg 8125

RESULT 9

X57305

ID X57305 standard; DNA: 8012 BP.

XX

AC X57305;

XX

DT 26-JUL-1999 (first entry)

XX

DE Sugar beet T-DNA containing cp4/epsps fragment.

XX

KW Sugar beet; transformation; T-DNA; Insertion; cp4/epsps; plant;

KW 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide;

KW tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.

OS Beta vulgaris.

XX W09923232-A1.  
PN  
XX  
PD  
XX  
XX  
PF  
XX  
XX  
PR 31-OCT-1997; 9705-0112003.  
XX  
XX (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
XX  
PI Mannerloef M, Steen P, Tenning PP;  
XX  
XX MPI; 1999-3113347/26.  
XX  
XX Glyphosate resistant transgenic sugar beet plants  
XX  
XX Claim 8; Page 24-29; 55pp; English.  
XX  
XX This invention describes a novel sugar beet plant, including its  
CC descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase  
CC (cp4/epsps) enzyme activity which is obtainable by Agrobacterium  
CC mediated transformation with a gene allowing expression of cp4/epsps  
CC in plants, where the plant lacks both right and left T-DNA border  
CC sequences. The transgenic sugar beet plants of the invention are capable  
CC of tolerating herbicide treatment with glyphosate (also known as  
CC N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.  
XX  
XX Sequence 8012 BP; 2096 A; 1855 C; 1879 G; 2182 T; 0 other;  
SQ

Query Match 49.5%; Score 640.2; DB 20; Length 8012;  
Best Local Similarity 84.3%; Pred. No. 7.9e-195;  
Matches 756; Conservative 0; Mismatches 138; Indels 3; Gaps 3;  
QY 1 ATGCTCAGAACCCAAAAAGTAGGATCGCTGGAGCCGGAATCGTGGCGGTATGCAAG 60  
DB 7116 atggctgagaaaccacaaagaggttggtgctgctggagctggaatcgtgtgttgcact 7175  
QY 61 GCGCTGATGCTTCAGCGCCGCGGATTCAAAGTCACCTTGATTCACCGGAACCCCTCCGTC 120  
DB 7176 gcttggatgcttcaacgctggtgattcaaggttacccttgattgatccaaaccaccacgggt 7235  
QY 121 GAAGCTGCATCGTTTGGGAATGCGCGATGCTTCAACGGCTCATCGCTCGTCCCTATGTCC 180  
DB 7236 gaagggtctcttcgttaacgctggttgcttcaacggttccctcgtgttcccaatgcc 7295  
QY 181 ATGCCGGGAACCTTGACGAGCGTGCAGCAAGTGGCTCCTTGACCGGATGGG-CCGTTGTCA 239  
DB 7296 atgccgggaacctgactagcgttccaaagtggcttcttgaccacaaagggtccattgcc 7355  
QY 240 ATCCGGTTACGTA-TTTCACCAACCATCATGCC-TGGTTGATTCGCTTTCTTAGCCGGA 297  
DB 7356 atccgtttccagctacttccaaaccatcatgcttgggtgattcgttctgctgctgga 7415  
QY 298 AGACCAAAACAAAGGTGAAGGAGCAGGCGAAAGCACCTCCGCAATCTCATCAAGTCCACCGTG 357  
DB 7416 agaccaacaagtggaaggaagtaagtaagtaagtaagtaagtaagtaagtaagtaagtg 7475  
QY 358 CCTCTGATCAAGTCATTTGGCGGAGGAGGCTGTATGCGAGCCATCTGTATCCGCCATGAAGGT 417  
DB 7476 ccttggatcaagtccttggctgagaggtgtagtgcataagcacttatccgttcacgaaggt 7535  
QY 418 CATCTGACCCCTATATCTGTCGAGAGCAGACTTCGCCAAGGACCCGCGAGGTTGGGAACGT 477  
DB 7536 cacttaccgtgtaccgttgagagagcagactctgcgaagaccgttgaggttgggaactt 7595  
QY 478 CGGCGTCTCAACGCTGTCTCCAGCCAGACTCCTCAGCGCCCATGCTTGGCGGATTTCCGAT 537  
DB 7596 cgtcgtctcaacggttctgactactcaaatcctcagcgtgatgctgattgcttgcgat 7655  
QY 538 CCGAACTTGTGCGCATGCGTTTACCAGGGCATTTCTTATAGAGAGAACGGTTCACAGATT 597

DB 7656 cctaactgtctcaagcctttaccagaaggaataccttatcgaagagaacggttcacaccalc 7715  
QY 598 AATCCGCAAGGGCTCGTGACCTCTTTCGGCGCTTTTATCCGCAACGGTGGCGAATTC 657  
DB 7716 aaccacaaggtctcgtaactctcttcttcgtcttcatacgtctcgttgcagaggttc 7775  
QY 658 GTATCTCGCGGTGTATCATCGGCTTTGAGACTGAAGTAGGGCGCTTAAAGGCATTTACAAC 717  
DB 7776 gtgtcgtcgtgttatcggaatcgagactgaaggtcgctgctctcaaggttatcaccacc 7835  
QY 718 ACGAACGGGCTTTCGGCGCTTGATGACAGCGTTCGCGAGCCGGCGCACACTCGAAATCA 777  
DB 7836 accaacggttctctgctgtgatgcagctgtgttgcaagctgtgacactccaagctc 7895  
QY 778 CTTCGCTAATTCGCTAGCGGATGACATCCGCTCGATACCGAACCTGGATATCATATCGTC 837  
DB 7896 ctgctaactcccttggatgacatccattggatacccaacgctggataccacatcgtg 7955  
QY 838 ATCCGGAATCCGGAAGCGCTCCACGCTTCGAGACCGATCGCTCAGGAAAAATTC 894  
DB 7956 atcgccaaccagaagctgtccacgtatttccaaactaccgactgcttcttgaaagttc 8012  
RESULT 10  
V30458/c  
ID V30458 standard; DNA; 534720 BP.  
XX  
AC V30458;  
XX  
DT 14-OCT-1998 (first entry)  
XX  
DE Rhizobium species plasmid pNGR234a.  
XX  
KW Symbiosis; open reading frame; ORF; plasmid; vector; transportation;  
KW degradation; metabolism; host range; nitrogen fixation; nodulation;  
XX  
OS Rhizobium sp.  
FH Key Location/Qualifiers  
FT CDS 417796..418671  
FT /\*tag= a  
FT /\*standard\_name= "ORF K1"  
FT /\*product= "oligopeptide permease"  
FT /\*note= "homologous to the OppC gene"  
FT CDS 418673..419680  
FT /\*tag= b  
FT /\*standard\_name= "ORF K2"  
FT /\*product= "oligopeptide permease"  
FT /\*note= "homologous to the Oppd gene"  
FT CDS 419677..420738  
FT /\*tag= c  
FT /\*standard\_name= "ORF K3"  
FT /\*product= "oligopeptide permease"  
FT /\*note= "homologous to the Oppf gene"  
FT CDS 420774..422159  
FT /\*tag= d  
FT /\*standard\_name= "ORF K4"  
FT /\*product= "encapsulation-like protein"  
FT /\*note= "homologous to the CapA gene"  
FT CDS 422628..424031  
FT /\*tag= e  
FT /\*standard\_name= "ORF K5"  
FT /\*product= "aminotransferase-like protein"  
FT /\*note= "homologous to the BioA gene"  
FT CDS 424056..425594  
FT /\*tag= f  
FT /\*standard\_name= "ORF K6"  
FT /\*product= "(semi)aldehyde dehydrogenase-like protein"  
FT complement (426949..428028)  
FT /\*tag= g  
FT /\*standard\_name= "ORF K7"



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FT /product= "transposase homologue"  
FT /note= "homologous to the tnp gene"  
FT 428292..429623  
FT /*tag= h  
FT /standard_name= "ORF K8"  
FT /product= "glutamate dehydrogenase-like protein"  
FT /note= "homologous to the GluDI gene"  
FT complement (430538..431284)  
FT /*tag= i  
FT /standard_name= "ORF K9"  
FT /product= "transposase homologue"  
FT complement (431296..432840)  
FT /*tag= j  
FT /standard_name= "ORF K10"  
FT /product= "transposase homologue"  
FT /note= "homologous to the Tnp gene"  
FT complement (433880..434110)  
FT /*tag= k  
FT /standard_name= "ORF K11"  
FT /product= "protein of unknown function"  
FT /note= "homologous to the FixJ gene"  
FT complement (434107..434433)  
FT /*tag= l  
FT /standard_name= "ORF K12"  
FT /product= "protein of unknown function"  
FT complement (434517..434711)  
FT /*tag= m  
FT /standard_name= "ORF K13"  
FT /product= "ferrodoxin/ferrodoxin-like protein"  
FT /note= "homologous to the fdxN gene"  
FT complement (434753..436234)  
FT /*tag= n  
FT /standard_name= "ORF K14"  
FT /gene= "nifB"  
FT /product= "protein involved in FeMo co-factor  
FT biosynthesis"  
FT complement (436460..438130)  
FT /*tag= o  
FT /standard_name= "ORF K15"  
FT /gene= "nifA"  
FT /product= "positive regulator of nif, fix and other  
FT genes"  
FT complement (438297..438590)  
FT /*tag= p  
FT /standard_name= "ORF K16"  
FT /gene= "fixX"  
FT /product= "protein required for nitrogenase activity"  
FT complement (438605..439912)  
FT /*tag= q  
FT /standard_name= "ORF K17"  
FT /gene= "fixC"  
FT /product= "protein required for nitrogenase activity"  
FT complement (439923..441032)  
FT /*tag= r  
FT /standard_name= "ORF K18"  
FT /gene= "fixB"  
FT /product= "protein required for nitrogenase activity"  
FT complement (441042..441899)  
FT /*tag= s  
FT /standard_name= "ORF K19"  
FT /gene= "fixA"  
FT /product= "protein required for nitrogenase activity"  
FT complement (442316..442636)  
FT /*tag= t  
FT /standard_name= "ORF K20"  
FT /product= "protein of unknown function"  
FT complement (443313..443879)  
FT /*tag= u  
FT /standard_name= "ORF K21"  
FT /product= "protein of unknown function"  
FT 444337..445029  
FT /*tag= v  
FT /standard_name= "ORF K22"
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FT /product= "ferrodoxin-like protein"  
FT /note= "homologous to the NifQ gene"  
FT 445088..446602  
FT /*tag= w  
FT /standard_name= "ORF K23"  
FT /gene= "dctA"  
FT /product= "C4-dicarboxylate transport protein"  
FT /note= "homologous to the DctAI gene"  
FT 446599..447843  
FT /*tag= x  
FT /standard_name= "ORF L1"  
FT /product= "cytochrome P450-like protein"  
FT /note= "homologous to the CamC gene"  
FT 447844..448500  
FT /*tag= y  
FT /standard_name= "ORF L2"  
FT /product= "gamma-hexachlorocyclohexane-dechlorinase-like  
FT protein"  
FT /note= "homologous to the LinA gene"  
FT 448497..450203  
FT /*tag= z  
FT /standard_name= "ORF L3"  
FT /product= "putative protein with degradative function"  
FT 450341..451396  
FT /*tag= aa  
FT /standard_name= "ORF L4"  
FT /product= "luciferase alpha-subunit-like protein"  
FT /note= "homologous to the LuxA gene"  
FT 452980..454494  
FT /*tag= ab  
FT /standard_name= "ORF L6"  
FT /gene= "nifD"  
FT /product= "alpha-subunit of FeMo protein of nitrogenase"  
FT 454590..456131  
FT /*tag= ac  
FT /standard_name= "ORF L7"  
FT /gene= "nifK"  
FT /product= "beta-subunit of FeMo protein of nitrogenase"  
FT 456187..457677  
FT /*tag= ad  
FT /standard_name= "ORF L8"  
FT /product= "protein involved in FeMo co-factor  
FT biosynthesis"  
FT /note= "homologous to the NifB gene"  
FT 457687..459096  
FT /*tag= ae  
FT /standard_name= "ORF L9"  
FT /product= "protein involved in FeMo co-factor  
FT biosynthesis"  
FT /note= "homologous to the FixF gene"  
FT 459093..459575  
FT /*tag= af  
FT /standard_name= "ORF L10"  
FT /product= "protein of unknown function"  
FT /note= "homologous to the Nifx gene"  
FT 459579..460067  
FT /*tag= ag  
FT /standard_name= "ORF L11"  
FT /product= "protein of unknown function"  
FT 460501..460920  
FT /*tag= ah  
FT /standard_name= "ORF L12"  
FT /product= "protein similar to part of the Fe protein  
FT of nitrogenase"  
FT /note= "homologous to the NifH gene"  
FT 461228..461545  
FT /*tag= ai  
FT /standard_name= "ORF L13"  
FT /product= "protein of unknown function"  
FT 463201..464739  
FT /*tag= aj  
FT /standard_name= "ORF L14"  
FT /product= "peptidase-like protein"
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FT CDS /note= "homologous to the bI-MPP gene"
FT 464736..466079
FT /*tag= ak
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FT /product= "processing protease-like protein"
FT /note= "homologous to the PP gene"
FT 466590..467021

Query Match 2.7%; Score 35.4; DB 19; Length 534720;
Best Local Similarity 50.9%; Pred. No. 4.7;
Matches 135; Conservative 0; Mismatches 126; Indels 4; Gaps 2;

QY 994 ACGCACCTCGAATCTTC-CAGCCCTCGCCCTCGAGTCTCTGAAGAACGATATTC 1052
Db 395468 ACGCACCTCGAGCATTCCTCGTCAATGACCCGAGGATGCAAAAGAAGCATC 395409

QY 1053 CAAATGGATGGGTTCGGCGGAGCATCCCGATTCCTCCCGTGAATGGCCGGGCAAC 1112
Db 395408 CTATTGGTCGGGTCTGCGCCCAATGACCGGAGGACCGCCGTCTATCGGCC---CAAC 395352

QY 1113 CCGGACACCCGACGTAATCTATGCTTTTCGGCCCATGGTCTATCTCGGCATGACAGGGGGGCC 1172
Db 395351 GAAGATCGCGGTCTCTCTTAACACCGGACGGGACGCGCCGTGGCTGGAGATGAGCTC 395292

QY 1173 GATGACCGAACGCTCTCTCAGAGCTCTCGGAGGCGAAGAACCTCAATCGACATTC 1232
Db 395291 CGGCTCTGCGCGGCTCTATCGGACCTGGTATCTGCGCGGAAGCCGAGATCGACGCCAC 395232

QY 1233 GCCTTCGCGACCAACCGCTTTGGT 1257
Db 395231 CGACCTCGCGTCAGCCGCTACGCT 395207

RESULT 11
V30459/c
ID V30459 standard; DNA; 536165 BP.
AC V30459;
XX
XX 06-JUL-1999 (first entry)
XX
XX Rhizobium species symbiotic plasmid pNGR234.
XX
XX Symbiosis; open reading frame; ORF; plasmid; vector; transportation;
XX degradation; metabolism; host range; nitrogen fixation; nodulation;
XX legume; plant; ds.
XX
XX Rhizobium sp.
XX
XX WO9802560-A2.
XX
XX 22-JAN-1998.
XX
XX 10-JUL-1997; 97WO-1B00950.
XX
XX 20-MAY-1997; 97GB-0010395.
XX 12-JUL-1996; 96EP-0730001.
XX
XX (MOLE-) INST MOLECULAR BIOTECHNOLOGY.
XX (BIOL-) LAB BIOLOGIE MOLECULAIRE PLANTES SUPERIE.
XX
XX Broughton WJ, Frelberg CB, Perret XP, Rosenthal A;
XX WPI; 1998-110606/10.
XX
XX New isolated symbiotic plasmid from Rhizobium sp. NGR234 - used to
XX develop products for modifying plant characteristics, e.g. nitrogen
XX fixation, synthesis of compounds and stress response
XX
XX Claim 1; Fig 3; 228pp; English.
XX
XX This is the nucleotide sequence of the plasmid pNGR234a isolated from
XX Rhizobium sp. NGR234. Open reading frames (ORF) derivable from the
```

```
CC nucleotide sequence are claimed. The nucleotide sequences or ORFs can
CC be used e.g. in the transportation of compounds to and from an organism
CC which is a host to at least one of the nucleotide sequences, ORFs or
CC proteins, the degradation and/or metabolism of organic, inorganic,
CC natural or xenobiotic substances in a host organism or the modification
CC of the host range, nitrogen fixation abilities; for obtaining a synthetic
CC minimal set of ORFs required for functional Rhizobium-legume symbiosis,
CC especially for nodulation efficiency on host plants.
XX
XX Sequence 536165 BP; 111291 A; 155755 C; 157864 G; 111255 T; 0 other;
SQ

Query Match 2.7%; Score 35.4; DB 19; Length 536165;
Best Local Similarity 50.9%; Pred. No. 4.7;
Matches 135; Conservative 0; Mismatches 126; Indels 4; Gaps 2;

QY 994 ACGCACCTCGAATCTTC-CAGCCCTCGCCCTCGAGTCTCTGAAGAACGATATTC 1052
Db 395468 ACGCACCTCGAGCATTCCTCGTCAATGACCCGAGGATGCAAAAGAAGCATC 395409

QY 1053 CAAATGGATGGGTTCGGCGGAGCATCCCGATTCCTCCCGTGAATGGCCGGGCAAC 1112
Db 395408 CTATTGGTCGGGTCTGCGCCCAATGACCGGAGGACCGCCGTCTATCGGCC---CAAC 395352

QY 1113 CCGGACACCCGACGTAATCTATGCTTTTCGGCCCATGGTCTATCTCGGCATGACAGGGGGGCC 1172
Db 395351 GAAGATCGCGGTCTCTCTTAACACCGGACGGGACGCGCCGTGGCTGGAGATGAGCTC 395292

QY 1173 GATGACCGAACGCTCTCTCAGAGCTCTCGGAGGCGAAGAACCTCAATCGACATTC 1232
Db 395291 CGGCTCTGCGCGGCTCTATCGGACCTGGTATCTGCGCGGAAGCCGAGATCGACGCCAC 395232

QY 1233 GCCTTCGCGACCAACCGCTTTGGT 1257
Db 395231 CGACCTCGCGTCAGCCGCTACGCT 395207

RESULT 12
X98168/c
ID X98168 standard; DNA; 405 BP.
AC X98168;
XX
XX 25-OCT-1999 (first entry)
XX
XX Nucleotide sequence of ORF33512 encoding a virulence factor.
XX
XX Human pathogen; virulence polypeptide; virulence factor;
XX pathogenic infection; Pseudomonas aeruginosa infection; ss.
XX
XX Pseudomonas aeruginosa.
XX
XX WO9927129-A1.
XX
XX 03-JUN-1999.
XX
XX 25-NOV-1998; 98WO-US25247.
XX
XX 25-NOV-1997; 97US-0066517.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX
XX Ausubel F, Cao H, Drenkard E, Goodman HM, Mahajan-Miklos S;
XX Rahme LG, Tan M, Tsongalis J;
XX WPI; 1999-357851/30.
XX
XX Virulence factors useful in developing disease treatments
XX
XX Disclosure; Fig 4; 228pp; English.
XX
XX The present sequence represents a Pseudomonas aeruginosa nucleic acid
XX sequence. P. aeruginosa is an opportunistic human pathogen present in
CC
```

CC soil, water and plants. The specification describes virulence polypeptides  
CC and nucleic acid sequence encoding such polypeptides. These sequences  
CC can be used to identify a compound which is capable of decreasing the  
CC expression of a pathogenic virulence factor. Compounds that inhibit  
CC the expression or activity of virulence factor polypeptides can be  
CC used to treat pathogenic infections, especially where the infection  
CC is a *P. aeruginosa* infection.  
CC note: the sequences given in the specification were poorly legible, and  
CC in some instances assumptions were made as to the identity of the base;  
CC it is therefore possible that the sequence given below is not entirely  
CC correct.  
XX  
SQ Sequence 405 BP; 98 A; 135 C; 97 G; 75 T; 0 other;

Query Match 2.6%; Score 34; DB 20; Length 405;  
Best Local Similarity 52.9%; Pred. No. 0.4;  
Matches 73; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 16 AAAAAGTAGGATCGCTGGAGCCGGAAATCGTCGGCGTATGACCGCGCTGATGCTTCAG 75  
DB 146 AGAGATGTAGTAGTGGTGGCGCTGGCGTCATCGGCTGTTGACCGCGGGAGCTGGCG 87  
QY 76 CGCCCGGATTCAAAGTCACCTTGATTCACCGCAACCCCTCCGCGCAAGGTCCATCGTTT 135  
DB 86 CTCGCCGAGCTCGCGGTGACCCCTGCTGGAGCGGGCGAGAGTGGCGTGAAGCATCCTGG 27  
QY 136 GGGATGCGGGATGCTTC 153  
DB 26 GCGGAGCGGGATGCTC 9

RESULT 13  
X98167/c  
ID X98167 standard; DNA: 603 BP.  
XX  
AC X98167;  
XX  
DT 25-OCT-1999 (first entry)  
XX  
DE Nucleotide sequence of ORF33205 encoding a virulence factor.  
XX  
KW Human pathogen; virulence polypeptide; virulence factor;  
KW pathogenic infection; *Pseudomonas aeruginosa* infection; ss.  
XX  
OS *Pseudomonas aeruginosa*.  
XX  
PN WO9927129-A1.  
XX  
PD 03-JUN-1999.  
XX  
PF 25-NOV-1998; 98WO-US25247.  
XX  
PR 25-NOV-1997; 97US-0066517.  
XX  
PA (GEO ) GEN HOSPITAL CORP.  
XX  
PI Ausubel F, Cao H, Drenkard E, Goodman HM, Mahajan-Miklos S;  
PI Rahme LG, Tan M, Tsongalis J;  
XX  
DR WPI; 1999-357851/30.  
XX  
PT Virulence factors useful in developing disease treatments  
XX  
PS Disclosure; Fig 3; 228pp; English.

CC The present sequence represents a *Pseudomonas aeruginosa* nucleic acid  
CC sequence. *P. aeruginosa* is an opportunistic human pathogen present in  
CC soil water and plants. The specification describes virulence polypeptides  
CC and nucleic acid sequence encoding such polypeptides. These sequences  
CC can be used to identify a compound which is capable of decreasing the  
CC expression of a pathogenic virulence factor. Compounds that inhibit  
CC the expression or activity of virulence factor polypeptides can be

CC used to treat pathogenic infections, especially where the infection  
CC is a *P. aeruginosa* infection.  
CC note: the sequences given in the specification were poorly legible, and  
CC in some instances assumptions were made as to the identity of the base;  
CC it is therefore possible that the sequence given below is not entirely  
CC correct.  
XX  
SQ Sequence 603 BP; 119 A; 219 C; 171 G; 94 T; 0 other;

Query Match 2.6%; Score 34; DB 20; Length 603;  
Best Local Similarity 52.9%; Pred. No. 0.49;  
Matches 73; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 16 AAAAAGTAGGATCGCTGGAGCCGGAAATCGTCGGCGTATGACCGCGCTGATGCTTCAG 75  
DB 453 AGAGATGTAGTAGTGGTGGCGCTGGCGTCATCGGCTGTTGACCGCGGGAGCTGGCG 394  
QY 76 CGCCCGGATTCAAAGTCACCTTGATTCACCGCAACCCCTCCGCGCAAGGTCCATCGTTT 135  
DB 393 CTCGCCGAGCTCGGGTGAACCCCTGCTGGAGCGGGCGAGAGTGGCGTGAGGCATCCTGG 334  
QY 136 GGGATGCGGGATGCTTC 153  
DB 333 GCGGAGCGGGATGCTC 316

RESULT 14  
X98164  
ID X98164 standard; DNA: 1137 BP.  
XX  
AC X98164;  
XX  
DT 25-OCT-1999 (first entry)  
XX  
DE Nucleotide sequence of ORF33705c encoding a virulence factor.  
XX  
KW Human pathogen; virulence polypeptide; virulence factor;  
KW pathogenic infection; *Pseudomonas aeruginosa* infection; ss.  
XX  
OS *Pseudomonas aeruginosa*.  
XX  
PN WO9927129-A1.  
XX  
PD 03-JUN-1999.  
XX  
PF 25-NOV-1998; 98WO-US25247.  
XX  
PR 25-NOV-1997; 97US-0066517.  
XX  
PA (GEO ) GEN HOSPITAL CORP.  
XX  
PI Ausubel F, Cao H, Drenkard E, Goodman HM, Mahajan-Miklos S;  
PI Rahme LG, Tan M, Tsongalis J;  
XX  
DR WPI; 1999-357851/30.  
XX  
PT Virulence factors useful in developing disease treatments  
XX  
PS Disclosure; Fig 3; 228pp; English.

CC The present sequence represents a *Pseudomonas aeruginosa* nucleic acid  
CC sequence. *P. aeruginosa* is an opportunistic human pathogen present in  
CC soil water and plants. The specification describes virulence polypeptides  
CC and nucleic acid sequence encoding such polypeptides. These sequences  
CC can be used to identify a compound which is capable of decreasing the  
CC expression of a pathogenic virulence factor. Compounds that inhibit  
CC the expression or activity of virulence factor polypeptides can be  
CC used to treat pathogenic infections, especially where the infection  
CC is a *P. aeruginosa* infection.  
CC note: the sequences given in the specification were poorly legible, and  
CC in some instances assumptions were made as to the identity of the base;  
CC it is therefore possible that the sequence given below is not entirely

CC correct.

XX Sequence 1137 BP; 173 A; 351 C; 413 G; 200 T; 0 other;

Query Match 2.6%; Score 34; DB 20; Length 1137;

Best Local Similarity 52.9%; Pred. No. 0.67; Mismatches 65; Indels 0; Gaps 0;

Matches 73; Conservative 0;

QY 16 AAAAAAGTAGGCATCGCTGGAGCGGGAATCGTCGGCGCTATGCACGGCGCTGATGCTTCAG 75

Db 49 agagatgtagtagtggtaggcgtggtgcatcgccgtgtgaccgcccggagctggcg 108

QY 76 CGCCGGCGGATTCAAAGTCAACCTTGATTGACCCGGAACCTCTCTGGCGAAGGTGCATCGTTT 135

Db 109 ctgcgcggactcggtgacccctggtgagcgggagagatggcgtaggcatactctgg 168

QY 136 GGGAAATCCGGATGCTTC 153

Db 169 gcgggagcgggatcgtc 186

RESULT 15

X98035/c  
ID X98035 standard; DNA; 42235 BP.

XX AC X98035;

XX DT 25-OCT-1999 (first entry)

XX DE Nucleotide sequence of cosmid B148.

XX KW Human pathogen; virulence polypeptide; virulence factor;

XX KW pathogenic infection; Pseudomonas aeruginosa infection; ss.

XX OS Pseudomonas aeruginosa.

XX XX WO927129-A1.

XX XX 03-JUN-1999.

XX XX 25-NOV-1998; 98WO-US25247.

XX PR 25-NOV-1997; 97US-0066517.

XX PA (GEHO ) GEN HOSPITAL CORP.

XX PI Ausubel F, Cao H, Drenkard E, Goodman HM, Mahajan-Miklos S;

XX PI Rahme LG, Tan M, Tsongalis J;

XX DR WPI; 1999-357851/30.

XX XX Virulence factors useful in developing disease treatments

XX XX Disclosure; Fig 2; 228pp; English.

XX XX

CC The present sequence represents a Pseudomonas aeruginosa nucleic acid

CC sequence. P. aeruginosa is an opportunistic human pathogen present in

CC soil water and plants. The specification describes virulence polypeptides

CC and nucleic acid sequence encoding such polypeptides. These sequences

CC can be used to identify a compound which is capable of decreasing the

CC expression of a pathogenic virulence factor. Compounds that inhibit

CC the expression or activity of virulence factor polypeptides can be

CC used to treat pathogenic infections, especially where the infection

CC is a P. aeruginosa infection.

CC note: the sequences given in the specification were poorly legible, and

CC in some instances assumptions were made as to the identity of the base;

CC it is therefore possible that the sequence given below is not entirely

CC correct.

XX XX

SQ Sequence 42235 BP; 9002 A; 13134 C; 12218 G; 7876 T; 5 other;

Query Match

Best Local Similarity 52.9%; Score 34; DB 20; Length 42235;

Matches 73; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

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Db 33657 AGAGATGATAGTGGTAGGCGCTGATCGCGCTGTTGACCGCCCGGGAGCTGGCG 33598

QY 76 CGCCGGCGGATTCAAAGTCAACCTTGATTGACCCGGAACCTCTCTGGCGAAGGTGCATCGTTT 135

Db 33597 CTCGCCGCGACTGCGGGTGACCCCTGCTGGAGCGGCGGAGAGTGGCGGTGAGGCATCTCTGG 33538

QY 136 GGGAAATCCGGATGCTTC 153

Db 33537 GCGGGAGCGGGATCGTC 33520

Search completed: January 1, 2001, 03:32:11

Job time: 19539 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2000, 19:09:36 ; Search time 157.96 Seconds  
(without alignments)  
1238.001 Million cell updates/sec

Title: US-08-484-274-4  
Perfect score: 1293  
Sequence: 1 ATCTGTGAGAACACACAAAA.....AAACGGGTCCGGCAAGTTAA 1293

Scoring table:

IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 262060 seqs, 75620496 residues

Total number of hits satisfying chosen parameters: 524120

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: /cgn2\_6/ptodata/2/lna/PCTUS\_COMB.seq.\*  
7: /cgn2\_6/ptodata/2/lna/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1293	100.0	1689	1	US-08-391-339-3
4	1260	97.4	1692	2	US-08-484-274A-3
5	1255.2	97.1	1296	1	US-08-391-339-6
6	1255.2	97.1	1296	2	US-08-484-274A-6
7	1160.8	89.8	1296	1	US-08-391-339-7
8	1160.8	89.8	1296	2	US-08-484-274A-7
9	928.8	71.8	1296	1	US-08-391-339-8
10	928.8	71.8	1296	2	US-08-484-274A-8
11	925.6	71.6	1296	1	US-08-391-339-17
12	925.6	71.6	1296	2	US-08-484-274A-17
13	56.2	4.3	69	1	US-08-391-339-30
14	56.2	4.3	69	2	US-08-484-274A-30
15	54.6	4.2	69	1	US-08-391-339-33
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21	47.6	3.7	62	1	US-08-391-339-27
22	47.6	3.7	62	2	US-08-484-274A-27
23	47.2	3.7	68	1	US-08-391-339-32
24	47.2	3.7	68	2	US-08-484-274A-32
25	33	2.6	41	1	US-08-391-339-29
26	33	2.6	41	2	US-08-484-274A-29

c	27	33	2.6	2241	5	US-09-144-759-17	Sequence 17, Appl
c	28	33	2.6	2295	5	US-09-144-759-19	Sequence 19, Appl
c	29	33	2.6	2301	5	US-09-144-759-21	Sequence 21, Appl
c	30	31.6	2.4	8931	5	US-09-028-934-28	Sequence 28, Appl
c	31	31.4	2.4	2970	6	PCT-US92-06391-1	Sequence 1, Appl
c	32	31.2	2.4	3358	3	US-08-469-537A-104	Sequence 104, App
c	33	31	2.4	1531	2	US-08-449-986-1	Sequence 1, Appl
c	34	31	2.4	1531	3	US-08-756-855-1	Sequence 1, Appl
c	35	30.2	2.3	2880	1	US-08-462-484-3	Sequence 3, Appl
c	36	30.2	2.3	2880	2	US-08-441-147-3	Sequence 3, Appl
c	37	30.2	2.3	2880	6	PCT-US95-07536-3	Sequence 3, Appl
c	38	29.6	2.3	1300	4	US-08-440-845D-8	Sequence 8, Appl
c	39	29.2	2.3	471	1	US-08-474-177-1	Sequence 1, Appl
c	40	29.2	2.3	471	2	US-08-487-033-1	Sequence 1, Appl
c	41	29.2	2.3	471	3	US-08-480-810-1	Sequence 1, Appl
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c	45	29.2	2.3	471	5	US-09-120-130-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1  
US-08-391-339-4  
; Sequence 4, Application US/08391339  
; Patent No. 5463175  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dennis R. Hoerner, Jr.,  
; ADDRESSEE: Monsanto Co. BB4F,  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391,339  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/156,968  
; FILING DATE:  
; APPLICATION NUMBER: US/07/717,370  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner, Dennis R., Jr.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10533)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1293 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1293  
US-08-391-339-4

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Query Match      100.0%; Score 1293; DB 1; Length 1293;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGCTGAGAACCAACAAAAAGTAGGCATCGCTGGAGCGGGAATCGTCGGGGTATGCACG 60

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RESULT 2
US-08-484-274A-4
; Sequence 4, Application US/08484274A
; Patent No. 5776760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barcy, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,274A
; FILING DATE: 07 June 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)789-2679
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1293 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1293
; US-08-484-274A-4
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Query Match      100.0%; Score 1293; DB 2; Length 1293;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 781 GCTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAACGTTGATATCATATCGTCATC 840  
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QY 901 ACACCTATGGAATGGGCTTGGCTGCGGGTACGGTTGAGTTGCTGGGCTCACAGCC 960  
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QY 1081 CCGGATTCGCTCCCGGATTGGCGGGCAACCCGAGACCCGAGCTAATCTATGCTTTC 1140  
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Db 1261 GGCAATCAAGCAACCGGTCGGCAAGTTAA 1293  
RESULT 3  
US-08-391-339-3  
; Sequence 3, Application US/08391339  
; Patent No. 5463175  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dennis R. Hoerner, Jr.,  
; ADDRESSEE: Monsanto Co. B4F  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391,339  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/156,968  
; FILING DATE:  
; APPLICATION NUMBER: US/07/17,370  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner, Dennis R., Jr.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10533)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1689 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-391-339-3  
Query Match 100.0%; Score 1293; DB 1; Length 1689;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGCTCTGAGAACCACAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGGTATGCAGG 60  
Db 120 ATGCTCTGAGAACCACAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGGTATGCAGG 179  
QY 61 GCGCTGATGCTTACGCGCGCGGATTCAAAGTCACCTTTGATTTGACCCGCAACCCCTCTCGC 120  
Db 180 GCGCTGATGCTTACGCGCGCGGATTCAAAGTCACCTTTGATTTGACCCGCAACCCCTCTCGC 239  
QY 121 GAAGTGCATCGTTTGGGAATCCCGGATGCTTCAACGGCTCATCGCTGCTCCCTATGTCC 180

Db 240 GAAGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTGTCCTTATGTCC 299  
Qy 181 ATGCCGGAACCTTGACGAGCGTCCGGAAGTGGCTTCTTGACCGGATGGCGGTGTCAA 240  
Db 300 ATGCCGGAACCTTGACGAGCGTCCGGAAGTGGCTTCTTGACCGGATGGCGGTGTCAA 359  
Qy 241 TCCGGTTCAGCTATTTCAACCATCATGCCCTGGTTGATTCGCTTTCTGTTAGCCGGAAGA 300  
Db 360 TCCGGTTCAGCTATTTCAACCATCATGCCCTGGTTGATTCGCTTTCTGTTAGCCGGAAGA 419  
Qy 301 CCAACAAAGTGAAGGAGCGGCAAGCACTCCGCAATCTCATCAAGTCCACGCTGCT 360  
Db 420 CCAACAAAGTGAAGGAGCGGCAAGCACTCCGCAATCTCATCAAGTCCACGCTGCT 479  
Qy 361 CTGATCAAGTCATTTGGCGGAGAGGCTGATCGAGCCATCTGATCCGCATGAAGTTCAT 420  
Db 480 CTGATCAAGTCATTTGGCGGAGAGGCTGATCGAGCCATCTGATCCGCATGAAGTTCAT 539  
Qy 421 CTGACCGTATATCTGGAGAGACAGACTTCGCCAAGAGACCGCGGAGTTGGGAACTCGGG 480  
Db 540 CTGACCGTATATCTGGAGAGACAGACTTCGCCAAGAGACCGCGGAGTTGGGAACTCGGG 599  
Qy 481 CGTCTCAACGGTGTTCGCACGCAGATCTCAGCGCGATGCTTGGCGGATTTCCGATCCG 540  
Db 600 CGTCTCAACGGTGTTCGCACGCAGATCTCAGCGCGATGCTTGGCGGATTTCCGATCCG 659  
Qy 541 AACTTGTGCGATGCGTTTACCAAGGGATCTTATAGAAGAACGCTGCACGATTAAT 600  
Db 660 AACTTGTGCGATGCGTTTACCAAGGGATCTTATAGAAGAACGCTGCACGATTAAT 719  
Qy 601 CCGAAGGGTCGTGACCTCTTCTTTCGGCGTTTATPCGGGAACGGTGGGGAATTCGTA 660  
Db 720 CCGAAGGGTCGTGACCTCTTCTTTCGGCGTTTATPCGGGAACGGTGGGGAATTCGTA 779  
Qy 661 TCTCGCGTGCATCGCTTTGACACTGAAGTAGGGCTTAAAGCATTTACAAACAG 720  
Db 780 TCTCGCGTGCATCGCTTTGACACTGAAGTAGGGCTTAAAGCATTTACAAACAG 839  
Qy 721 AACGGCGTTCGCGCGTTGATGACAGCGTTGTGCGAGCGCGCACACTCGAAATCACTT 780  
Db 840 AACGGCGTTCGCGCGTTGATGACAGCGTTGTGCGAGCGCGCACACTCGAAATCACTT 899  
Qy 781 GCTAATTCGCTAGCGGATGACATCCCGCTCGATACCAACGTTGATATCATCTCATC 840  
Db 900 GCTAATTCGCTAGCGGATGACATCCCGCTCGATACCAACGTTGATATCATCTCATC 959  
Qy 841 GCGAATCCGGAAGCGCTCCACGATTCGAGACCGATGCTCAGGAATTCATCCG 900  
Db 960 GCGAATCCGGAAGCGCTCCACGATTCGAGACCGATGCTCAGGAATTCATCCG 1019  
Qy 901 ACACCTATGGAATGGGGCTTCGCGTGGCGGTACGGTTGAGTTGCGTGGGCTCACAGCC 960  
Db 1020 ACACCTATGGAATGGGGCTTCGCGTGGCGGTACGGTTGAGTTGCGTGGGCTCACAGCC 1079  
Qy 961 GCTCCTAACTGGAACCTGGCGATGCTCTATACGACCGCTCGAAACTTCCTCCAGCC 1020  
Db 1080 GCTCCTAACTGGAACCTGGCGATGCTCTATACGACCGCTCGAAACTTCCTCCAGCC 1139  
Qy 1021 CTGCGGCTCGAGTCTGGAAGAACGATATTCGAAATGGATGGGTTCCGCGCGAGCATC 1080  
Db 1140 CTGCGGCTCGAGTCTGGAAGAACGATATTCGAAATGGATGGGTTCCGCGCGAGCATC 1199  
Qy 1081 CCGGATTCGCTCCCGGTGATTGGCGGGCAACCGGACACCCGACGTAATCTATGCTTC 1140  
Db 1200 CCGGATTCGCTCCCGGTGATTGGCGGGCAACCGGACACCCGACGTAATCTATGCTTC 1259  
Qy 1141 GGCATGCTCATCTCGGCATTCAGAGGGCGCGATGACCGAAGCTCTGTCAGAGCTC 1200  
Db 1260 GGCATGCTCATCTCGGCATTCAGAGGGCGCGATGACCGAAGCTCTGTCAGAGCTC 1319  
Qy 1201 CTGCGAGCGGAAAGACCTCAATCGACATTTTCGCCCTTCGCACCAACCGCTTTGGTATT 1260  
Db 1320 CTGCGAGCGGAAAGACCTCAATCGACATTTTCGCCCTTCGCACCAACCGCTTTGGTATT 1379

Qy 1261 GCAGAAATCAAGCAACGGTCCGCAAGTTAA 1293  
Db 1380 GCAGAAATCAAGCAACGGTCCGCAAGTTAA 1412

RESULT 4

US-08-484-274A-3  
; Sequence 3, Application US/08484274A  
; Patent No. 5776760  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,274A  
; FILING DATE: 07 June 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Patterson, Melinda L.  
; REGISTRATION NUMBER: 33,062  
; REFERENCE/DOCKET NUMBER: MOBI130 38-21(13560)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (713)789-2679  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1692 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-484-274A-3

Query Match 97.4%; Score 1260; DB 2; Length 1692;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1293; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

Qy 1 ATGTCTGAGAACCAACAAAAAGTAGGCATCGCTGGAGCCGGAATCGTCGGCGTATGCACG 60  
Db 120 ATGTCTGAGAACCAACAAAAAGTAGGCATCGCTGGAGCCGGAATCGTCGGCGTATGCACG 179  
Qy 61 GCGCTGATGCTTACGCCCGCGGATTCAAAGTCACTTGTATGACCCGAAACCCCTCCTGGC 120  
Db 180 GCGCTGATGCTTACGCCCGCGGATTCAAAGTCACTTGTATGACCCGAAACCCCTCCTGGC 239  
Qy 121 GAAGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC 180  
Db 240 GAAGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC 299  
Qy 181 ATGCCGGGAACCTTGACGAGCGTCCGGAAGTGGCTCTTGACCCGAT-GGGCCGTTGTCA 239  
Db 300 ATGCCGGGAACCTTGACGAGCGTCCGGAAGTGGCTCTTGACCCGATGGGGCCGTTGTCA 359  
Qy 240 ATCCGGTTCAGCTA-TTTTCCAACCATCATG-CCTGGTTGATTTCGCTTTCTGTTAGCCGGA 297  
Db 360 ATCCGGTTCAGCTATTTTCCAACCATCATGCCCTGGTTGATTTCGCTTTCTGTTAGCCGGA 419  
Qy 298 AGACCAACAAGTGAAGGAGCAGCGGCAAGCACTCCGCAATTCATCAAGTCCACCGGTG 357  
|||||



Db 420 AGACCAAAAGGTGAAGGAGCAGCGGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 479  
Qy 358 CTTCTGATCAATCATYTCGGGAGAGGCTGATCGAGCCATCTGATCGGCATGAAGT 417  
Db 480 CTTCTGATCAATCATYTCGGGAGAGGCTGATCGAGCCATCTGATCGGCATGAAGT 539  
Qy 418 CATCTGACCGTATATCTGTTGGAGAACACATTCGCCAAGGACCGGGAGGTTGGAACTG 477  
Db 540 CATCTGACCGTATATCTGTTGGAGAACACATTCGCCAAGGACCGGGAGGTTGGAACTG 599  
Qy 478 GGGCTCTCAACGGTGTTCGGACCGCAGATCTCTACGCGCGATGCTTTCGGGATTCGAT 537  
Db 600 GGGCTCTCAACGGTGTTCGGACCGCAGATCTCTACGCGCGATGCTTTCGGGATTCGAT 659  
Qy 538 CGGAATTTGTCGATGCTTTACCAAGGGCATTCCTATAGAGAGAACGGTCACACGAT 597  
Db 660 CGGAATTTGTCGATGCTTTACCAAGGGCATTCCTATAGAGAGAACGGTCACACGAT 719  
Qy 598 ATCCGCAAGGGCTGTCGACCTCTTGTTCGGCGTTTATCGCAACGGTGGCAATTC 657  
Db 720 ATCCGCAAGGGCTGTCGACCTCTTGTTCGGCGTTTATCGCAACGGTGGCAATTC 779  
Qy 658 GTATCTGCGCGTGTCTATCGGCTTTGAGACTGAAGGTAGGGCGCTTAAAGGCATTCACACC 717  
Db 780 GTATCTGCGCGTGTCTATCGGCTTTGAGACTGAAGGTAGGGCGCTTAAAGGCATTCACACC 839  
Qy 718 ACGAACGGCTTTGCGCGTGTGATGACAGCGGTGTTCGAGCGCGCGCACACTCGAAATCA 777  
Db 840 ACGAACGGCTTTGCGCGTGTGATGACAGCGGTGTTCGAGCGCGCGCACACTCGAAATCA 899  
Qy 778 CTTGCTAATTCGCTAGGCGATGACATCCGCTCGATACCGACGTGGATATCATATCTGTC 837  
Db 900 CTTGCTAATTCGCTAGGCGATGACATCCGCTCGATACCGACGTGGATATCATATCTGTC 959  
Qy 838 ATCCGGAATCCGGAAGCGCTCCAGCATTCGAGCAGCGATGCTCAGGAAATTCATC 897  
Db 960 ATCCGGAATCCGGAAGCGCTCCAGCATTCGAGCAGCGATGCTCAGGAAATTCATC 1019  
Qy 898 GCGACACCTATGGAATGGGGTTGCGCGTGGGGGTACGGTTGAGTTCGCTGGGCTACA 957  
Db 1020 GCGACACCTATGGAATGGGGTTGCGCGTGGGGGTACGGTTGAGTTCGCTGGGCTACA 1079  
Qy 958 GCGGCTCTAATCGAAACGTGCGCATGCTCTATACGACGCTCGAAACTCTTCCA 1017  
Db 1080 GCGGCTCTAATCGAAACGTGCGCATGCTCTATACGACGCTCGAAACTCTTCCA 1139  
Qy 1018 GCGCTCGCGCTTGGAGTTCTGAAGACGATATCCAAATGGATGGGTTCGCGCCGAGC 1077  
Db 1140 GCGCTCGCGCTTGGAGTTCTGAAGACGATATCCAAATGGATGGGTTCGCGCCGAGC 1199  
Qy 1078 ATCCCGGATTCGCTCCCGTGTATGGCGGGGAAACCCGACACCGACGTAATCTATGCT 1137  
Db 1200 ATCCCGGATTCGCTCCCGTGTATGGCGGGGAAACCCGACACCGGAGTAACTATGCT 1259  
Qy 1138 TTGCGCATGTGTCATCTCGGATGACAGGGCGCGGATGACGCAACGCTCGTCTCAGAG 1197  
Db 1260 TTGCGCATGTGTCATCTCGGATGACAGGGCGCGGATGACGCAACGCTCGTCTCAGAG 1319  
Qy 1198 CTTCTCGGAGCGGAAAGACCTCAATGACATTTTCGCCCTTCGCAACCAACCGCTTGGT 1257  
Db 1320 CTTCTCGGAGCGGAAAGACCTCAATGACATTTTCGCCCTTCGCAACCAACCGCTTGGT 1379  
Qy 1258 ATTGGCAATCAAGCAACGGTCCGCGAAGTTAA 1293  
Db 1380 ATTGGCAATCAAGCAACGGTCCGCGAAGTTAA 1415

RESULT 5

US-08-391-339-6

; Sequence 6, Application US/08391339

; Patent No. 5463175

; GENERAL INFORMATION:

; APPLICANT: Kishore, Ganesh M.

; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dennis R. Hoerner, Jr.,  
; ADDRESSEE: Monsanto Co, B4F,  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391,339  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/156,968  
; FILING DATE:  
; APPLICATION NUMBER: US/07/717,370  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner, Dennis R., Jr.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10533)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1296 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (recombinant)  
; US-08-391-339-6

Query Match 97.1%; Score 1255.2; DB 1; Length 1296;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 1290; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

Qy 1 ATGTCTGAGAACACAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGTATGCACG 60

Db 1 ATGGCTGAGAACACAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGTATGCACG 60

Qy 61 GGGCTGATGCTTACGCGCGGGATTCAAAGTCACCTTGATTGACCCGNAACCTCCTGGC 120

Db 61 GGGCTGATGCTTACGCGCGGGATTCAAAGTCACCTTGATTGACCCGNAACCTCCTGGC 120

Qy 121 GAAGTGATGCTTTGGGAATCGCGGATGCTTCAACGGCTCATCGTCGTCCTATGTCC 180

Db 121 GAAGTGATGCTTTGGGAATCGCGGATGCTTCAACGGCTCATCGTCGTCCTATGTCC 180

Qy 181 ATCCCGGAAACTTCACGAGCGTCCGAAAGTGGCTCCTTGACCCGAT-GGGCGGTGTCA 239

Db 181 ATCCCGGAAACTTCACGAGCGTCCGAAAGTGGCTCCTTGACCCGATGGGCGGTGTCA 240

Qy 240 ATCCCGGTTCAGCTA-TTTCCAACCATCATG-CCTGGTGTGATTGCGTTTCTGTAGCCGA 297

Db 241 ATCCCGGTTCAGCTATTTTCCAACCATCATGCTGCTGGTGTGATTGCGTTTCTGTAGCCGA 300

Qy 298 AGACCAACAAGGTGAAGGAGCGGGAAGCACTCCGCAATCTCATCAAGTCCACGGTG 357

Db 301 AGACCAACAAGGTGAAGGAGCGGGAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360

Qy 358 CTTCTGATCAAGTCAATTCGCGGAGGAGGCTGATCGGAGCATCTGATCGGCCATGAAGT 417

Db 361 CTTCTGATCAAGTCAATTCGCGGAGGAGGCTGATCGGAGCATCTGATCGGCCATGAAGT 420

QY 418 CATCTGACCGGTATATCGTGAGAGACAGACTTCCCAAGAGACCCGCGAGGTGGGAACGTG 477  
Db 421 CATCTGACCGGTATATCGTGAGAGACAGACTTCCCAAGAGACCCGCGAGGTGGGAACGTG 480  
QY 478 CGCGCTCTCAACGGTGTTCGACGACGATCTCAGCCCGCATCGGTTCGCGGATTCGAT 537  
Db 481 CGCGCTCTCAACGGTGTTCGACGACGATCTCAGCCCGCATCGGTTCGCGGATTCGAT 540  
QY 538 CCGAACCTGTTCGCGATCGGTTCACCAAGGGATTCCTATAGAAGAGACCGGTTCACACGAT 597  
Db 541 CCGAACCTGTTCGCGATCGGTTCACCAAGGGATTCCTATAGAAGAGACCGGTTCACACGAT 600  
QY 598 AATCCGCAAGGGTCTGTGACCTCTTGTTCGCGGTTTTATPCGCAACGGTTCGCGGATTC 657  
Db 601 AATCCGCAAGGGTCTGTGACCTCTTGTTCGCGGTTTTATPCGCAACGGTTCGCGGATTC 660  
QY 658 GTATCTCGCGGTCTATCGCGCTTTGACACTGAAGGTAGGCGCTTAAAGGCATTTACAC 717  
Db 661 GTATCTCGCGGTCTATCGCGCTTTGACACTGAAGGTAGGCGCTTAAAGGCATTTACAC 720  
QY 718 ACGAACCGGCTTTCGCGGTGTGATGACGCGGTTCGCGCGGCGCACACTCCAAATCA 777  
Db 721 ACGAACCGGCTTTCGCGGTGTGATGACGCGGTTCGCGCGGCGCACACTCCAAATCA 780  
QY 778 CTTCGCTAATTCGCTAGCGATGACATCCCGCTCGATACCGCAACGGTTCGATATCATGTC 837  
Db 781 CTTCGCTAATTCGCTAGCGATGACATCCCGCTCGATACCGCAACGGTTCGATATCATGTC 840  
QY 838 ATCCGGAATCCGGAAGCGCTCCACGATTTCCGACGACCGATGGCTCAGGAAATTCATC 897  
Db 841 ATCCGGAATCCGGAAGCGCTCCACGATTTCCGACGACCGATGGCTCAGGAAATTCATC 900  
QY 898 GCGACACTTATGGAATGGGGTTCGCGGTGGCGGTACGGTTGAGTTTCGCTGGGCTCACA 957  
Db 901 GCGACACTTATGGAATGGGGTTCGCGGTGGCGGTACGGTTGAGTTTCGCTGGGCTCACA 960  
QY 958 GCGGCTCTTAATCGGAACGTGGCGATGTGCTCTATACGACGCTCGAAACTTCCTCCA 1017  
Db 961 GCGGCTCTTAATCGGAACGTGGCGATGTGCTCTATACGACGCTCGAAACTTCCTCCA 1020  
QY 1018 GCGCTCGCGCTCGGAGTCTGAAGAAGCATATTTCCAAATGGATGGGTTCGCGCGGAGC 1077  
Db 1021 GCGCTCGCGCTCGGAGTCTGAAGAAGCATATTTCCAAATGGATGGGTTCGCGCGGAGC 1080  
QY 1078 ATCCCGGATTCGCTCCCGCTGATTGGCGGCGCAACCCGACACCCGACGTAATCTATGCT 1137  
Db 1081 ATCCCGGATTCGCTCCCGCTGATTGGCGGCGCAACCCGACACCCGACGTAATCTATGCT 1140  
QY 1138 TTCCGCGCATGGTCAATCTCGGCATGACAGGGGCGCGATGACCGCAACGCTCTCAGAG 1197  
Db 1141 TTCCGCGCATGGTCAATCTCGGCATGACAGGGGCGCGATGACCGCAACGCTCTCAGAG 1200  
QY 1198 CTCTCCGCGCGGAAAGACTTCAATCGACATTTCCGCCCTTCGCAACCAACCGCTTTGGT 1257  
Db 1201 CTCTCCGCGCGGAAAGACTTCAATCGACATTTCCGCCCTTCGCAACCAACCGCTTTGGT 1260  
QY 1258 ATTGGCAATCCCAAGCAACCGGTCGCGCAAGTTAA 1293  
Db 1261 ATTGGCAATCCCAAGCAACCGGTCGCGCAAGTTAA 1296

RESULT 6

US-08-484-274A-6  
; Sequence 6, Application US/08484274A  
; Patent No. 576760  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433

CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210-4433  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: PatentIn Release #1.0, version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,274A  
FILING DATE: 07 June 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Patterson, Melinda L.  
REGISTRATION NUMBER: 33,062  
REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (713)789-2679  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1296 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (recombinant)  
US-08-484-274A-6

Query Match 97.1%; Score 1255.2; DB 2; Length 1296;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1290; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

QY 1 ATGCTCAGAACCAACAAAGTAGGCATCGTCGACCGCAATCGTCGCGGTATGCACG 60  
Db 1 ATGCTCAGAACCAACAAAGTAGGCATCGTCGACCGCAATCGTCGCGGTATGCACG 60  
QY 61 GCGCTGATGCTTTCAGCGCCGCGGATTCAAGATCACCTTGATTGACCGCAACCCCTCTGGC 120  
Db 61 GCGCTGATGCTTTCAGCGCCGCGGATTCAAGATCACCTTGATTGACCGCAACCCCTCTGGC 120  
QY 121 GAAGGTGCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGCTATGTCC 180  
Db 121 GAAGGTGCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGCTATGTCC 180  
QY 181 ATGCCGGGAAACTTGACGAGCTGCCGAAGTGGCTCTTGACCCGAT-GGGCCCTTGTC 239  
Db 181 ATGCCGGGAAACTTGACGAGCTGCCGAAGTGGCTCTTGACCCGATGTTGTCA 240  
QY 240 ATCCGGTTCAGCTA-TTTTCAACCATCATG-CTTGGTTGATTTCGCTTTCTGTTAGCCGGA 297  
Db 241 ATCCGGTTCAGCTATTTTCAACCATCATGCGCCCTGGTTGATTTCGCTTTCTGTTAGCCGGA 300  
QY 298 AGACCAACAAAGGTGAAGGAGCAGCGGAAAGCATCTCCGCAATCTCATCAAGTCACCGGTG 357  
Db 301 AGACCAACAAAGGTGAAGGAGCAGCGGAAAGCATCTCCGCAATCTCATCAAGTCACCGGTG 360  
QY 358 CCTCTGATCAAGTCATTGGCGGAGGAGCTGATCGGAGCCATCTGATCCGCCATGAAGGT 417  
Db 361 CCTCTGATCAAGTCATTGGCGGAGGAGCTGATCGGAGCCATCTGATCCGCCATGAAGGT 420  
QY 418 CATCTGACCGGTATATCGTGAGAGACAGACTTCCCAAGAGACCCGCGAGGTGGGAACGTG 477  
Db 421 CATCTGACCGGTATATCGTGAGAGACAGACTTCCCAAGAGACCCGCGAGGTGGGAACGTG 480  
QY 478 CGCGCTCTCAACGGTGTTCGACGACGATCTCAGCGCGCATGCTGCGGGATTCGAT 537  
Db 481 CGCGCTCTCAACGGTGTTCGACGACGATCTCAGCGCGCATGCTGCGGGATTCGAT 540  
QY 538 CCGAACCTGTTCGCGATCGGTTCACCAAGGGATTCCTATAGAAGAGACCGGTTCACACGAT 597  
Db 541 CCGAACCTGTTCGCGATCGGTTCACCAAGGGATTCCTATAGAAGAGACCGGTTCACACGAT 600

QY 598 AATCCGCAAGGCGCTGACGCTCTGTTCCGCGCTTTATCCGCAACGGTCCGCAATTC 657  
Db 601 AATCCGCAAGGCGCTGACGCTCTGTTCCGCGCTTTATCCGCAACGGTCCGCAATTC 660  
QY 658 GTATCTGGCGGTGTCATCGGCTTTGAGACTGAAGTAGGGCGCTTAAAGGCATTACAAC 717  
Db 661 GTATCTGGCGGTGTCATCGGCTTTGAGACTGAAGTAGGGCGCTTAAAGGCATTACAAC 720  
QY 718 AGCAAGCGGTTCGCGGCTTGATCGAGCGGTGTCGAGCGCGGCGACACTCGAATCA 777  
Db 721 AGCAAGCGGTTCGCGGCTTGATCGAGCGGTGTCGAGCGCGGCGACACTCGAATCA 780  
QY 778 CTTGCTAATTCCTAGGCGATCACATCCGCTCGATACCGAACGTCGATATCATATCGTC 837  
Db 781 CTTGCTAATTCCTAGGCGATCACATCCGCTCGATACCGAACGTCGATATCATATCGTC 840  
QY 838 ATCGGGAATCCGGAAGCGCTCCAGCGATTCGAGACCGGATGCGTCAGGAAATTCATC 897  
Db 841 ATCGGGAATCCGGAAGCGCTCCAGCGATTCGAGACCGGATGCGTCAGGAAATTCATC 900  
QY 898 GCGACACCTATGGAATGGGCTTCGCTGCGGGGTAGGTTGAGTTGCTGGGCTCACA 957  
Db 901 GCGACACCTATGGAATGGGCTTCGCTGCGGGGTAGGTTGAGTTGCTGGGCTCACA 960  
QY 958 GCGGCTCCTAATCGAAAGTCGCGATGCTCTATACGACGCTCGAAACCTCTTCCA 1017  
Db 961 GCGGCTCCTAATCGAAAGTCGCGATGCTCTATACGACGCTCGAAACCTCTTCCA 1020  
QY 1018 GCGCTCGGCGCTCGAGTCTTGAAGAAGCATATTCGAATGATGGGTTCCGGCGGAGC 1077  
Db 1021 GCGCTCGGCGCTCGAGTCTTGAAGAAGCATATTCGAATGATGGGTTCCGGCGGAGC 1080  
QY 1078 ATCCCGGATTCGCTCCCGTGATGGCGGGCAACCGGACACCGACGTAATCTATGCT 1137  
Db 1081 ATCCCGGATTCGCTCCCGTGATGGCGGGCAACCGGACACCGACGTAATCTATGCT 1140  
QY 1138 TTCGCGCATGTCATCTCGGATGACAGGGCGCGATCACCGCAACGCTCGTCTCAGAG 1197  
Db 1141 TTCGCGCATGTCATCTCGGATGACAGGGCGCGATCACCGCAACGCTCGTCTCAGAG 1200  
QY 1198 CTCCTCGAGGCGAAAGACCTCAATCGACATTTCCGCCCTTCGCAACCAACCGCTTGGT 1257  
Db 1201 CTCCTCGAGGCGAAAGACCTCAATCGACATTTCCGCCCTTCGCAACCAACCGCTTGGT 1260  
QY 1258 ATTGGCAATCCAGCAACGGGTCGGCAAGTTAA 1293  
Db 1261 ATTGGCAATCCAGCAACGGGTCGGCAAGTTAA 1296

RESULT 7  
US-08-391-339-7  
; Sequence 7, Application US/08391339  
; Patent No. 5463175  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Phosphatase Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dennis R. Hoerner, Jr.,  
; ADDRESSEE: Monsanto Co. B44F  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391,339

; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/156,968  
; FILING DATE:  
; APPLICATION NUMBER: US/07/717,370  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner, Dennis R., Jr.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10533)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1296 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (recombinant)  
; US-08-391-339-7  
  
Query Match 89.8%; Score 1160.8; DB 1; Length 1296;  
Best Local Similarity 95.0%; Pred. No. 0;  
Matches 1231; Conservative 0; Mismatches 62; Indels 3; Gaps 3;  
  
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Db 1 ATGGCTGAGAACACAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTATGCACT 60  
QY 61 GCGCTGATGCTTTAGCGCGCGGGAATTCAAAGTCACCTGATTGACCCGAACCTCTCTGC 120  
Db 61 GCTTTGATGCTTCAACGCTGCTGGATTCAAAGTCACCTGATTGACCCGAACCTCTCTGC 120  
QY 121 GAAGTGCACTCTTTGGGAATCGCGGATGCTTTCAACGGCTCATCTCGCTATGTC 180  
Db 121 GAAGTGCACTCTTTGGGAATCGCGGATGCTTTCAACGGCTCATCTCGCTATGTC 180  
QY 181 ATCCGCGGAAATTCGAGAGCGTGGCGAAGTGGCTCTTTGAGCCGAT -GGGCGGTTGTCA 239  
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QY 240 ATCCGCTTCAGCTA -TTTCCAAACCATCATG -CCTGTTGATTGCTGTTCTGTTAGCCGA 297  
Db 241 ATCCGCTTCAGCTAATTTCCAAACCATCATGCTGCTGTTGATTGCTGTTCTGTTAGCCGA 300  
QY 298 AGACCAAAACAGGTGAAGAGCAGCGGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 357  
Db 301 AGACCAAAACAGGTGAAGAGCAGCGGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360  
QY 358 CCTCTGATCAAGTCAATTTGGCGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT 417  
Db 361 CCTCTGATCAAGTCAATTTGGCGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT 420  
QY 418 CATCTGACCGTATATCGTGGAGAACGACACTTCGCGCAAGAGCCGCGAGGTTGGGAATTC 477  
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QY 478 CGGCGTCTCAACGGTGTTCGCGACGAGATCCCTCAGCGCGCGATGCTGCGGGATTCGAT 537  
Db 481 CGGCGTCTCAACGGTGTTCGCGACGAGATCCCTCAGCGCGCGATGCTGCGGGATTCGAT 540  
QY 538 CCGAACTTGTGCTGCTGCTTTTACCAAGGCGATCTTATAGAGAGAACGCTCACAGATT 597  
Db 541 CCTAACTTGTGCTGCTGCTTTTACCAAGGCGATCTTATAGAGAGAACGCTCACAGATT 600  
QY 598 AATCCGCAAGGCTCGTGACCTCTTTGTTCCGCGCTTTTATCCGCAACGGTCCGCAATTC 657  
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QY 658 GTATCTGCGCGTGTCTATCGGCTTGAAGTAGGGCGCTTAAAGGCATTACAAC 717  
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Db 841 ATCCGGAATCCGGAAGCCCTCCACGCATTCGACGACCGATGCGTCAGGAAATTCATC 900  
Qy 898 GCGACACCTATGAAATGGGGCTTCGCGTGGCGGGTACGGTTGAGTTCGCTGGGCTCACA 957  
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Qy 958 GCGGCTCCTAACTGGAACGTCGGATGTCGCTATACCGACGCTCGGAAACTTCCTCCA 1017  
Db 961 GCTGCTCCTAACTGGAACGTCGGATGTCGCTATACCGACGCTCGGAAACTTCCTCCA 1020  
Qy 1018 GCGCTCGGCGCTCGGAGTTCTGAAGAACGATATTCMAATGATGGGTTCGCGCGGAGC 1077  
Db 1021 GCGCTCGGCGCTCGGAGTTCTGAAGAACGATATTCMAATGATGGGTTCGCTGCTAGC 1080  
Qy 1078 ATCCCGGATTCGCTCCCGCTGATGGCCGGGCAACCCGACACCGACGATATCTATGCT 1137  
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Db 1141 TTGCTGACGGTCATCTCGGTATGACAGGTGCTCCAAATGACTGCAACTCTCGTCTCAGAG 1200  
Qy 1198 CTCCTCGCAGGCGAAAGACCTCAATCGACATTCGCGCTTCGCGCAACAAACGCTTTGCT 1257  
Db 1201 CTCCTCGCAGGCGAAAGACCTCAATCGACATTCGCGCTTCGCGCAACAAACGCTTTGCT 1260  
Qy 1258 ATTGCAATCCCAAGCAACGGGTCGCGCAAGTTAA 1293  
Db 1261 ATTGCAATCCCAAGCAACGGGTCGCGCAAGTTAA 1296

RESULT 9

US-08-391-339-8  
: Sequence 8, Application US/08391339  
: Patent No. 5463175  
: GENERAL INFORMATION:  
: APPLICANT: Kishore, Ganesh M.  
: APPLICANT: Barry, Gerard F.  
: TITLE OF INVENTION: Glyphosate Tolerant Plants  
: NUMBER OF SEQUENCES: 33  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Dennis R. Hoerner, Jr.,  
: ADDRESSEE: Monsanto Co. B4F  
: STREET: 700 Chesterfield Village Parkway  
: CITY: St. Louis  
: STATE: Missouri  
: COUNTRY: USA  
: ZIP: 63198  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/391,339  
: FILING DATE:  
: CLASSIFICATION: 800  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US/08/156,968  
: FILING DATE:  
: APPLICATION NUMBER: US/07/717,370  
: FILING DATE:  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Hoerner, Dennis R., Jr.  
: REGISTRATION NUMBER: 30,914  
: REFERENCE/DOCKET NUMBER: 38-21(10533)  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (314)537-6099  
: INFORMATION FOR SEQ ID NO: 8:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 1296 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: double

; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (synthetic)  
US-08-391-339-8  
Query Match 71.8%; Score 928.8; DB 1; Length 1296;  
Best Local Similarity 83.8%; Pred. No. 0;  
Matches 1086; Conservative 0; Mismatches 207; Indels 3; Gaps 3;  
Qy 1 ATGCTGTGAGAACACAAAAAGTAGGCATCGGTGGAGCGGAATCGTCGCGGTATGCACG 60  
Db 1 ATGGCTGTGAGAACACAAAGAGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTTCGACT 60  
Qy 61 GCGCTGATGCTTCAGCGCCGCGGATTCAAAGTACCTTGATTGACCGCAACCCCTCTGGC 120  
Db 61 GCTTTGATGCTTCAGCTGCTGGATTCAAGGTTACCTTGATTGATCCAAACCCACCAGGT 120  
Qy 121 GAAGGTGCAATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGCTCATATGTCC 180  
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Db 181 ATGCCAGGAAACTTGAAGTGGCTTCCAAAGTGGCTTCTTGACCCCAATGGGTCCATTTGTC 240  
Qy 240 ATCCGCTTCAGCTA-TTTCCAAACCATCATGCC-TGGTTGATTGCTTCTCTGTAGCCGA 297  
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Qy 298 AGACCAAAAGGTGAAGGAGCAGCGGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 357  
Db 301 AGACCAAAAGGTGAAGGAGCAAGCTAAGGCACTCCGTAACCTCATCAAGTCCACTGTG 360  
Qy 358 CCTCTGATCAAGTCATTGGCGAGGAGGCTGATGCGAGCATCTGATCGCCCATGAAGGT 417  
Db 361 CCTTTGATCAAGTCTTGGCTGAGGAGGCTGATGCTTAGCCACCTTATCCGTCACGAAGGT 420  
Qy 418 CATCTGACCGTATATCGTGGAGAACGACATTCGCCAAGGACCGCGAGGTTGGGAACGT 477  
Db 421 CACCTTACCGTGTACCGTGGAGAACGACATTCGCCAAGGACCGCGTGGAGGTTGGGAACCT 480  
Qy 478 GCGCGTCTCAACGGTGTTCGACGCGAGATCCTCAGCGCGGATCGCTTGGCGGATTTCCGAT 537  
Db 481 CGTGTCTCAACGGTGTTCGATCAATCCTCAGCGCTGATGCAATGGCGTATTCGAT 540  
Qy 538 CCGAATTTGTCGATCGCTTTACCAAGGCAATCTTTATAGAAGAGAACGCTACACGAT 597  
Db 541 CCTAATTTGTCACGCTTTACCAAGGCAATCTTTATCGAAGAGAACGCTACACCATC 600  
Qy 598 AATCCGAAGGCTCGTGACCTCTTTGTTTGGCGTTTATTCGCGAACGGTGGCGGAATTC 657  
Db 601 AACCACAAAGGTCGCTGACTCTCTTTGTTTGGTTCGTTTCATCGCTAACCGGTGGAGGTT 660  
Qy 658 GTATCTGCGGCTCATCGCTTTGAGACTGAAAGTGAAGGCGCTTAAGCGCATTAACAAC 717  
Db 661 GTCTGTGCTGTGTTATCGGATTCGAGACTGAAAGGTCGCTCTCAAGGGGTATCACACC 720  
Qy 718 ACGAAGCGGCTTCTGGCGGTTGATGACGCGGTTGTTCGACGCGCGCACACTCGAATCA 777  
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Qy 838 ATCCGGAATCCGGAAGCCCTCCACGCAATTCGACACCGATGCGCTCAGGAAATTCATC 897  
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Db 901 GCTACTCTTATGGAGATGGGTCTTTCGTGTTGCTGGAACCGCTTGAGTTCCGTGCTCACT 960

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Db 961 GCTGCTCCTAACTGGAACGGTCGCTCACGTTCTCTACACTCACGCTCGTAAGTTGCTTCCA 1020
QY 1018 GCCCTCGCGCTCGCGAGTTCTGAAGAAGCATATCCAAATGGATGGGTTCCGGCGGAGC 1077
Db 1021 GCTCTCGCTCTCGCGAGTTCTGAAGAAGCTTACTCCAAGTGGATGGGTTTCGCTCCAAAGC 1080
QY 1078 ATCCGGGATTCGCTCCCGCTGATTTGGCGGGCAACCCGACACCCGACAGTAATCTATGCT 1137
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QY 1138 TTGGCCATGTGTCATCTCGGATGACAGGGGGCGGATGACCGCAACGCTGCTCTCAGAG 1197
Db 1141 TTGGTTCACGGTTCACCTCGGTATGACTGGTCTCCAATGACCGCAACCCCTCGTTTCTGAG 1200
QY 1198 CTCCTCGCAGCGGAACACCTCAATCAGCATTTTCGCCCTTCGCACCAACCGCTTTGCT 1257
Db 1201 CTCCTCGCAGGTGAGAAGACCTCTATCAGCATCTCTCCATTCGCACCAACCGTTTCGCT 1260
QY 1258 ATTGGCAATCAAGCAACCGGTCGCGCAAGTTAA 1293
Db 1261 ATTGTAAGTCCAAGCAACCGTCTGATCCTAA 1296

RESULT 10
us-08-484-274A-8
; Sequence 8, Application US/08484274A
; Patent No. 5776760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,274A
; FILING DATE: 07 June 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)789-2679
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
US-08-484-274A-8

Query Match 71.8%; Score 928.8; DB 2; Length 1296;
Best Local Similarity 83.8%; Pred. No. 0;
Matches 1086; Conservative 0; Mismatches 207; Indels 3; Gaps 3;

QY 1 ATGCTCTGAGAACCAACAAAAAGTAGGCTCGCTGAGCGCGGAATCGTCGGCGTATGCCAGG 60
Db 1 ATGCTGAGAACCAACAGAGGTGGTATCGCTGGAGCTGGAAATCGTTGGTGTTCACCT 60
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Db 61 GCCTTGATGCTTCAACGCTCGTGGATTCGAAGTTACCTTGAATTGATCCAAACCCACCAGGT 120
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Db 121 GAAGTGCCTTCTTTCGGTAACGGTGTGCTTCAACGGTTCCTCCGTTGTTTCCAATGTC 180
QY 181 ATGCCGGGAACCTTGACGAGCGTCGCCAAGTGGCTCTTGACCCGATGGG-CCGTTGTCA 239
Db 181 ATGCCAGGAACCTTGATAGCGTTCCAAAGTGGCTTCTTGACCCAATGGGTCCATTGTC 240
QY 240 ATCCGGTTCAGTA-TTTTCCAACCATCATGCC-TGGTTGATTTCGCTTCTCTAGCCCGGA 297
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QY 298 AGACCAAAACAAAGTGAAGGAGCAGCGGAAGCATCTCCGCAATCTCATCAAGTCCACGGTG 357
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QY 358 CCTCTGATCAAGTCATTTGGCGGAGGAGCTGATCGAGGCCATCTGATCCGCCATCAAGT 417
Db 361 CCTTGATCAAGTCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGT 420
QY 418 CATCTGACCGTATATCGTGAGAGCAGACTTCGCCAAGGACCCGCGGAGGTTGGGAACGTG 477
Db 421 CACCTTACCGTGTACCGTGAGAGCAGACTTCGCCAAGGACCCGTGGAGGTGGGAACCTT 480
QY 478 CGCGCTCTCAACGGTGTTCGACGCGCAGATCTCAGCGCGCATGCGTTGCGGGATTTGAT 537
Db 481 CGTCGCTCAACGGTGTTCGTAATCTCAACGCTGATGATGCTGCGGTGATTTGAT 540
QY 538 CGGAACCTTGCGCATGCGTTTACCAAGGGATCTTATAGAAGAGAACGGTCACACGATT 597
Db 541 CCTAATCTGTCTCAGCGCTTACCAAGGGATCTTATCGAAGAGAGCGGTCAACCCATC 600
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Db 601 AACCCACAAGGTCTCGTGACTCTCTTCTGTTCTGTTTCTATCGCTAACGGTGGAGATT 660
QY 658 GTATCTCGCGGTGTCTCGGCTTTGAGACTGAGGTAGGCGGCTTAAAGGATTTACAAAC 717
Db 661 GTCTCTGCTGCTGTATTCGGATTCGAGACTGAAGTGTGCTCTCAAGGGTATCACCAAC 720
QY 718 ACGAACGGCTTCTGCGCGTTGATGACGCTTGTCTCAGCGCGGACACACTCGAAATCA 777
Db 721 ACCAAGGTGTTCTTGTGTTGATGACGCTGTTGTTGACGCTGTGCACACTCCCAAGTCT 780
QY 778 CTTGCTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAACGTTGATATCATATCGTC 837
Db 781 CTTGCTAATTCCTTGGTGATGACATCCCATTTGGATACCGAACGTTGATACCACTCGTG 840
QY 838 ATCCGGAATCCGGAAGCGGTCTCAGCATTTCCGACGACCGATGCGTCAGGAAATTCATC 897
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QY 898 GGCACACCTATGAAAATGGGGCTTCGCGTGGCGGTACGTTGAGTTGCGTGGGCTCACA 957
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QY 958 GCGGCTCTTAACGTGAACCTGCGCATGTGCTCTATACGACGCTCGAANAACCTTCTTCCA 1017
Db 961 GCTGCTCCTAACTGGAAGCGTGTCTACACTCACGCTCGTAAAGTTCGTTCTTCCA 1020
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Db 1021 GCTCTCGCTCTCCCAAGTTCTGAAGAACGTTACTTCCAAGTGGATGGGTTTCCGTCGAAGC 1080
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Db 1261 ATTGCTAAGTCCCAAGCAACCTGGTCTGCATCCTAA 1296

RESULT 11

US-391-339-17  
; Sequence 17, Application US/08391339  
; Patent No. 5463175  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dennis R. Hoerner, Jr.,  
; ADDRESSEE: Monsanto Co. B4F  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391,339  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/156,968  
; FILING DATE:  
; APPLICATION NUMBER: US/07/17,370  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner, Dennis R., Jr.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10533)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1296 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (recombinant)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1296  
US-08-391-339-17

Query Match 71.6%; Score 925.6; DB 1; Length 1296;  
Best Local Similarity 83.6%; Pred. No. 0;  
Matches 1084; Conservative 0; Mismatches 209; Indels 3; Gaps 3;  
QY 1 ATGCTGAGACCAACCAAAAGTAGGCTATCGCTGGAGCGGGAATCGTCGGCGATGTCAGG 60  
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Db 121 GAAGGTGCAATTCGTTTGGAAATGCCGATGCTTTCACAGGCTCATCGCTCGCTCCATGTGCC 180  
QY 181 ATGCGGGGAAATTCGACGAGCGTGGCAAGTGGCTCTTTGACCCGATGGG - CCGTGTGCA 239  
Db 181 ATGCGGAGAAATTCGACAGCTTGGCTTCCAAAGTGGCTTCTTTGACCCAAATTTGGGTCCAATGTGCC 240  
QY 240 ATGCGGTTCAGCTA - TTTTCCAAACCATCATGGC - TGGTTCATTTTCGCTTCTGTAGCCGGA 297  
Db 241 ATCCGTTTCGGCTACTTTCCAAACCATCATGGCTTGGTGTGATTTCTTGTGCTGCTGA 300  
QY 298 AGACCAAAACAGGTGAAGGAGCAGCGCAAGACACTTCGCAATCTCATCAAGTCCACGGTG 357  
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QY 358 CCTCTGATCAAGTCATTTGGCGAGGAGGCTGATGGAGCCATCTGATCCGCCCATGAAGGT 417  
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QY 418 CATCTGACCGTATATCGTCGAAACAGACATTCGCCAAGGACCGCGGAGGTTTGGNACTG 477  
Db 421 CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAGGACCGCTGGAGGTTTGGNACTT 480  
QY 478 CGGCGTCTCAACGGTGTTCGCACGAGATCCCTCAGCGCCGATCGCTTTCGGGATTTTCGAT 537  
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QY 658 GTATCTGCGCGTGTCTCGGCTTTTGAGACTGAAGGTAGGGCGCTTAAAGCGATTCACACC 717  
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Db 721 ACCAAGGGTGTCTTGTCTGATGCGAGCTGTGTTCGACACTGGTCCACACTCCAAGTCT 780  
QY 778 CTTGCTAATTCGCTAGGGATGACATCCCGCTCGATACCGAACCTTGGATATCATATCGTC 837  
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QY 838 ATCGGGAATCCGGAAGCGGCTCCACGCAATTCGAGACCGGATCGCTCAGGAAATTCATC 897  
Db 841 ATCGCAACCCAGAAAGCTGCTCCACGATTTCCAACTACCGATGCTTCTCGAAAGTTTCATC 900  
QY 898 GCGACACCTATGGAATGGGGCTTCGCGTGGGGGTACGGTTGAGTTTCGCTGGGTTCACA 957  
Db 901 GCTACTCCTATGGAGATGGGTCTTCGCTGTTGCTGGAACCGTTTTCGCTGCTGCTCACT 960  
QY 958 GCGGCTCCTTAAGTGGAAAGCTGCGGATGTCCTTATACGACGCTCGGAAACCTTCTTCCA 1017  
Db 961 GCTGCTCCTTAAGTGGAGGCTGCTCAGCTTCTTCTACACTCGCGCTCGTAAGTTGCTTCCA 1020  
QY 1018 GCGCTCGGCGCTTCGAGTTTCTGAAGAACGATATTCCAAATGGATGGGTTTCGGCGCGAGC 1077  
Db 1021 GCTCTCGCTTCCTGCCAGTTCTCAAGAACGTTTACTCCAAGTGGATGGGTTTTCGCTCCAAGC 1080  
QY 1078 ATCCCGGATTCGCTCCCGCTGATTTGGCGGGCAACCCGAGACACCGACGCTATATCTATGCT 1137  
Db 1081 ATCCCGGATTCGCTTCCAGTGTGTTGGTCTGCTAGCCGCTACTCCAGACCGCTTATCTACGCT 1140  
QY 1138 TTTCCGCGATGTCATCTCGGATGACAGGGCGCGGATGACCGCAACGCTTCCTCTCAGAG 1197  
Db 1141 TTCGGTACGGGTACCTCGGTATGACTGGTGTCTCAATGACCGCAACCCCTCCTTCTGAG 1200

QY 1198 CTCCTCGCAGGCGGAAAGACCTCAATCGACATTTCCGCCCTTCGCACCAAAACCCGTTTGGT 1257  
Db 1201 CTCCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTCGCACCAAAACCCGTTTGGT 1260  
QY 1258 ATTGGCAATCCAAGCAAAACCGGTCGGGCAAGTTAA 1293  
Db 1261 ATTGGTAAGTCCAAGCAAAACCTGGTCTGCATCCCTAA 1296

RESULT 12

US-08-484-274A-17  
: Sequence 17, Application US/08484274A  
: Patent No. 5776760  
: GENERAL INFORMATION:  
: APPLICANT: Kishore, Ganesh M.  
: APPLICANT: Barry, Gerard F.  
: TITLE OF INVENTION: Glyphosate Tolerant Plants  
: NUMBER OF SEQUENCES: 33  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Arnold, White & Durkee  
: STREET: P.O. Box 4433  
: CITY: Houston  
: STATE: Texas  
: COUNTRY: USA  
: ZIP: 77210-4433  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/484,274A  
: FILING DATE: 07 June 1996  
: CLASSIFICATION: 435  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Patterson, Melinda L.  
: REGISTRATION NUMBER: 33,062  
: REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (713)789-2679  
: INFORMATION FOR SEQ ID NO: 17:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 1296 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: double  
: TOPOLOGY: linear  
: MOLECULE TYPE: DNA (recombinant)  
: FEATURE:  
: NAME/KEY: CDS  
: LOCATION: 1..1296  
US-08-484-274A-17

Query Match 71.6%; Score 925.6; DB 2; Length 1296;  
Best Local Similarity 83.6%; Pred. No. 0;  
Matches 1084; Conservative 0; Mismatches 209; Indels 3; Gaps 3;

QY 1 ATGGCTGAGAACCAAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGGTATGCACG 60  
Db 1 ATGGCTGAGAACCAACGAAGTGGTATCGCTGGAGCTGGAATCGTGGTGTTCACAT 60  
QY 61 GGGCTGATGCTTACGGCGCGGGATTCAAAGTCACCTGATTGACCCGAACCCCTCTGCG 120  
Db 61 GCTTTGATGCTTCAACGTCGTCGATTCAAGGTACCTTGATTGATCAAAACCCACCAAGT 120  
QY 121 CAAGCTGCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCGTCTCCCTATGTCC 180  
Db 121 GAAGGTGCTCTTTTCGGTAAACGCTGGTGGTTCACAGGTTCTCTCGGTGTTTCCAATGTC 180  
QY 181 ATGCCGGGAACCTTGACGAGCGTGCAGAGTGGCTCTTACCGCTGCTGCTCCCTATGTCC 239  
Db 181 ATGCCAGGAACCTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCAAATGGGTCATGTCC 240

QY 240 ATCCGGTTTCAGCTA-TTTTCCAACCATCATGCC-TGGTTGATTTCGCTTCTGTTAGCCGA 297  
Db 241 ATCCGGTTTCGGCTACTTTTCCAACCATCATGCC-TGGTTGATTTCGCTTCTGTTAGCCGA 300  
QY 298 AGACCAAAACAGGTGAAGGAGCAGCGGAAAGCAGCTTCGCAATCTCATCAAGTCCACGGTG 357  
Db 301 AGACCAAAACAGGTGAAGGAGCAGCTAAGGCAGCTTCGCTAAACCTCATCAAGTCCACACTG 360  
QY 358 CCTCTGATCAAGTCATTGGCGGAGGAGCTCATGGAGCCCATCTGATCCGCCCATGAAGGT 417  
Db 361 CCTTTGATCAAGTCTTTGGGCTGAGGAGCTGATGCTAGCCACCTTATCCGTCACGAAGGT 420  
QY 418 CATCTGACCGTATATCTGTGGAGAACGACATTCGCCAAGGACCGCGAGGTTCGGAACCTG 477  
Db 421 CACCTTACCGGTGTACCGTGGAGNAGCAGACTTCGCCAGGAGCGGTGGAGGTTCGGAACCT 480  
QY 478 CGGGCTCTCAACGGGTTCGCGACGACAGATCTCAGCGCCGATGCGTTGCGGGATTTTCGAT 537  
Db 481 CGTCTCTCAACGGGTTCGCTACTCAATCCTCAGCGCTGATGCAATTCGCTGATTTCCAT 540  
QY 538 CGAACTTGTGCGATGCTTTTACCAAGGGCATCTTATAGAGAGAGACGGTCCACAGATT 597  
Db 541 CCTAACTTGTCTACGGCTTTTACCAAGGGAATCTTATCGAAGAGAGACGGTCCACACCATC 600  
QY 598 AATCCGCAAGGCTCGTGACCCCTCTTGTTCGGGCGTTTATTCGGCAACGGTGGGCAATTC 657  
Db 601 AACCCACAAGTCTCGTGACTCTCTTGTTCGTCGTTTCATCGCTAACGGTGGAGAGTTC 660  
QY 658 GTATCTCGCGGTGTATCGGCTTTTGAGACTGAAGTAGGGCGCTTAAAGGCATTTACAACC 717  
Db 661 GTGTCTCTCGTGTATTCGGAATTCGAGACTGAAGTCTGCTCTCAAGGGTATCACCAACC 720  
QY 718 ACGAAGCGGCTTCTGGCGGTTGATGACAGCGTTCTGCAGCGCGCGCACACTCGAATCA 777  
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QY 778 CTTCCTAATTTCGGTAGCGGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCTC 837  
Db 781 CTTGCTAACTCCCTTGGTGATGACATCCCATCCATTTGGATACCGAAGCTGGATACCATCTG 840  
QY 838 ATCGGAATCCGAAGCGGCTCCACGCAATTCGACGACCGGATGCGTCAGGAAAATTCATC 897  
Db 841 ATCGCCAAACCCAGAAGCTGCTCCACGTAJTCCAACTACCGATGCTTCTGGAAGTTTCATC 900  
QY 898 GCGACACCTATGAAATGGGCGTTCGCGTGGCGGTACGGTTGAGTTCGCTGGCGCTCACA 957  
Db 901 GCYACTCCTATGGAGATGGGTCTTCGTGCTGGAACCGTTGAGTTCGCTGGCTGCTCACT 960  
QY 958 GCGCTCTCTAACTGGAAACGTGCGCATGTGCTCTATACGACGCTCGAANAATTCCTTCCA 1017  
Db 961 GCTGCTCCTAACTGGAAAGCTGCTACGTTCTCTACACTCGCGCTCGTAAGTTGCTTCCA 1020  
QY 1018 GCCTTCGCGCTCGGAGTTCCTGAAGAACGATATTTCCAAATGGATGGGTTCCGCGCGAGC 1077  
Db 1021 GCTCTCGCTCTCCAGTTCCTGAAGAACGTTACTTCCAAAGTGGATGGTTCGCTCCAAGC 1080  
QY 1078 ATCCCGGATTCGGTCCCGCTGATTGGCGGCAACCCGACACCCGACGTAATCTATGCT 1137  
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QY 1138 TTCCGGCATGGTCACTTCGGCATGACAGGGCGCGGATGACCGCAACGCTCTGCTCAGAG 1197  
Db 1141 TTCCGGTCACGTCACCTCGGTATGACTGGTGTCTCAATGACCGCAACCCCTGTTTCTGAG 1200  
QY 1198 CTCTCGCAGGCCAAAGACCTCAATCGACATTTTCGGCTTCGCAACCAACCCGTTTGGT 1257  
Db 1201 CTCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTCGCAACCAACCCGTTTGGT 1260  
QY 1258 ATTGGCAAAATCCAAGCAAAACGGGTCGGGCAAGTTAA 1293  
Db 1261 ATTGGTAAGTCCAAGCAAAACCTGGTCTGCATCCCTAA 1296



```

: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/484,274A
: FILING DATE: 07 June 1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Patterson, Melinda L.
: REGISTRATION NUMBER: 33,062
: REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (713)789-2679
: INFORMATION FOR SEQ ID NO: 30:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 69 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (synthetic)
: US-08-484-274A-30

Query Match 4.3%; Score 56.2; DB 2; Length 69;
Best Local Similarity 88.4%; Pred. No. 9.4e-10;
Matches 61; Conservative 0; Mismatches 8; Indels 0; Gaps

QY 711 TACAACACACGAGCGGTTCTGCGCGTTGATGAGCGGTTGTCGACGCGCGCACACTC 770
      ||||||| ||||| ||||||| ||||||| ||||||| ||||| ||||| |||||||
Db 1 TACAACCACTAACGGTGTCTGCGCTGTGATGCGAGCTGTTGTTGCAGCTGTTGTTGCACACTC 60

QY 771 GAATACACT 779
      |||||||
Db 61 TAAATCACT 69

RESULT 15
US-08-391-339-33
: Sequence 33, Application US/08391339
: Patent No. 5463175
: GENERAL INFORMATION:
: APPLICANT: Kishore, Ganesh M.
: APPLICANT: Barry, Gerard F.
: TITLE OF INVENTION: Glyphosate Tolerant Plants
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dennis R. Hoerner, Jr.,
: ADDRESSEE: Monsanto Co. 884F
: STREET: 700 Chesterfield Village Parkway
: CITY: St. Louis
: STATE: Missouri
: COUNTRY: USA
: ZIP: 63198
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/391,339
: FILING DATE:
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/156,968
: FILING DATE:
: APPLICATION NUMBER: US/07/717,370
: FILING DATE:

```

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; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 69 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
US-08-391-339-33

Query Match      4.2%; Score 54.6; DB 1; Length 69;
Best Local Similarity 87.0%; Pred. No. 3.3e-09;
Matches 60; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1125 CGTAATCTATGCTTTTCGGCCATGTCATCTCGGCATGACAGGGGGCCCGCATGACGGCAAC 1184
      ||||||||||||| || || ||||||||||| ||||||| || || ||||| |||||
Db 1 CGTAATCTATGCTTTTCGGTCACGGTCATCTCGGTATGACAGGTGCTCCAATGACTGCAAC 60

Qy 1185 GCTCGTCTC 1193
      |||||||
Db 61 TCTCGTCTC 69
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Search completed: January 1, 2001, 03:17:38  
Job time: 29282 sec

GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2000, 18:03:01 ; Search time 3327.86 Seconds  
(without alignments)  
2402.255 Million cell updates/sec

Title: US-08-484-274-4

Perfect score: 1293

Sequence: 1 ATCTCAGAACCAACAAAA.....AAACGGGTCGGCAAGTTAA 1293

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_est3:\*

4: gb\_est4:\*

5: gb\_est5:\*

6: gb\_est6:\*

7: gb\_est7:\*

8: gb\_est8:\*

9: gb\_est9:\*

10: gb\_est10:\*

11: gb\_est11:\*

12: gb\_est12:\*

13: gb\_est13:\*

14: gb\_est14:\*

15: gb\_est15:\*

16: gb\_est16:\*

17: gb\_est17:\*

18: gb\_est18:\*

19: gb\_est19:\*

20: gb\_est20:\*

21: gb\_est21:\*

22: gb\_est22:\*

23: gb\_est23:\*

24: gb\_est24:\*

25: gb\_est25:\*

26: gb\_est26:\*

27: gb\_est27:\*

28: gb\_est28:\*

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32: gb\_est32:\*

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36: gb\_est36:\*

37: gb\_est37:\*

38: gb\_est38:\*

39: gb\_est39:\*

40: gb\_est40:\*

41: em\_estba:\*

42: em\_estfun:\*

43: em\_esthuml:\*

44: em\_esthum2:\*

45: em\_esthum3:\*

46: em\_esthum4:\*

47: em\_esthum5:\*

48: em\_esthum6:\*

49: em\_esthum7:\*

50: em\_esthum8:\*

51: em\_esthum9:\*

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54: em\_esthum12:\*

55: em\_esthum13:\*

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57: em\_esthum15:\*

58: em\_esthum16:\*

59: em\_esthum17:\*

60: em\_esthum18:\*

61: em\_esthum19:\*

62: em\_esthum20:\*

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65: em\_estin3:\*

66: em\_estin4:\*

67: em\_estom:\*

68: em\_estovi:\*

69: em\_estov2:\*

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73: em\_estpl4:\*

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77: em\_estro3:\*

78: em\_estro4:\*

79: em\_estro5:\*

80: em\_estro6:\*

81: em\_estro7:\*

82: em\_estro8:\*

83: em\_estro9:\*

84: em\_estro10:\*

85: em\_estro11:\*

86: em\_estro12:\*

87: em\_estro13:\*

88: gb\_gss1:\*

89: gb\_gss2:\*

90: gb\_gss3:\*

91: gb\_gss4:\*

92: em\_gss1:\*

93: em\_gss2:\*

94: em\_gss3:\*

95: em\_gss4:\*

96: gb\_gss5:\*

97: gb\_gss6:\*

98: gb\_gss7:\*

99: gb\_gss8:\*

100: gb\_gss9:\*

101: em\_gss5:\*

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104: em\_gss8:\*

105: em\_gss9:\*

106: em\_gss10:\*

107: em\_gss11:\*

108: gb\_gss10:\*

109: gb\_gss11:\*

110: em\_gss12:\*

111: gb\_gss12:\*

112: gb\_gss13:\*

113: gb\_gss14:\*

114: gb\_gss15:\*

115: gb\_gss16:\*

116: gb\_gss17:\*

117: gb\_gss18:\*  
118: gb\_gss19:\*  
119: em\_gss13:\*  
120: gb\_gss20:\*  
121: gb\_gss21:\*  
122: gb\_gss22:\*  
123: gb\_gss23:\*  
124: gb\_gss24:\*  
125: em\_gss14:\*  
126: em\_gss15:\*  
127: em\_gss16:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	44.4	3.4	434	124	Al160534 Leishmania
C 2	37.4	2.9	702	96	AQ328054 Leishmania
C 3	36.4	2.8	634	19	AW097371 rs43a11.y
C 4	36	2.8	380	22	AW500960 UI-HF-BP0
C 5	36	2.8	389	22	AW501280 UI-HF-BP0
C 6	36	2.8	895	123	AL307658 Tetraodon
C 7	35.4	2.7	226	5	AA644181 ab63a02.s
C 8	35	2.7	360	16	AV190084 AV190084
C 9	35	2.7	382	36	C47876 C47876 Yuj1
C 10	35	2.7	517	17	AV386799 AV386799
C 11	34.8	2.7	171	17	AV316270 AV316270
C 12	34.8	2.7	205	18	AV413471 AV413471
C 13	34.8	2.7	251	18	AV418303 AV418303
C 14	34.8	2.7	271	24	AW19954 LjNEST12e
C 15	34.8	2.7	273	18	AV427698 AV427698
C 16	34.8	2.7	300	18	AV406977 AV406977
C 17	34.8	2.7	349	18	AV412853 AV412853
C 18	34.8	2.7	416	18	AV425451 AV425451
C 19	34.8	2.7	423	18	AV407852 AV407852
C 20	34.8	2.7	452	18	AV423367 AV423367
C 21	34.6	2.7	429	18	AV408636 AV408636
C 22	34.6	2.7	429	18	AV415123 AV415123
C 23	34	2.6	258	39	W09527 ma01b07.r1
C 24	34	2.6	261	36	D40242 RICS2075A.R
C 25	34	2.6	425	7	AA871231 VQ32902.r
C 26	34	2.6	433	4	AA542047 vk43d01.r
C 27	34	2.6	614	21	AW254765 ML105 pep
C 28	34	2.6	636	97	AQ447252 mgx80006C
C 29	33.8	2.6	296	16	AV139416 AV139416
C 30	33.8	2.6	360	36	C41677 C41677 Yuj1
C 31	33.8	2.6	935	123	AL245876 Tetraodon
C 32	33.6	2.6	409	35	BE411304 ISC004.B1
C 33	33.6	2.6	460	15	AU088715 AU088715
C 34	33.6	2.6	724	35	BE454097 HVSMEH008
C 35	33.2	2.6	353	36	C13125 C13125 Yuj1
C 36	33.2	2.6	398	15	AU082174 AU082174
C 37	33.2	2.6	494	14	AL387587 MCBQ43E07
C 38	33.2	2.6	676	34	BE248875 WF023D11D
C 39	33	2.6	472	36	BE516792 NFE620_G0
C 40	33	2.6	884	123	AL247657 Tetraodon
C 41	32.8	2.5	222	19	AV536254 AV536254
C 42	32.8	2.5	311	24	AW735014 pa46d04.y
C 43	32.8	2.5	400	14	AL364994 AL364994
C 44	32.8	2.5	427	18	AV426876 AV426876
C 45	32.8	2.5	587	25	AW916227 EST347531

ALIGNMENTS

RESULT 1  
P149R/c

LOCUS DEFINITION	P149R	434 bp	DNA	GSS	16-MAR-2000
Leishmania major Friedlin PAC P149 right end-sequence, genomic survey sequence.					
ACCESSION	AL160534				
VERSION	AL160534.1	GI:7258935			
KEYWORDS	GSS.				
SOURCE	Leishmania major.				
ORGANISM	Leishmania major.				
REFERENCE	1 (bases 1 to 434)				
AUTHORS	Ivens,A.C., Lewis,S.M., Bagherzadeh,A., Zhang,L., Chan,H.M. and Smith,D.F.				
TITLE	A physical map of the Leishmania major Friedlin genome				
JOURNAL	Genome Res. 8 (2), 135-145 (1998)				
MEDLINE	98146435				
REFERENCE	2 (bases 1 to 41)				
AUTHORS	Taylor,R.G., Huckle,E.E.J., Ivens,A.C., Rajandream,M.A. and Barrell,B.G.				
TITLE	Direct Submission				
JOURNAL	Submitted (14-MAR-2000) Leishmania major Friedlin genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and alicat@sanger.ac.uk				
COMMENT	see http://www.ebi.ac.uk/parasites/leish.html Details of Leishmania sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/Lmajor/ The primer sequence can be obtained from alicat@sanger.ac.uk.				
FEATURES	Location/Qualifiers				
source	1. .434				
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	/strain="Friedlin"				
	/db_xref="taxon:5664"				
	/clone="PAC P149"				
BASE COUNT	76 a 131 c 157 g 70 t				
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Query Match	3.4%;	Score 44.4;	DB 124;	Length 434;	
Best Local Similarity	54.2%;	Pred. No. 0.02;			
Matches	90;	Conservative	0;	Mismatches	76;
				Indels	0;
				Gaps	0;
Qy	34	GGAGCCGAATGTCGGGGTATGCAGCGCTGATGCTTCAGCGCGCGGATTCAAATC	93		
Db	357	GGCCCGCGCATTCGGTGTTCAGCACCGCATCGGCCCTCGCGGCACCGAGTC	298		
Qy	94	ACCTTGATGACCGAACCCCTCTGGCGAAGTGCATCGTTTGGGAATGCCGGATGCTTC	153		
Db	297	GTTCTTGTGATGCTTATC	238		
Qy	154	AACGGCTCATCGTCCCTTCCTATGTCATGCGCGGAACTTGAACA	199		
Db	237	CAGCGCAGCGGTGCAGCGCTATCGTTCCCGCGCGACTGGAAGA	192		
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DEFINITION	nbxb0042102f CUGI Rice BAC Library Oryza sativa genomic clone				
ACCESSION	nbxb0042102f				
VERSION	AQ328054.1	GI:4119904			
KEYWORDS	GSS.				
SOURCE	Oryza sativa				
ORGANISM	Oryza sativa				
REFERENCE	1 (bases 1 to 702)				
AUTHORS	Wing,R.A. and Dean,R.A.				
TITLE	A BAC End Sequencing Framework to Sequence the Rice Genome				
JOURNAL	Unpublished (1998)				
COMMENT	Contact: Wing RA Clemson University Genomics Institute				





QY	1110	AACCCGGACACCCGAGCTAATCTATGCTTTTCGGCCATGGTCTATCTCGCATGACACAGGGCC	1169
QY	1110	AACCCGGACACCCGAGCTAATCTATGCTTTTCGGCCATGGTCTATCTCGCATGACACAGGGCC	1169
Db	137	AGCTCCGTCGAAGGCTATAGCTTCAGTCGGCGCCAGAGCCAAAGTCTTGAAGCCCGAGAC	196
QY	1170	GCGGATGACCGCAACGCTCGTCTCAGAGCTCCTCGCAGCGCAAAAGAGCTTCAATCGCAT	1229
Db	197	GAGCGAGGTCTCCATCTCGGTCTGAGAGAGCCCGCCGCGAGAGAGAGCGCGCTCACCNT	256
QY	1230	TTTCGCCCTTCGCAACCAAC	1248







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BASE COUNT      61 a 76 c 55 g 59 t
ORIGIN
/clone_lib="Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; isolate=MiyakoJima MG-20"
Query Match      2.7%; Score 34.8; DB 18; Length 251;
Best Local Similarity 58.8%; Pred. No. 12;
Matches 60; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 4 TCTGAGAACACAAAAAGTAGGCATCGCTGGAGCCGGAATCGTGGCGGTATGCACGGCG 63
    || || || || || || || || || || || || || || || || || || || || ||
Db 11 TCGCGCAGCAGAGAAGATTCTGGTCACCGGGGTGCGCGCTTCATCGGCACCTCACACGGTG 70
    || || || || || || || || || || || || || || || || || || || || ||

Qy 64 CTGATGCTTCAGCGCCGCGGATTCAAAGTCACCTTGATTGAC 105
    | |||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 71 GTTCAGCTTCTCCATGACGGCTTCCATGCTCCATCATCGAC 112
    || || || || || || || || || || || || || || || || || || || || ||

RESULT 14
AW719954      271 bp mRNA EST 19-APR-2000
LOCUS
LjNEST12e2r Lotus japonicus nodule library 5 and 7 week-old Lotus
japonicus cDNA 5', mRNA sequence.
ACCESSION
AW719954
VERSION
AW719954.1 GI:7614480
KEYWORDS
EST.
SOURCE
Lotus japonicus.
ORGANISM
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Lotus.
REFERENCE
1 (bases 1 to 271)
AUTHORS
Colebatch,G., Freund,S., Trevisk,B and Udvardi,M.
TITLE
Lotus japonicus root nodule ESTs: tools for functional genomics
JOURNAL
Unpublished (2000)
COMMENT
Contact: Udvardi MK
Molecular Plant Nutrition
Max Planck Institute of Molecular Plant Physiology
Am Muehlenberg 1, 14476 Golm, Germany
Fax: 49 331 567 8250
Email: udvardi@mpimp-golm.mpg.de
Seq primer: T7
High quality sequence stop: 271.
FEATURES
Location/Qualifiers
1..271
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/organism="Lotus japonicus"
/db_xref="taxon:34305"
/clone_lib="Lotus japonicus nodule library 5 and 7
week-old"
/dev_stage="5 and 7 week-old plants"
/note="Organ: Nodule; Vector: pSPORT1; Site_1: SalI;
Site_2: NotI; The library was prepared using mRNA
extracted from nodules of 5 and 7 week-old Lotus plants.
Nodules were induced by, and contained Mesorhizobium
strain R7A."
BASE COUNT      62 a 89 c 49 g 71 t
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/clone_lib="Lotus japonicus nodule library 5 and 7
week-old"
/dev_stage="5 and 7 week-old plants"
/note="Organ: Nodule; Vector: pSPORT1; Site_1: SalI;
Site_2: NotI; The library was prepared using mRNA
extracted from nodules of 5 and 7 week-old Lotus plants.
Nodules were induced by, and contained Mesorhizobium
strain R7A."
Query Match      2.7%; Score 34.8; DB 24; Length 271;
Best Local Similarity 58.8%; Pred. No. 13;
Matches 60; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 4 TCTGAGAACACAAAAAGTAGGCATCGCTGGAGCCGGAATCGTGGCGGTATGCACGGCG 63
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Db 96 TCGCGCAGCAGAGAAGATTCTGGTCACCGGGGTGCGCGCTTCCATCGGCACCTCACACGGTG 155
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Qy 64 CTGATGCTTCAGCGCCGCGGATTCAAAGTCACCTTGATTGAC 105
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LOCUS
AV427698 Lotus japonicus young plants (two-week old) Lotus
japonicus cDNA clone MM085C02_r 5', mRNA sequence.
ACCESSION
AV427698
VERSION
AV427698.1 GI:7787904
KEYWORDS
EST.
SOURCE
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ORGANISM
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Lotus.
REFERENCE
1 (bases 1 to 273)
AUTHORS
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE
Generation of 7137 non-redundant expressed sequence tags from a
legume, Lotus japonicus
JOURNAL
DNA Res. 7 (2), 127-130 (2000)
MEDLINE
20277479
COMMENT
Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES
Location/Qualifiers
1..273
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/dev_stage="Lotus japonicus young plants (two-week old)"
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Search completed: January 1, 2001, 01:12:42
Job time: 25781 sec
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GenCore version 4.5

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OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 03:14:54 ; Search time 7299.04 Seconds  
(without alignments)  
775.497 Million cell updates/sec

Title: US-08-484-274-6

Perfect score: 1296

Sequence: 1 ATGGCTGAGNACCACAAAA.....AACGGGTCCGGCAAGTTAA 1296

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues

Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: gb\_om.\*

4: gb\_ov.\*

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9: gb\_pr1.\*

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11: gb\_pr3.\*

12: em\_fun.\*

13: em\_hum1.\*

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22: em\_ro.\*

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25: em\_un.\*

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91: gb\_sy.\*  
92: gb\_un.\*  
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94: gb\_vl2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1296	100.0	1296	5	II5326
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4	1255.2	96.9	1293	5	AR016592
5	1255.2	96.9	1293	5	II5325
6	1255.2	96.9	1689	5	II5324
7	1201.6	92.7	1296	5	AR016594
8	1201.6	92.7	1296	5	II5327
9	961.6	74.2	1296	5	AR016595
10	961.6	74.2	1296	5	II5328
11	958.4	74.0	1296	5	AR016604
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15	78.8	6.1	2289	2	PSEKSDA	M69159 Pseudomonas
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17	56.2	4.3	69	5	AR016619	Sequence
18	56.2	4.3	69	5	115349	Sequence 30
19	56.2	4.3	69	5	115382	Sequence 33
20	50.6	3.9	65	5	AR016614	Sequence 33
21	50.6	3.9	65	5	115347	Sequence 28
22	49	3.8	1540	2	EHU17017	u17017 Ectothiorho
23	48.2	3.7	61	5	AR016617	Sequence
24	48.2	3.7	61	5	115350	Sequence 31
25	47.6	3.7	62	5	AR016613	Sequence 31
26	47.6	3.7	62	5	115346	Sequence 27
27	47.2	3.6	68	5	AR016618	Sequence 32
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36	37	2.9	10236	1	AE000097	Rhizobium
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## ALIGNMENTS

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DEFINITION Sequence 6 from patent US 5463175.
ACCESSION 115326
VERSION 115326.1 GI:1250234
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 1296)
TITLE Barry,G.F. and Kishore,G.M.
JOURNAL Glyphosate tolerant plants
PATENT: US 5463175-A 6 31-OCT-1995;
FEATURES Location/Qualifiers
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source
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DEFINITION Sequence 3 from patent US 5776760.
ACCESSION AR016591
VERSION AR016591.1 GI:3972868
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 1692)
TITLE Barry,G.Francis and Kishore,G.Murthy.
JOURNAL Glyphosate tolerant plants
PATENT: US 5776760-A 3 07-JUL-1998;
FEATURES Location/Qualifiers
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ACCESSION AR016592  
VERSION AR016592.1 GI:3972869  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1293)  
AUTHORS Barry,G.Francis and Kishore,G.Murthy.  
TITLE Glyphosate tolerant plants  
JOURNAL Patent: US 5776760-A 4 07-JUL-1998;  
FEATURES Location/Qualifiers  
source 1..1293  
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Db 538 CCGAACTTGTTCGCATCGCTTTACCAAGGGCATTTATAGAAGAGAACCGTTCACACGATT 597
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Db 598 AATCGCAAGGGCTCGTGACCTCTTTGTTTCGGCGTTTATCGGAAACCGTTCGGCAATTC 657
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Qy 1141 TTCGCGCACGGTCATCTCGGATGACAGGGGGCGGATGACCGCAACCGTCTGCTCAGAG 1200
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Db 1198 CTCCTCGCAGGCGAAAGACCTCAATCGACATTTGCGCCCTTCGCAACCAACCGCTTGGT 1257
Qy 1261 ATTGCAAAATCCAAAGCAACGGGTCGGCAAGTTAA 1296
Db 1258 ATTGCAAAATCCAAAGCAACGGGTCGGCAAGTTAA 1293
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RESULT 5
I15325
LOCUS I15325 1293 bp DNA PAT 02-APR-1996
DEFINITION Sequence 4 from patent US 5463175.
ACCESSION I15325
VERSION I15325.1 GI:1250233
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1293)
AUTHORS Barry,G.F. and Kishore,G.M.
TITLE Glyphosate tolerant plants
JOURNAL Patent: US 5463175-A 4 31-OCT-1995;
FEATURES
source
1..1293
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BASE COUNT 286 a 367 c 359 g 281 t
ORIGIN
Query Match 96.9%; Score 1255.2; DB 5; Length 1293;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1290; Conservative 0; Mismatches 3; Indels 3; Gaps 3;
Qy 1 ATGGGCTGAGAACCAAAAAGTAGGCATCGCTGGAGCCGGAATCGTCGGCGGTATGCACG 60
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Db 61 GCGCTGATCTTCAGCGCCGCGGATTTCAAAGTCACCTTGATGACCCGAACCTCTCTGGC 120
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Qy 181 ATGCCGGGAAACTTTCAGAGCGTCCGGAAGTGGCTCCTTTGACCCGATGGGGCGGTTGTCA 240
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Db 298 AGACCAAAACAGGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 357
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Db 358 CCTCTGATCAAGTTCATTTGGCGGAGGAGGCTGATGCGAGGACCATCTGATCCGCCATGAAGGT 417
Qy 421 CATCTGACCGTATATCGTGGAGAGCAGACTTCGCCCAAGAGACCGCGGAGGTTGGGAAC 480
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Qy 481 CGGCGTCTCAACGGTGTTCGACGCGAGATCCTCAGCGCGGATGCGTTGGGGGATTTCCGAT 540
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Qy 541 CCGAACTTGTTCGCATCGCTTTACCAAGGGCATTTCTTATAGAAGAGAACCGTTCACACGATT 600
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Qy 1081 ATCCCGGATTCGCTCCCGGTGATTGGCCGGCAACCCGGACACCCCGACGTAATCTATGCT 1140  
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Qy 1141 TTCCGGCCACGGTCTATCTCGGCATGACAGGGGCGCGGATGACCGGAACGCTCGTCTCAGAG 1200  
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RESULT 6  
I15324 1689 bp DNA PAT 02-APR-1996  
LOCUS Sequence 3 from patent US 5463175.  
DEFINITION I15324  
ACCESSION I15324  
VERSION I15324.1 GI:1250232  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 1689)  
TITLE Barry,G.F. and Kishore,G.M.  
JOURNAL Glyphosate tolerant plants  
FEATURES Patent: US 5463175-A 3 31-OCT-1995;  
Location/Qualifiers  
1. .1689  
BASE COUNT 381 a 479 c 468 g 360 t 1 others  
ORIGIN

Query Match 96.9%; Score 1255.2; DB 5; Length 1689;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1290; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

Qy 1 ATGGCTGAGAACCAACAAAAAGTAGGCATCGCTGGAGCCGGAATCGTCGGCGTATGCAAG 179  
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Qy 61 GCGCTATGCTTCAGCGCCGCGGATTCAAAGTCAACCTGATGACCCGACCCCTCTCGGC 120  
Db 180 GCGCTATGCTTCAGCGCCGCGGATTCAAAGTCAACCTGATGACCCGACCCCTCTCGGC 239  
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Db 240 GAAGTGTGATCGTTTGGGAATGCGGATGCTTCAAGGGCTCATCGCGTCGCTATGTCC 299  
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Db 300 ATGCCGGGAACTTTGACGAGCTGCCGAGTGGCTCCTTGACCCGATGGGGCGCGTTGTCA 358  
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AR016594 1296 bp DNA PAT 05-DEC-1998  
LOCUS Sequence 7 from patent US 5776760.  
DEFINITION AR016594  
ACCESSION AR016594  
VERSION AR016594.1 GI:3972871  
KEYWORDS .  
SOURCE Unknown.

ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1296)  
AUTHORS Barry.G.Francis and Kishore,G.Murthy.  
TITLE Glyphosate tolerant plants  
JOURNAL Patent: US 5776760-A 7 07-JUL-1998;  
FEATURES  
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        1..1296  
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BASE COUNT 287 a 344 c 332 g 333 t  
ORIGIN

Query Match 92.7%; Score 1201.6; DB 5; Length 1296;  
Best Local Similarity 95.4%; Pred. No. 0;  
Matches 1237; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1 ATCGCTGAGAACCAACAAAGTAGGCATCGCTGGAGCGGAATCGTCGCGCTATGCCAG 60  
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DB 1261 ATTGCAAAATCCAAACGACGGTCCGCAAGTTAA 1296

RESULT 8  
LOCUS I15327 1296 bp DNA PAT 02-APR-1996  
DEFINITION Sequence 7 from patent US 5463175.  
ACCESSION I15327  
VERSION I15327.1 GI:1250235  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1296)  
AUTHORS Barry.G.F. and Kishore,G.M.  
TITLE Glyphosate tolerant plants  
JOURNAL Patent: US 5463175-A 7 31-OCT-1995;  
FEATURES  
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        1..1296  
        /organism="unknown"  
BASE COUNT 287 a 344 c 332 g 333 t  
ORIGIN

Query Match 92.7%; Score 1201.6; DB 5; Length 1296;  
Best Local Similarity 95.4%; Pred. No. 0;  
Matches 1237; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1 ATGGCTGAGAACCAACAAAGTAGGCATCGCTGGAGCGGAATCGTCGCGCTATGCACG 60  
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DB 61 GCTTTGATGCTTCAACGTCGTGATTCAAAGTCACCTTGATTGACCCGGAACCCCTCTGGC 120  
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DB 121 GAAGGTGCATCTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGTCCTATGTGCC 180  
QY 181 ATCCCGGGAAACTTGACGAGCGTCGCGAAGTCGGCTTGCATCCCGATGGGGCGTTGTCA 240  
DB 181 ATCCCGGGAAACTTGACGAGCGTCGCGAAGTCGGCTTGCATCCCGATGGGGCGTTGTCA 240

QY 241 ATCCGGTTACAGTATTTTCCAAACCATCATGCCCTGGTGTGATTCGCTTTCTCTTACGCCGA 300  
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RESULT 9  
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LOCUS AR016595 1296 bp DNA PAT 05-DEC-1998  
DEFINITION Sequence 8 from patent US 5776760.  
ACCESSION AR016595  
VERSION AR016595.1 GI:3972872  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1296)  
AUTHORS Barry,G.Francis and Kishore,G.Murthy.  
TITLE Glyphosate tolerant plants  
JOURNAL Patent: US 5776760-A B 07-JUL-1998;  
FEATURES Location/Qualifiers  
source 1..1296  
BASE COUNT 271 a 359 c 305 g 361 t  
ORIGIN  
  
Query Match 74.2%; Score 961.6; DB 5; Length 1296;  
Best Local Similarity 83.9%; Pred. No. 9.5e-248;  
Matches 1087; Conservative 0; Mismatches 209; Indels 0; Gaps 0;  
  
QY 1 ATGGCTGAGAACCCACAAAAAGTAGGCATCGCTGGAGCGGAATCTCGCGCGTATGCCAG 60  
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Db 1 ATGGCTGAGAACCCACAAAGGTTGGTATCGCTGGAGCTGGAACTCGTTGGTGTTCGACT 60  
QY 61 GCGGTGATGCTTACGCGCCGCGGATTCAAAGTCACTTTGATTTGACCCGAACCCCTCTGCG 120  
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Db 61 GCTTTGATGCTTCAACGTCGTGGATTCAGGTACCTTTGATTTGATTCGCAAAACCACAGT 120  
QY 121 GAAGTGCATCGTTGGGAATCCCGGATGCTTCAACGGCTCATCGTCTGCTCGCTATGTGCC 180  
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Db 121 GAAGTGCCTTTTCGCGTAACGCTGGTTGCTTCAACGGTTCCTCGCTGTGTTCCAATGTCC 180  
QY 181 ATGCGCGGAAACTTGACGAGGCTGCCGAAGTGGCTTTCACCCGATGGGCGCTTGTCAC 240  
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Db 181 ATGCGAGAAACTTGACTAGCTAGCTTCCAAAGTGGCTTCTTGACCCAATGGTCCATTTGCC 240  
QY 241 ATCGGTTACGCTATTTTCCAAACCATCATGCCCTGGTGTGATTTGCTGTGTAGCCGGA 300  
|||||  
Db 241 ATCGGTTTACGCTACTTTTCCAAACCATCATGCCCTGGTGTGATTTGCTGTGTGCTGCTGA 300  
QY 301 AGACCAACAGGTGAGGAGCAGCGGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360  
|||||  
Db 301 AGACCAACAGGTGAGGAGCAGCTAAGGCACCTCCGTAAGCTCATCAAGTCCACCTGTG 360  
QY 361 CCTCTGATCAAGTCTATTTGGCGGAGAGGCTGATCGGAGCCATCTGATCCGCCATCAAGGT 420  
|||||  
Db 361 CCTTTGATCAAGTCTTTCGCTGAGGAGCTGATGCTAGCCACCTTATCCGCTCACCAGGT 420  
QY 421 CATCTGACCGTATATCTGTGAGAGACGACATTCGCGCAAGGACCGCGGAGGTGGGAACGTG 480  
|||||  
Db 421 CACCTTACCGTGTACCGGTGGAGAGCAGACTTCGCGCAAGGACCGCTGGAGGTGGGAACCT 480  
QY 481 CGGCGTCTCAACGGTGTTCGCAACCCAGATCTCTAGCGCCGATGCTTGGGGATTTTCGAT 540  
|||||  
Db 481 CGTCTCTCAACGGTGTTCGTAACCTCTCAGCGCTGATGCTGCTGATTTTCGATTTTCGAT 540  
QY 541 CCGAACTTGTTCGGATGCGTTTACCAAGGGCATCTTATAGAAGAGAACGGTTCACACGATT 600  
|||||  
Db 541 CCTAACTTGTCTACGCGCTTTTACCAAGGGATCTTATAGAAGAGAACGGTTCACACCATC 600  
QY 601 AATCCGCAAGGGTCTGTGACCCCTCTTGTTCGGCGTTTTATFCGCGAACGGTGGCGAATTT 660  
|||||  
Db 601 AATCCCAAGGCTCTGTGACTCTCTTGTTCGTTCTGCTGCTTCACTCGCTTAACCGGTTC 660  
QY 661 GTATCTCGCGGTGTCATCGGCTTTGAGACTGAAGTGTAGGCGCTTAAAGGCATTTACAAACC 720  
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Db 661 GTGCTGCTGTATTCGCGGATTCGAGACTGAAGTGTGCTCTCAAGGGTATTCACCAACC 720

QY	721	ACGAAGGGGTTCTGGCCGTTGATGACAGCGTTGTGCGAGCGGGCCACACTCGAATCA	780
Db	121	GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCCTATATGTCC	180
QY	781	CTTGCTAAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC	840
Db	181	ATGCCGGGAACTTGACGAGCGTGCAGAGTGGCTCCTTGACCCGATGGGCGGTGTGCA	240
QY	841	ATCGGAAATCCGGAAGCCCTCCACGATTCGACGACCGATGCGGTAGGAAATTCATC	900
Db	841	ATCGCAACCCAGAGCTGCTCCACGATATCCAACTACCGATGCTTCTGGAAGTTTCATC	900
QY	901	GGACACCTATGGAATGGGCTTCCGCTGGCGGTACGGTTGAGTTCCGTCGGCTCACA	960
Db	901	GCTACTCCTATGGAGATGGGTCTGCTGTGCTGGAAACCGTTTCAGTTCCGTCGTTCACT	960
QY	961	GCGGCTCCTAACTGGAAACGTCGCGATGCTCTATACGACGCTCGAAACCTTCTTCCA	1020
Db	961	GCTGCTCCTAACTGGAAACGTCGCGATGCTCTATACGACGCTCGAAACCTTCTTCCA	1020
QY	1021	GCCCTGCGCCCTCGGAGTTCTGAAGAACGATATTCGCAATGGATGGGTTCCGGCCGAGC	1080
Db	1021	GCTCTGCTCCTGAGGAGTCTGAGAACGTTACTCCAACTGAGTGGTTCCGTCGCAAGC	1080
QY	1081	ATCCCGGATTCGCTCCCGTGTATGGCGGGCAACCCGACACCGACGTATCTATGCT	1140
Db	1081	ATCCAGATATTCCTTCCAGTGTATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1140
QY	1141	TTGCGGACGCTTACGCGGCGGATTCGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1200
Db	1141	TTGCGGACGCTTACGCGGCGGATTCGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1200
QY	1261	ATTGCAATTCACGAACGAGGTCGGCAAGTTAA	1296
Db	1261	ATTGTAAGTCCAAAGCAACTGGCTCGATCTAA	1296
RESULT	10		
LOCUS	115328		
DEFINITION	Sequence 8 from patent US 5463175.	PAT	02-APR-1996
ACCESSION	115328		
VERSION	115328.1	GI:1250236	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1296)		
AUTHORS	Barry,G.F. and Kishore,G.M.		
TITLE	Glyphosate tolerant plants		
JOURNAL	Patent: US 5463175-A 8 31-OCT-1995;		
FEATURES	Location/Qualifiers		
source	1..1296		
BASE COUNT	271 a 359 c 305 g	361 t	
ORIGIN			
Query Match	74.2%;	Score 961.6;	DB 5; Length 1296;
Best Local Similarity	83.9%;	Pred. No. 9.5e-248;	
Matches 1087;	Conservative	0; Mismatches 209;	Indels 0; Gaps 0;
QY	1	ATGGCTGAGAACCAAAAAGTAGCATCGCTGGAGCGGGAATCGTCGGCGATGTCAGG	60
Db	1	ATGGCTGAGAACCAAAAAGTAGCATCGCTGGAGCGGGAATCGTCGGCGATGTCAGG	60
QY	61	GGGCTGATGCTTACGCGGCGGATTCGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	120
Db	1141	TTGCGGACGCTTACGCGGCGGATTCGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1200

Db	61	GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTGATTGATCAAAACCCACAGGT	120
QY	121	GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCCTATATGTCC	180
Db	121	GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCCTATATGTCC	180
QY	181	ATGCCGGGAACTTGACGAGCGTGCAGAGTGGCTCCTTGACCCGATGGGCGGTGTGCA	240
Db	181	ATGCCAGGAACTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCAAATGGGTCCTATGTCC	240
QY	241	ATCCCGTTTCAGCTATTTTCCAAACCATCATGCGCTGCTGATTGCGTTTCTGTTAGCCGGA	300
Db	241	ATCCCGTTTCAGCTATTTTCCAAACCATCATGCGCTGCTGATTGCGTTTCTGTTAGCCGGA	300
QY	301	AGACCAAAACGAGTGAAGGAGCAGGCAAGCACTCCGCAATCTCATCAAGTCCACGGTG	360
Db	301	AGACCAAAACGAGTGAAGGAGCAGGCAAGCACTCCGCAATCTCATCAAGTCCACGGTG	360
QY	361	CCTCTGATCAAGTCAATTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT	420
Db	361	CCTTTGATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGT	420
QY	421	CATCTGACCGTATATCGTGAAGAGCAGACTTCGCCAAGGAGCAGGTTGGGAACTG	480
Db	421	CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAAGGAGCAGGTTGGGAACTG	480
QY	481	CGCGCTCTCAACGGTGTTCGCACGAGATCCTCAGCGCCGATGCGTTGCGGGATTTTCGAT	540
Db	481	CGTCTCTCAACGGTGTTCGCTACTCAATCTCAGCGCTGATGCAATTTGCGATTTTCGAT	540
QY	541	CGGACTTCTCGATCGCTTTTACCAGGCAATCTTTATAGAAGAACGCTCACAGATT	600
Db	541	CCTAAGTCTCTCACGCCCTTACCAGGCAATCTTTATAGAAGAACGCTCACAGATT	600
QY	601	AATCCGCAAGGCTCGTGACCTCTTGTTCGCGCTTTTATCCGCAAGCGTGGCGAATTT	660
Db	601	AACCCAAAGGCTCGTGACTCTTGTTCGCTGCTTTCATCGTAAACGTTGGAGAGTTT	660
QY	661	GTATCTGCGCTGTCACTCGGCTTTGAGACTGAAGGTAGGCGCTTAAAGGCAATTAACAAC	720
Db	661	GTGCTGCTCGTGTATCGGATTCGAGACTGAAGGTGCTCTCAAGGATTAACCAACC	720
QY	721	ACGAAGGGGTTCTGGCCGTTGATGACAGCGTTGTGCGAGCGGGCCACACTCGAATCA	780
Db	721	ACCAAGGGTCTTCTGCTGTTGATGACAGCTGTGTTGACAGCTGCTGCTCAAGGATTAACCA	780
QY	781	CTTGCTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGCTGATATCATATCGTC	840
Db	781	CTTGCTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGCTGATATCATATCGTC	840
QY	841	ATCGGAAATCCGGAAGCCCTCCACGATTCGACGACCGATGCGGTAGGAAATTCATC	900
Db	841	ATCGCAACCCAGAGCTGCTCCACGATATCCAACTACCGATGCTTCTGGAAGTTTCATC	900
QY	901	GGACACCTATGGAATGGGCTTCCGCTGGCGGTGACGGTTGAGTTCCGTCGGCTCACA	960
Db	901	GCTACTCCTATGGAGATGGGTCTGCTGTGCTGGAACCGTTGAGTTCCGTCGCTCACT	960
QY	961	GCGGCTCCTTAACCTGGAACGTCGCGATGCTCTATACGACGCTCGGAAACCTTCTTCCA	1020
Db	961	GCTGCTCCTTAACCTGGAACGTCGCTGCTGCTTCTTCTACACTGACGCTGTAAGTTGCTTCCA	1020
QY	1021	GCCCTGCGCCCTCGGAGTTTCTGAAGAACGATATTCGCAATGGATGGGTTCCGGCCGAGC	1080
Db	1021	GCTCTGCTCCTGAGGAGTCTGAGAACGTTACTCCAACTGAGTGGTTCCGTCGCAAGC	1080
QY	1081	ATCCCGGATTCGCTCCCGTGTATGGCGGGCAACCCGACACCGACGTATCTATGCT	1140
Db	1081	ATCCAGATATTCCTTCCAGTGTATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1140
QY	1141	TTGCGGACGCTTACGCGGCGGATTCGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1200
Db	1141	TTGCGGACGCTTACGCGGCGGATTCGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1200

Qy	1201	CTCCTCGCAGCGGAAAGACCTCAATCGACATTTTCGCCCTTCGCACCAACACCGCTTTGGT	1260
Db	1201	CTCCTCGCAGGTGAGAGACCTCTATCGACATCTCTCCATTTCGCACCAACCGTTTCGGT	1260
Qy	1261	ATTGCGCAATCCAAAGCAACCGGTCCGCAAGTTAA	1296
Db	1261	ATTGTTAAGTCCAAAGCAACGTGCTCGATCTTAA	1296
RESULT 11			
AR016604	AR016604	1296 bp	DNA
LOCUS	Sequence 17 from patent US 5776760.		PAT
DEFINITION	Sequence 17 from patent US 5776760.		
ACCESSION	AR016604		
VERSION	AR016604.1	GI:3972881	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1296)		
AUTHORS	Barry,G.Francis and Kishore,G.Murthy.		
TITLE	Glyphosate tolerant plants		
JOURNAL	Patent: US 5776760-A 17 07-JUL-1998;		
FEATURES	Location/Qualifiers		
source	1..1296		
BASE COUNT	267 a	360 c	309 g
ORIGIN	360 t		
Query Match 74.0%; Score 958.4; DB 5; Length 1296;			
Best Local Similarity 83.7%; Pred. No. 6.9e-247;			
Matches 1085; Conservative 0; Mismatches 211; Indels 0; Gaps 0;			
Qy	1	ATGGCTGAGAACCAAAAAAGTAGGCATCGCTGGAGCGCGGAATCGTCGGCGTATGCACG	60
Db	1	ATGGCTGAGAACCAAGAAAGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTTCACAT	60
Qy	61	GGCGTGATGCTTCAGCGCGCGGATTCAAAGTCACCTTGATTGACCCGAACCTCTCTGCG	120
Db	61	GCTTTGATGCTTCACGCTCGTGATTCAGGTTACCTTGATGATCCAAACCCACCAAGT	120
Qy	121	GAAGTGATCGTTTGGGAATCCGGATGCTTTCAACGGCTCATCCGTCGCTATGTCC	180
Db	121	GAAGTGCTCTTTCGGTAAACGCTGGTTCCTCAACGGTTCCTCGGTTGTTCCAATGTCC	180
Qy	181	ATCCCGGAAACTTCACGAGCGTGGCGAAGTGGCTTCCTTGACCCGATGGGCGGTGTCA	240
Db	181	ATGCCAGGAAACTTGACTAGCGTTCCAAAGTGGCTTCCTTGACCCATGGGTTCCATTTGCC	240
Qy	241	ATCCGGTTTCAGCTATTTCCCAACCATCATGCCCTGGTTGATTGCGTTTCTGTAGCGCGA	300
Db	241	ATCCGTTTCGGCTACTTCCCAACCATCATGCCCTGGTTGATTGCGTTTCTGTGCTGGA	300
Qy	301	AGACCAACAAGGTGAAGGAGCAGCGGAAAGACACTCCGCAATCTCATCAAGTCCACGGTG	360
Db	301	AGACCAACAAGGTGAAGGAGCAGCTAAGGCACCTCCGTAACCTCATCAAGTCCACTGTG	360
Qy	361	CCTGTGATCAAGTCAATTTGGCGGAGAGGCTGATGGAGCCATCTGATCCGCCATGAAGT	420
Db	361	CCTTTGATCAAGTCTTGGCTGAGGAGGCTGATGAGCCACCTTATCCGTCACCAAGGT	420
Qy	421	CATCTGACCGTATATGCTGGGAGACGACTTCGCCAAGGACCGGAGGTTGGGAACGTG	480
Db	421	CACCTTACCGTGTACCGTGGGAGAACGACTTCGCCAGGACCGTGGAGGTTGGGAACTT	480
Qy	481	CGCGCTCTCAACGGTGTTCGCACCGCAGATCCCTACGCGCGATGCGTTGCGGGATTTGCAT	540
Db	481	CGTCTCTCAACGGTGTTCGTAATCCCTACGCGCTGATGCATTTGCGTGTGATTTCCGAT	540
Qy	541	CCGAACCTTGTCCGATTCGCTTTACCAAGGCGCATTTCTATAGAAGAACCGGTACACGATT	600
Db	541	CCGAACCTTGTCCGATTCGCTTTACCAAGGCGCATTTCTATAGAAGAACCGGTACACCATC	600

Db	541	CTTAACCTTGTCTCACGCCCTTTTACCAAGGGAATCCTTTATCGAAGAGAACCGGTACACCATC	600
Qy	601	AATCCGCAAGGGCTCGTGACCCCTCTTGTTCGGCGTTTATCGGGAACCGGTGGCGAATTT	660
Db	601	AACCCACAAGTCTCGTGACTCTCTTGTTCGTCGTTTCATCGCTAACGGTGGAGAGTTC	660
Qy	661	GTATCTCGCGGTCTCATTCGGCTTTGAGACTGAAAGGTAGGGCGCTTAAAGGCAATTTACACC	720
Db	661	GTGTCTGCTGCTTATTCGGATTTCGAGACTGAAGGTGCTCTCTCAAGGGTATCACCAAC	720
Qy	721	ACGAACGGCGTCTTGGCCGTTGATGCAAGCGTTGTCGACGCGCGCACACTCAAAATCA	780
Db	721	ACCAACGGGTGTTTGTCTGTTGATGCAAGTGTGTTGTCAGCTGGTGACACTCAAGTCT	780
Qy	781	CTTGCTAAATTCGCTAGCGATGACATCCCGCTCGATACCGAACGCTGGATATCATATCGTC	840
Db	781	CTTGCTAAATTCCTTGGTGATGACATCCCATTTGATACCGAACGCTGGATACCATCGTG	840
Qy	841	ATCGGAATTCGGAAGCGCTCCACGATTCGAGACGACCGATGCGTCAGGAAATTCATC	900
Db	841	ATCGCAACCCAGAAGCTGCTCCACGATTTCCAACTACCGATGCTTCTGGAAGTTCATC	900
Qy	901	GCACACCTATGGAATGGGGCTTCGCGTGGCGGTAGGTTGAGTTTCGCTGGGCTCACA	960
Db	901	GCTACTCTTATGAGATGGGTCTTCGTGTTGCTGGAACCGTTGAGTTTCGCTGGTCTCACT	960
Qy	961	GCGCTCCTAACTGGAACGTCGCGATGCTCTATACGACACGCTCGAATACTTCTTCCA	1020
Db	961	GCTGCTCCTAACTGGAAGCGTCTCAGTTCCTACACTCGCGCTCGTAACTTCTTCCA	1020
Qy	1021	GCCTCGCGCTCGGAGTTCTGAAGACGATATTCAAATGGATGGGTTCGCGCCGAGC	1080
Db	1021	GCTCTCGCTCCTGCCAGTCTGAAGAACGTTACTCCAAGTGGATGGGTTCGCTCCAAGC	1080
Qy	1081	ATCCCGATTCGCTCCCGTGATTGGCCGGCAACCCGACACCCGAGTATCTATGCT	1140
Db	1081	ATCCCGATTCCTTCCAGTATTTGGTCTGCTACCCGCTACTCCAGACGTTATCTACGCT	1140
Qy	1141	TTCCGGCACCGTCTATCTCGGCATGACAGGGCGCGGATGACCGAACGCTCGTCTCAGAG	1200
Db	1141	TTCCGGTCACGGTCACCTCGGTATGACTGGTGTCTCCATGACCGCAACCCCTGTTCTGAG	1200
Qy	1201	CTCCTCGCAGCGGAAAGACCTCAATCGACATTTTCGACATTTTCGACCAACCGCTTTGGT	1260
Db	1201	CTCCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTCGCAACCAACCGCTTCGGT	1260
Qy	1261	ATTGGCAATCCAAAGCAACGGTCCGCAAGTTAA	1296
Db	1261	ATTGGTAAGTCCAAAGCAACGTTGGTCTGCAATCTTAA	1296
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IL5337	IL5337	1296 bp	DNA
LOCUS	Sequence 17 from patent US 5463175.		PAT
DEFINITION	Sequence 17 from patent US 5463175.		
ACCESSION	IL5337		
VERSION	IL5337.1	GI:1250245	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1296)		
AUTHORS	Barry,G.F. and Kishore,G.M.		
TITLE	Glyphosate tolerant plants		
JOURNAL	Patent: US 5463175-A 17 31-OCT-1995;		
FEATURES	Location/Qualifiers		
source	1..1296		
BASE COUNT	267 a	360 c	309 g
ORIGIN	360 t		
Query Match 74.0%; Score 958.4; DB 5; Length 1296;			

Db	1021	GCTCTCGCTCCTGCCAGTTCTTGAAGAAGCTTTACTCCAAAGTGGATGGGTTTCCGCTCCAAGC	1080
Qy	1081	ATCCCGGATTCCGCTCCCGGTGATTGGCGGGCAACCCGGACACCCGACGTAATCTATGCT	1140
Db	1081	ATCCCGGATTCCGCTCCCGGTGATTGGCGGGCAACCCGGACACCCGACGTAATCTATGCT	1140
Qy	1141	TTCGGCCACGGTCAATCTCGGATGACAGGGCGCGGATGACCGCAACCGCTTTGGT	1200
Db	1141	TTCGGTCACGGTCACTCCGGTATGACTGGTGCTCCAATGACCGCAACCGCTTTCTGAG	1200
Qy	1201	CTCTCGCAGCGGAAAGACCTCAATCGACGATTTTCGGCCCTTCGCACCAACCGCTTTGGT	1260
Db	1201	CTCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTCGACCAACCGTTTCGGT	1260
Qy	1261	ATTGGCAATCCAAAGCAACGGGTCGGCAAGTTAA	1296
Db	1261	ATTGGTAGTCCAGCAAACTGGTCTGCATCTAA	1296
RESULT 13			
LOCUS A59869 1631 bp DNA PAT 06-MAR-1998			
DEFINITION Sequence 1 from Patent WO9706269.			
ACCESSION A59869			
VERSION A59869.1 GI:3715060			
KEYWORDS			
SOURCE Arabidopsis sp.			
ORGANISM Arabidopsis sp.			
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis.			
AUTHORS Jepson, I.			
TITLE INDUCIBLE HERBICIDE RESISTANCE			
JOURNAL Patent: WO 9706269-A 1 20-FEB-1997;			
ZENECA LTD (GB)			
FEATURES			
source Location/Qualifiers			
1..1631			
/organism="Arabidopsis sp."			
/db_xref="taxon:29726"			
BASE COUNT	342 a	454 c	381 g 454 t
ORIGIN			
Query Match 67.8%; Score 878.8; DB 5; Length 1631;			
Best Local Similarity 80.2%; Pred. No. 1.7e-225;			
Matches 1079; Conservative 0; Mismatches 217; Indels 50; Gaps 2;			
Qy	1	ATGCTGAGAACCAACAAAAAGTAGGCATCCTCGAGCCGGAATCGTCGGCGTATGCACG	60
Db	274	ATGCTGAGAACCAACAAAGAGTTGGTATCCTCGAGCTGGAATCGTTGGTGTTCGACT	333
Qy	61	CGCTGTATGCTTACGCGCGCGGATTCAAAGTCACTTGTATGACCGCAACCCCTCTGGC	120
Db	334	CTTTGTATGCTTCAACGTCGCGGATTCAAAGGTTACCTTGTATTCCAAAACCCACAGGT	393
Qy	121	GAAGTGATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCGCTGCTCCCTATGTCC	180
Db	394	GAAGTGCTCTTTTCGGTAACGCTGGTTGCTTCAACGGTTCTCCGTTGTTCCAAATGTCC	453
Qy	181	ATGCGGGAAACTTCAGACAGCGTCCGGAAGTGGCTTCCTTGACC-----	223
Db	454	ATGCCAGAACTTGACTAGCGTTCCAAAGTGGCTTCTGGATCCTGTTGTAATTCAGC	513
Qy	224	-----CGATGGGCGGTTGTCAATCCGGTTTCAGCTATTTTCCAAACCATCATGCCCTG	275
Db	514	TTAGGGATCCAAATGGTCCATGTCCATCCGTTTCAGCTACTTTCCAAACCATCATGCCCTG	573
Qy	276	GTTGATTCGCTTTCTGTAGCCGGAAGACCAACAAAGGTGAAGGAGCGGCAAGCACT	335
Db	574	GTTGATTCGTTTCTGTGCTGGAAGACCAACAAAGGTGAAGGAGCAAGCTAAGGCACT	633
Qy	336	CCGCAATCTCATCAAGTCCACGGTGCCTTCTCATCAAGTTCATTTGGCGGAGGAGGCTGATGC	395



Db	634	CCGTAACCTCATCAAGTCCACCTGTGCTTTTGATCAAGTCTTGGCTGAGAGGCTGATGC	693
Qy	396	GAGCCATCTGATCCGATCAAGGTCATCTGACCGTATATCTGTTGGAGAGACGACTTCGC	455
Db	594	TAGCCACCTTATCCGTCACAGAGGTCACTTACCGTGTACCGTGGAGAGACGACTTCGC	753
Qy	456	CAAGGACCGGAGGTTGGAACTCGGGCGTCTCAACGGTGTTCGCACGACGATCTCTCAG	515
Db	754	CAAGGACCGTGGAGTTGGAACTTCTGTCGTCTCAACGGTGTTCGTACTCAAACTCTCAG	813
Qy	516	CGCCGATCGTGTGGGGATTTTCGATCGGAACCTTGTTCGCATGCGTTTACCAAGGCAATTC	575
Db	814	CGCTGATGCAATTCGCTGATTTTCGATCCTAACTTGTCTCAGCGCTTTTACCAAGGAATCT	873
Qy	576	TATGAAGACGAACGGTCACACGATTAATCCGAAGGCTCGTGACCCCTCTTGTTCGGCG	635
Db	874	TATCGAAGAGAGGGTCACACCACTCAACCCACAAGGTCTCGTGACTCTCTTGTTCGTGC	933
Qy	636	TTTTATCCGAAGCGTGGCGAATTTGTATCTGCGCGTGTATCTCGGCTTTGAGACTGAAG	695
Db	934	TTTCATCGCTAACGGTGGAGTTCTGTCTCTCTGTTTATCGGATTCGAGACTGAAG	993
Qy	696	TAGGCGCGTTAAAGGCATTTACAACACGAGACGGCTTCTGGCGTTTGATGCAGCG----	750
Db	994	TCGTGCTCTCAAGGGTATCACCAACCAACCGGTGTTCTTGTGTGTGATGCTGCAGTGT	1053
Qy	751	-----GTTGTCCGACCGCGCCACACTCGAAATCACTTGCTAAAT	790
Db	1054	GTGAATTTCAAGCTTACTGCAAGTTGTTGCAAGCTGGTGCACACTCCAAGTCTCTTTGCTA	1113
Qy	791	CGCTAGGCGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTCATCGCGAATC	850
Db	1114	CCCTTGGTATGATACATCCCATTCGATACCGAAGCTGGATACCACTCGTGTATCGCAAC	1173
Qy	851	CGGAAGCGGCTCCACGATTTCCGACGACCGATCGCTCAGGAATAATTCATCGGACACCTA	910
Db	1174	CAGAAGCTGCTCCACGATTTCCAACTACCGATCTCTTGGAAGTTTCATCGCTACTCCTA	1233
Qy	911	TGGAATTTGGGCTTCGGTCGGCGGTACGGTTACGTTTCGCTGGCTCAGCGGCTCCTA	970
Db	1234	TGGAGTTGGGCTTCGGTTGCTTGGAAACGGTTGAGTTGCTGCTGCTCCTGCTGCTCTA	1293
Qy	971	ACTGGAACGTGGCGATGTGCTCTATACGACGCTCGAAACCTCTTCCAGCGCTCGCGC	1030
Db	1294	ACTGGAACGTGCTCAGTTCTCTACACTCGTCTCGTAACTGCTTCCAGCTCTCGCTC	1353
Qy	1031	CTGCGAGTTCTGAAGAAGCATATTCGAAATGGATGGGTTTCGGCGGACGATCCCGGAT	1090
Db	1354	CTGCGAGTTCTGAAGAAGCATATTCGAAATGGATGGGTTTCGGCGGACGATCCCGAT	1413
Qy	1091	CGCTCCCGTGATTTGGCGGGCAACCGGACCCGACCTGATCTATGCTTTCGGCCACG	1150
Db	1414	CCCTTCAGTGATGGTGGTGTGCTACCGGTACTCCAGAGTTATCTACGCTTTTCGGTCA	1473
Qy	1151	GTCACTTCGGCATGACAGGGGCGCGATGACCCCAACGCTGCTCTCAGAGCTCTCGCAG	1210
Db	1474	GTCACTTCGGATGACTGGTGTCTCAATGACCGCAACCTCGTTCTGAGCTCTCTCGCAG	1533
Qy	1211	GCGAAGAAGCCTCAATCGACATTTCCGCTTTCGACCAACCGCTTTGATTTGGCAAT	1270
Db	1534	GTGAAGAAGCCTCATCGACATCTCTCAATTCGACCAACCGTTTCGGTATTTGGTAAGT	1593
Qy	1271	CCAAGCAACCGGTCGGCAAGTTAA	1296
Db	1594	CCAAGCAACCTGGCTCGCATCTAA	1619

RESULT 14

PSEAKSD

LOCUS 3430 bp DNA BCT 26-APR-1993

DEFINITION *Pseudomonas putida* alpha-ketoglutarate semialdehyde dehydrogenase gene, complete cds.

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Db 2627 CCTGAGTCACGCCAGGCACTGAGCGGTTCGCCACCGCATCCACAGCAGCGGTGCGG 2686
QY 502 ACGCAGATCCTCAGCGCCGATCGTTGGCGGATTTTCGATCCGAACCTTGTGCGATCGTTT 561
Db 2687 GTGACGCTGTGTCGCGCGAAACCGTGCAGGAGCGAGCGCCCACTGAGCCCGTCACTG 2746
QY 562 ACCAAGGCGATTCCTATAGAAGAACAGCGTACACAGATTAATCCGACAGGCGTCTGTACC 621
Db 2747 CTGGCGGCGGTGTTCTTTCCGCGCACCGCGGCATTCATCGACCCCTTACCGGGTTGTGTC 2806
QY 622 CTCTTTGTTTCGGCGTTTATCCGAACGCTGCGGAATTTGTATCTGCGCGTGTCTCATCGGC 681
Db 2807 GAATCTGTTGGAAGCGCCNAGCCAGCGCGTGCCTGTTGTTTCAGCGCGCAGGTCCGATGCC 2866
QY 682 TTTGAGACTGAAGTAGGCGGCTTAAGAGCAATACAAACACAGGCGGTCTTGGCCCGTT 741
Db 2867 GGGCAATTCACAGCGCGGCGTGAGCCTGGCGACGACCAAGGACGCTCAATGCCCGC 2926
QY 742 GATGACGCGGTTCGCGACCGCGGCACACTCGCAATCACTTGTCTAATTCGCTAGCGGAT 801
Db 2927 CAGGTGCTGATCAGCTGTGGTGCCCATTTCTGCGAAACTGACCGCGCGCTGACGGGCAAG 2986
QY 802 GACATCCCGCTCGATACGCAAGCTGGATATCATATCGTCATCGCGAATCCCGAAGCCGCT 861
Db 2987 CGGTTACCGCTGGACACAGACCGCGTTACCACCTGATGTTCCCGGGTGAGCACCAGCGC 3046
QY 862 CCACGCAATTCGACAGCAGCGATCGCTCAGGAAATTCATCGCGACACCTATGGAATGGGG 921
Db 3047 CTGCGGCTTTGCAGTCACCTTCGCTGGAGCGCAAGTTCATCATCAGCCCAATGG-CCGAAG 3105
QY 922 CTTCGCGTGGCGGGTAGGTTGAGTTTCGCTGGGCTCACAGCGCTCTCAACTGGAACGT 981
Db 3106 TTGCGCCCTGGCGGACGCGTGAGTTTCGCGCGGCTGGAGACCCGCAAGCATGCAACGG 3165
QY 982 GCGCATGTGCTCTATACGACACCTCGAAGACTTCTTCCAGCCCTTCGCGCTCGAGTTCT 1041
Db 3166 GCATGCGAGTTGCA-----CCGGTTGAGCAAGGGGTGTTCCGGCAAGACTTGAGCGTCG 3220
QY 1042 GAAGAACGATATTCNAATGSGGTTCGCGCGGAGCATCCCGGATTCGCTCCCGCGT 1101
Db 3221 AAGCGCGCA---CGCGGTGAGTGGCTTCGCGGCTTCGTTACCGGACTTCGCTGCGGTG 3276
QY 1102 ATTTGCGCGGCAACCGGACACCCGACGTAATCTATGCTTTCGCGCAGCGTCACTCGGC 1161
Db 3277 ATCGACAGGG---TGTGTGATGGCGGTGCTGTGTGGCGTTTGGGCATCAGCACCTGGGG 3333
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Db 3334 TTGACCCAGCGCGCGTGACGCG 3356
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RESULT 15

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PSEKSDA      PSEKSDA      2289 bp      DNA      BCT      26-APR-1993
LOCUS         Pseudomonas putida alpha-ketoglutarate semialdehyde dehydrogenase
DEFINITION   gene, complete cds.
ACCESSION    M69159
VERSION      M69159.1 GI:151317
KEYWORDS     ketoglutarate semialdehyde dehydrogenase.
SOURCE       Pseudomonas putida (strain ATCC 12633) DNA.
ORGANISM     Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
              Pseudomonas.
              1 (bases 1 to 2289)
              Burlingame, R.P., Maruya, A., Ally, A.H., Ally, D. and Backman, K.C.
              Nucleotide sequences of hydroxyproline-specific alpha-ketoglutarate
              semialdehyde dehydrogenase genes from two strains of Pseudomonas
              putida
              Unpublished (1991)
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PLAFSVAGGDTASALAGCPVYVKAHSAHPCTSELVRAVARAKVOKSLAPGVFSLLF
GSGREVGIALVSDPRIKAVGTGSGRGMALINAAQARLEIPVVAENSSINPVLLFP
AALBARGEALAGFVASLTGAGOFCTNPLVMARQGPALDAFIKAAANLVORSPAOT
MLTQGLISAVENGVEVTLAENTHAQTVAVGRAKREPVPCTVVRHPCGSGFSECALQAE
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NGWPTGVEVCDAMVHGDFPATSDATTSVGTAAILRLRPVCYQDFDPTLLPAALQH
GNPLQRLRLDGRPRPTCTNPLPTIATT"
BASE COUNT      378 a      766 c      734 g      411 t
ORIGIN

Query Match      6.1%; Score 78.8; DB 2; Length 2289;
Best Local Similarity 54.5%; Pred. No. 2e-10;
Matches 158; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

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Db 1728 GCCAACAAATCGCCACGACATAACCGCTCATCGGCGGGGAATCATCGCGCTCGCGCG 1787
QY 64 CTGATGCTTCAGCGCGCGGATTCAAAGTCACTTGATTGACCGAACCCTCCTGGCGAA 123
Db 1788 CTGCAACTGGCGCGCTGGGGCTGCGGTGACGGTCGTCGACGACGAGGAGCCGCCAT 1847
QY 124 GGTGCATCGTTTGGGAATCCGGATGCTTCAACGGCTCATCCGTCGTCCCTATGTCCATG 183
Db 1848 GGTGCTCTGTTCCGGAATCGCGGCGATCTGCGGACCGAGCAGGTGTTTCCCATCGCGGAT 1907
QY 184 CCGGGAACCTTACGAGCGGTGCGGAAGTGGCTTCCTTGACCCCGATGGGCGCGTTGTCAATC 243
Db 1908 TTTGCGATCCTGAACGCTTGCCATGCGCATGAGACCGCATGGGCGCGTTGCGGCTG 1967
QY 244 CGGTTTCAGCTATTTTCCAAACCATCATGCCCTGCTGTTGATTGCTTTTCTGTT 293
Db 1968 GACTGGAAGTACATGCCGCGCGCCCTGCGGTGTTTGGCCCGGCTACTGTT 2017
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Search completed: January 1, 2001, 03:15:19  
Job time: 29203 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 03:32:11 ; Search time 263.11 Seconds  
(without alignments)  
1850.400 Million cell updates/sec

Title: US-08-484-274-6  
Perfect score: 1296  
Sequence: 1 ATGGCTGAGNACCACAAAA.....AACGGGTCCGGCAAGTTAA 1296

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 18781343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /SID56/gcgdata/geneseq/geneseqn/NA1981.DAT:\*
- 3: /SID56/gcgdata/geneseq/geneseqn/NA1982.DAT:\*
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- 12: /SID56/gcgdata/geneseq/geneseqn/NA1991.DAT:\*
- 13: /SID56/gcgdata/geneseq/geneseqn/NA1992.DAT:\*
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- 20: /SID56/gcgdata/geneseq/geneseqn/NA1999.DAT:\*
- 21: /SID56/gcgdata/geneseq/geneseqn/NA2000.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1294.4	99.9	1321	13 Q20833	Manipulated glypho
2	1288	99.4	1692	13 Q22705	Glyphosate oxidore
3	1252	96.6	1689	13 Q20832	Glyphosate oxidore
4	1200	92.6	1321	13 Q20834	Modified glyphosat
5	961.6	74.2	1296	13 Q20835	Synthetic glyphosa
6	961.6	74.2	8418	20 X57309	Sugar beet T-DNA c
7	878.8	67.8	1631	18 T85664	CPT1-COX gene fusi
8	673	51.9	8798	20 X57308	Sugar beet T-DNA c
9	671.4	51.8	8012	20 X57305	Sugar beet T-DNA c
10	37	2.9	534720	19 V30458	Rhizobium species
11	37	2.9	536165	19 V30459	Rhizobium species
12	35	2.7	38734	20 Z32020	Human METHI relate

C 13	34	2.6	405	20	X98168	Nucleotide sequenc
C 14	34	2.6	603	20	X98167	Nucleotide sequenc
C 15	34	2.6	922	19	V15073	Hybrid DNA compris
C 16	34	2.6	1137	20	X98164	Nucleotide sequenc
C 17	34	2.6	1209	12	Q12569	Protease2 open rea
C 18	34	2.6	1513	12	Q12567	Alkaline protease
C 19	34	2.6	42235	20	X98035	Nucleotide sequenc
C 20	33	2.5	423	18	T80725	Type II topoisomer
C 21	33	2.5	2455	21	Z45836	cDNA of intestinal
C 22	33	2.5	2821	21	Z45837	cDNA of intestinal
C 23	33	2.5	5059	20	X84332	Stealth virus nucl
C 24	32.8	2.5	1140	20	X36611	Pseudomonas oxidat
C 25	32.8	2.5	2830	21	A23429	cDNA encoding huma
C 26	32.6	2.5	534720	19	V30458	Rhizobium species
C 27	32.6	2.5	536165	19	V30459	Rhizobium species
C 28	32.4	2.5	1546	12	Q12568	Protease2 and beta
C 29	32.4	2.5	3172	12	Q12566	Alkaline protease
C 30	31.4	2.4	690	19	V64538	M. tuberculosis im
C 31	31.4	2.4	690	19	V44429	Mycobacterium tube
C 32	31.4	2.4	690	20	Z19339	M. tuberculosis an
C 33	31.4	2.4	690	20	Z19127	M. tuberculosis re
C 34	31.4	2.4	1755	19	V03306	Bacterium OC9a pho
C 35	31.4	2.4	2241	21	Z51469	Vector pVGRXR enco
C 36	31.4	2.4	2295	21	Z51470	Vector pVGRXR-5A/5
C 37	31.4	2.4	2301	21	Z51471	Control vector pVg
C 38	31.2	2.4	1116	20	X81700	DNA encoding a fru
C 39	31.2	2.4	1359	21	Z53148	Neisseria gonorrhoe
C 40	31.2	2.4	1359	21	Z53150	Neisseria meningit
C 41	31.2	2.4	3358	20	V70229	Human receptor tyr
C 42	31.2	2.4	35099	19	V27112	Adenovirus 17. Ma
C 43	31	2.4	1531	18	T46195	Maize insecticidal
C 44	30.8	2.4	611	21	Z80753	Human colon cancer
C 45	30.8	2.4	1837	20	Z16889	Human gene express

ALIGNMENTS

RESULT 1

- Q20833
- ID Q20833 standard; DNA; 1321 BP.
- XX
- AC Q20833;
- XX
- DT 01-MAY-1992 (first entry)
- XX
- DE Manipulated glyphosate oxidoreductase gene.
- XX
- KW Recombinant; GOR; resistance; ss.
- XX
- OS Bacterial isolate LBAA.
- XX
- FH Key Location/Qualifiers
- FT CDS 9..1304
- FT /\*tag= a
- FT /note= "encodes wild type glyphosate oxidoreductase"
- XX
- PN W09200377-A.
- XX
- PD 09-JAN-1992.
- XX
- PF 24-JUN-1991; 91WO-US04514.
- XX
- PR 24-JUN-1991; 91US-0717370.
- XX
- XX 25-JUN-1990; 90US-0543236.
- XX
- PA (MONS ) MONSANTO CO.
- XX
- PI Kishore GM, Barry GF;
- XX
- DR WPI, 1992-041559/05.
- XX
- XX P-PSDB; R20642.



PR	24-JUN-1991;	91US-0717370.	
PR	25-JUN-1990;	90US-0543236.	
XX			
XX	(MONS )	MONSANTO CO.	
XX			
XX	Kishore GM,	Barry GF;	
XX			
XX	WPI: 1992-041559/05.		
DR	P-PSDB; R22262.		
XX			
PT	Gene encoding glyphosate oxido-reductase enzyme - used to transform plants to produce plants tolerant to glyphosate herbicide		
PT	herbicide		
XX			
PS	Claim 1; Fig 2; 142pp; English.		
CC	The sequence is that of a gene encoding a glyphosate oxidoreductase (GOR) enzyme. It was obtd. from bacterial isolate LBAA. It is used to transform plants such that they express the enzyme sufficiently to enhance the glyphosate tolerance of the plant. Transformed plants resistant to glyphosate can be obtd. so that weeds can be selectively controlled in fields contg. crops. This sequence (fig 2) contains apparent discrepancies (see feature table) with a supposedly identical sequence (SEQ ID No.3 in the specification), since it is unclear from the specification which of these is correct, both sequences have been indexed. See also Q20833-Q20841 and Q20832 - the alternative sequence for the GOR gene.		
XX			
SQ	Sequence 1692 BP; 381 A; 478 C; 471 G; 361 T; 1 other;		
	Query Match	99.4%;	Score 1288; DB 13; Length 1692;
	Best Local Similarity	99.6%;	Pred. No. 0;
	Matches 1291; Conservative	0;	Mismatches 5; Indels 0; Gaps 0;
QY	1	ATGGCTGAGAACCAAAAAGTAGCATCGCTGGAGCCGGGAATCGTCGGGCTATGCACG 60	
Db	120	atgctgagaaccacaaaaagtaggcatcgcctggagccggaa tcgtcggcgtatgcacg 179	
QY	61	GCCTCATGCTTTCAGCGCCCGGATTCAAAGTCACTTTGATTGACCCGAACCTCTCTGGC 120	
Db	180	gcgctgatgcttcagcgcgcggattcaaaagtcacctgatgaccggaagcctcctggc 239	
QY	121	GAAGTGTCATGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGCTCGTCCCTATGTC 180	
Db	240	gaaggtgcacgtttgggaatccggatgcttcaacggctcctcgtcgtccctatgtcc 299	
QY	181	ATGCCGGGAACCTTGACGAGCGTGCAGAGTGGCTCCTTGACCCGATGGCGCGTGTGCA 240	
Db	300	atgccgggaacttgacgagcgtgcggaagtggctccttgacccgatggggccgtgtgca 359	
QY	241	ATCCGCTTCAGCTATTTTCCAAACCATCATGCCCTGGTTGATTCGCTTTCTGTAGCCGGA 300	
Db	360	atccggttcagctattttccaaacatcatgccttggttgatcgtcttctgttagccgga 419	
QY	301	AGACAAACAAGGTGAAGAGCAGCGCAAGCACCTCCGCAATCTCATCAAGTCCACGCTG 360	
Db	420	agaccaacaaggtgaaggagcagggaagcactccgcaactcatcaagtccacggtg 479	
QY	361	CCTCTGATCAAGTCATTTGGCGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT 420	
Db	480	cctctgatcaagtcatttggcggaggagcgtgatgcgagccatctgatccgcgatgaaggt 539	
QY	421	CATCTCACCGTATATCGTGAGAGCACACTTCCCAAGGACCGCGGAGGTTGGGAACGTG 480	
Db	540	catctgaccgtatatactgtggagaagcagacttcgccaagagccgcggaggttgggaaactg 599	
QY	481	CGGCTCTCAACGGTGTTCGACGACGAGATCCTCAGCGCCGATGCGTTGCGGGATTTCGAT 540	
Db	600	cggcgtcctaacggtgttcgcacgcagatcctcagcgcgatgctgtcgggatttcgat 659	
QY	541	CCGAACCTTGTCGATCGGTTTACCAAGGGCATTCCTTATAGAGAGAACGGTCAACAGTAT 600	



KW Recombinant; GOR; resistance; ss.  
XX Bacterial isolate LBAA.  
OS  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 9..1304  
FT /\*tag= a  
FT /note= \*encodes wild type glyphosate oxidoreductase"  
XX  
XX W09200377-A.  
XX  
XX  
XX 09-JAN-1992.  
XX 24-JUN-1991; 91WO-US04514.  
XX 24-JUN-1991; 91US-0717370.  
PR 25-JUN-1990; 90US-0543236.  
XX  
XX (MONS ) MONSANTO CO.  
PA  
XX  
XX Kishore GM, Barry GF;  
PI  
XX  
XX WPI; 1992-041559/05.  
DR P-PSDB; R20642.  
XX  
XX Gene encoding glyphosate oxido-reductase enzyme - used to  
PT transform plants to produce plants tolerant to glyphosate  
PT herbicide  
XX  
XX Claim 1; Page 102; 142pp; English.  
XX  
XX The sequence is that of the gene encoding a glyphosate oxidoreductase  
CC (GOR) enzyme which has been modified using mutagenic primers. The  
CC gene sequence was redesigned to eliminate as much as possible the  
CC following sequences or sequence features (while avoiding the  
CC introduction of unnecessary restriction sites), stretches of G's  
CC and C's of 5 or more, A + T rich regions (predominantly) that could  
CC function as polyadenylation sites or potential RNA destabilisation  
CC regions, and codons not frequently found in plant genes. The G + C %  
CC of the GOR gene was reduced from 56% in the manipulated version  
CC (Q20833) to 52% in the modified version. However it still encodes  
CC the wild type GOR enzyme. It was obtd. from bacterial isolate LBAA.  
CC It is used to transform plants such that they express the enzyme  
CC sufficiently to enhance the glyphosate tolerance of the plant.  
CC Transformed plants resistant to glyphosate can be obtd. so that  
CC weeds can be selectively controlled in fields contg. crops.  
CC See also Q20832-Q20841 and Q22705.  
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XX Sequence 1321 BP; 293 A; 349 C; 339 G; 340 T; 0 other;  
SQ

Query Match 92.6%; Score 1200; DB 13; Length 1321;  
Best Local Similarity 95.4%; Pred. No. 0;  
Matches 1236; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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DB 9 atggctgagaaacacaaaaagtaggcatcgctggagctggaatcgttggtgatgcact 68  
QY 61 GCGCTGATGCTTCACGCCGCGGATTCAAAGTCACCTTCGATTGACCCGAACCTCCTGGC 120  
DB |||||  
DB 69 gctttagtctcaacgctcgtagattcaaaagtcacctgattgacccgaacctcctggc 128  
QY 121 GAAGGTGCATCGTTTGGGAATCCCGATGCTTCAACGGCTCATCGCTCGCTCCCTATGTGC 180  
DB |||||  
DB 129 gaagtgatcgtttgggaatccggatgcttcaacggctcatcgtcgctccctatgtcc 188  
QY 181 ATGCGGGGAAACTTGACGAGCGTGCGGAAGTGGCTCCTTTGACCCGATGGGCGGTGTCA 240  
DB |||||  
DB 189 atgcggaacttgacgagcgtgcgaagtggctccttgacctgacccgatggggcgtgtca 248  
QY 241 ATCCGGTTGACGTATTTTCCACCACCATGCGCTGGTTGATTTCGCTTCTGTAGCCGGA 300  
DB |||||

DB 249 atccggttcagctattttccaaccatcatgcccgtgattgattcgttttctgttagccgga 308  
QY 301 AGACCAAAACAGGTGAAGGAGGAGCGGCAAGACTCCGCAATCTCATCAAGTCCACGGTG 360  
DB |||||  
DB 309 agacaaaacaagtggaagagcagcgaaagcaactccgcaatctcateaagtcacagggg 368  
QY 361 CCTCTGATCAAGTCAATGCGGAGGAGGCTGTATGCGAGCCATCTGTATCGCCCATGAAGGT 420  
DB |||||  
DB 369 cctctgatcaagtcattggcgaggaggtgatgtagcgccatctgatccgccatgaaggt 428  
QY 421 CATCTCACCGTATATCGTGSAGAAGCAGACTTCGCCCAAGACCGCGGAGGTGGGAACTC 480  
DB |||||  
DB 429 catctgaccgtatatctcgtggagaagcagacttcgccaagaccgcggaggttggcaactg 488  
QY 481 CGGCGTCTCAACGGTGTTCGCACGAGATCCTCAGCGCGCATGCGTTCGGGATTTTCGAT 540  
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DB 489 cggcgctcaacggtgttcgcagcagatccctctctgctgatgcttctgctgattcogat 548  
QY 541 CCGAAGTCTCGATGCGTTTACCAAGGGCATTTCTATTAGAGAGAACGGTTCACAGATT 600  
DB |||||  
DB 549 cctaaacttgctgcatgcttttaccgaaggcattctctatagaagagaacggtcacagatt 608  
QY 601 AATCCGCAAGGGCTCGTGACCCCTCTTGTTCGGCGTTCATCCGCAACGGTGGCGAATT 660  
DB |||||  
DB 609 aatccgcaaggctcgtgacctcttcttccggcgttttatcgcgaacggtggcgaaatt 668  
QY 661 GTATCTGCCGCTGTATCGGCTTTGAGACTGAAGGTAGGCGGCTTAAAGGCATTAACAAC 720  
DB |||||  
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QY 721 AGAAGCGGCTTCTGGCGCTTGTATGACAGGGTGTTCGACGCGGCGCACACTCGAANATCA 780  
DB |||||  
DB 729 actaaacggtgttcgctgttgatgcagctgttctgagcaggtgtgcacacttaataca 788  
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DB |||||  
DB 789 ctgtctaattcgtgagcgatgacatcccgctcgaaccgaacgctggatcatcatcgtc 848  
QY 841 ATCGCGAATCCGGAAGCGCTCCACGCATTCGACGACCGACGATCGCTCAGGAAATTCATC 900  
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QY 1261 ATTGGCAATCCAAAGCAACGGGTCCGGCAAGTTAA 1296  
DB |||||  
DB 1269 attggcaaatccaaagcaaacgggtccgcggaagtaa 1304

ID	Q20835	standard; DNA; 1296 BP.	
AC	Q20835;		
XX			
DT	01-MAY-1992	(first entry)	
XX			
DE	Synthetic	glyphosate oxidoreductase gene.	
XX			
KW	Recombinant;	GOR; resistance; ss.	
XX			
OS	Synthetic.		
XX			
PH	Key	Location/Qualifiers	
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FT		/*tag= a	
XX			
PN	W09200377-A.		
XX			
PD	09-JAN-1992.		
XX			
PF	24-JUN-1991;	91WO-US04514.	
XX			
PR	24-JUN-1991;	91US-0717370.	
PR	25-JUN-1990;	90US-0543236.	
XX			
PA	(MONS )	MONSANTO CO.	
XX			
PI	Kishore GM,	Barry GF;	
XX			
XX			
DR	WPI; 1992-041559/05.		
DR	P-PSDB; R20642.		
XX			
PT	Gene encoding	glyphosate oxido-reductase enzyme - used to	
PT	transform	plants to produce plants tolerant to glyphosate	
PT	herbicide		
XX			
PS	Claim 1;	Page 1032; 142pp; English.	
XX			
CC	The sequence is that of the gene encoding a glyphosate oxidoreductase (GOR) enzyme, the gene sequence was synthesised so that it could be redesigned to eliminate as much as possible the following sequences or sequence features (while avoiding the introduction of unnecessary restriction sites), stretches of G's and C's of 5 or more; A + T rich regions (predominantly) that could function as polyadenylation sites or potential RNA destabilisation regions, and codons not frequently found in plant genes. The G + C% for the synthetic gene is 51% and the potential to form short, high energy, hair-pin structures is reduced. However it still encodes the wild type GOR enzyme. It is used to transform plants such that they express the enzyme sufficiently to enhance the glyphosate tolerance of the plant. Transformed plants resistant to glyphosate can be obt'd. so that weeds can be selectively controlled in fields contg. crops. See also Q20832-Q20841 and Q22705.		
XX			
SQ	Sequence	1296 BP; 271 A; 359 C; 305 G; 361 T; 0 other;	
Query Match 74.2%; Score 961.6; DB 13; Length 1296;			
Best Local Similarity 83.9%; Pred. No. 3.7e-297;			
Matches 1087; Conservative 0; Mismatches 209; Indels 0; Gaps 0;			
Qy	1	ATGCGCTGAGAACCAAAAAGTAGCGTCGGAGCCGGAATGCTCGCGGATGACG 60	
Db	1	atggctgagaaacacaaagattagcgtcgagccgggaatgctcggcgatgacg 60	
Qy	61	CGCGTGTGCTTACGCGCGCGGATTCAAAAGTCACCTTGATTGACCCGACCCCTCCTGGC 120	
Db	61	gcttgatgctcgaacgcgtggattcaaggttacccctgattgattcaaaaccccggt 120	
Qy	121	GAAGGTCATCGTTTGGGAATGCGGTATGCTTCAACGGCTCATCGCTCGTCCCTATGTCC 180	
Db	121	gaaggctctcttcgttaacgcgtggttgccttaacaggttccctcgtgttccaatgtcc 180	

Qy	181	ATGCGCGGAAACTTTGACGAGCGTGCCGGAAGTGGCTTCCCTTGGACCCGAYGGGCGGTTGTCA 240	
Db	181	atgcaggaaacttgactagcgttccaaagtggctcttgacccaatgggtccattgtcc 240	
Qy	241	ATCGGGTTACGCTATTTTCCAAACCATATGCCCTGGTTGATTTCGCTTCTGTAGCCGGA 300	
Db	241	atccggttcagctactcttccaaaccatcatgctctgggttgattcgtttcttctgtgctgga 300	
Qy	301	AGACCAAAACAAGGTGAAGGAGCAGCGGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360	
Db	301	agaccaaaacagggtgaaggagcaagcactccgtaacctcatcaagtccaactgtg 360	
Qy	361	CCTCTGATCAAGTCAATTCGGCGAGAGGCTGATGGAGCCATCTGATGATCGGCAATCAAGGT 420	
Db	361	ctcttgatcaagtccttgctgaggagcgtgatgctagccaccttatcgtcaacgaagt 420	
Qy	421	CATCTGACCGTATATCTGTGGAGAACGACACTTCGCCAAGACCGCGGAGGTGGGAACGTG 480	
Db	421	caccttacccgtgtaccgtggagagcagactctgcgaaggaccgtggagggttgggaactt 480	
Qy	481	CGGGTCTCAACCGGTGTCGCACGCAGATCTCTACGCGCGATGCGTTTCGGGATTTTCGAT 540	
Db	481	cgtcgctcaacogtgcgttactcaaatctcgaagcgtgatgcattcgtgatctcgtat 540	
Qy	541	CCGAACCTTGTCCGATGCGCTTTACCAAGGCGCATTTCTATAGAGAGAACGGTCACACGATT 600	
Db	541	ctaacttgctcagcgcctttaccaagggaatccttatcgaagagacggtccacaccatc 600	
Qy	601	AATCGGCAAGGCTCGTGACCCCTCTTGTTCGGCGCTTTTATTCGGCAACGGTGGCGAATTT 660	
Db	601	aaccacaaagctcgtgactctcttctcgtcttcctcgtctcgttaacacggtggagagttc 660	
Qy	661	GTATCTGGCGCTGATCATCGGCTTTGAGACTGAAGGTAGGCGCTTTAAAGGCATTATCAACC 720	
Db	661	gtgctcgtcgtgttatcgcgattcgaagcgtgaagcgtgctctcaagggtatcaccacc 720	
Qy	721	ACGAACGCGTTCTGGCGGTTGATGCACGCGTTGTCGACGCGCGCGCACACTCGAAATCA 780	
Db	721	accaacggtgtctctgctgtgatgcagctgtgtgtgcagctggtgcacactccaagctc 780	
Qy	781	CTTCTAATTCGCTAGGCGATGACATCCGCTCGATACCGAACGTTGGATATCATATCTGTC 840	
Db	781	cttctactcctcccttggtagacatcccatgtagacacgctggatataccacatcgtg 840	
Qy	841	ATCGCGAATTCGGAGCGCTCCACGCATTCGACGACCGATGCGTCAGGAAAATTTATC 900	
Db	841	atcgcaaccacgaagcgtgctccacgtattccaactaccagatgctctcggaaagtctac 900	
Qy	901	CGGACACTATGGAAATGGGGCTTCGCGTGGCGGTACGGTTGAGTTTCGCTGGGCTCACA 960	
Db	901	gctactcctatggagatgggtctctcgtgtgtggtggaacgcttgagttcgtcgttctcact 960	
Qy	961	GCCGCTCTAACTGSAACGTCGCGATGCTCTATACGACGCTCGGAAAACCTTCTTCCA 1020	
Db	961	gctgctcctaactggaagcgtgctcaogtctctacactcgcctcgttaagtgtctcca 1020	
Qy	1021	GCCCTCGCGCTCGAGTTCTGAAGAACGATATTCCAAATGGATGGGTTCGGCGCGAGC 1080	
Db	1021	gctctcgtcctcgcagttctgaagaacgttactccaagtggatgggttccgcgtccaagc 1080	
Qy	1081	ATCCCGGATTCGCTCCCGGTGATTTGGCGGGCAACCCCGACACCCGACGCTAATCTATGCT 1140	
Db	1081	atcccgatctccctccagtgattggtcgtgtaccogtactccagacgttatctacgct 1140	
Qy	1141	TTGCGCACGCTCATCTCGGCATGACAGGGCGCGGATGACCGCAACGCTCTGCTCAGAG 1200	
Db	1141	ttcgggtcacggtccaccctcgttatgactgggtgctccaatgaccgcaacctggttctcag 1200	
Qy	1201	CTCCTCGCAGCGCAAAAGACCTCAATGCACATTTTCGCCCTTCGCACCAACACCGTTTGGT 1260	
Db	1201	ctcctcgcagtgagaagacctctatgcacatctctccattcgcaccaaacccgttctcggt 1260	
Qy	1261	ATTGGCAAAATCCAAAGCAACCGGTCGCCGCAAGTTAA 1296	



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Db 1261 attggtgaagtcacaaactggtctctgcaccta 1296
      ||||| || ||||| ||||| ||||| ||||| |||||
RESULT 6
X57309
ID X57309 standard; DNA; 8418 BP.
XX
AC X57309;
XX
DT 26-JUL-1999 (first entry)
XX
DE Sugar beet T-DNA containing cp4/epsps #2.
XX
KW Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plant;
KW 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide;
KW tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.
XX
OS Beta vulgaris.
XX
PN WO922322-A1.
XX
PD 14-MAY-1999.
XX
PF 29-OCT-1998; 98MO-EP06859.
XX
PR 31-OCT-1997; 97US-0112003.
XX
PA (NOVS ) NOVARTIS AG.
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI Mannerloef M, Steen P, Tenning PP;
XX
DR WPI; 1999-313347/26.
XX
PT Glyphosate resistant transgenic sugar beet plants
XX
PS Claim 15; Page 36-41; 55pp; English.
XX
CC This invention describes a novel sugar beet plant, including its
CC descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase
CC (cp4/epsps) enzyme activity which is obtainable by Agrobacterium
CC mediated transformation with a gene allowing expression of cp4/epsps
CC in plants, where the plant lacks both right and left T-DNA border
CC sequences. The transgenic sugar beet plants of the invention are capable
CC of tolerating herbicide treatment with glyphosate (also known as
CC N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.
XX
SQ Sequence 8418 BP; 2170 A; 1976 C; 1976 G; 2296 T; 0 other;

Query Match 74.2%; Score 961.6; DB 20; Length 8418;
Best Local Similarity 83.9%; Pred. No. 9.5e-297;
Matches 1087; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

QY 1 ATGGCTGAGAACCAAAAAGTAGGCATCGCTGAGCGGGAATCGTCGGCGATGACG 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7095 atggctgagacacaaagaagtgtgtagctgtagagctggaagtcgtgttgtaact 7154
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GCGCTGATGCTTTCAGCGCGCGGATTCAAAGTCACCTTGATTGACCCGACCCCTCTGGC 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7155 gctttgatgcttcaacgctcggtgattcaaggtttaacttgattgattccaaacccaccaggt 7214
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 AAAGGTGATCGTTTGGGAATCCCGGATTCCTTCAACGGCTCATCGTCTCGCTATGTCC 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7215 gaagtgctctcttcggtaaacgctggttgcctcaacggttccctcgttcttccaatgtcc 7274
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 ATGCGGGAAACTTGACGAGCGTCCGAAGTGCGTCTTGACCCGATGGCGCGGTGTGCA 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7275 atgcaggaaacttgactagcgttccaaagtgccttcttgaccacaatgggtccattgtcc 7334
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 ATCCGGTTCAGCTATTTTCCAAACCATCATGCGCTGGTGTGATTGCTTTTGTAGCCGGA 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 7  
T85664

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Db 7335 atcgtttcagtaacttttccaaaccatcatcgtcgttggtgatcgttcttctgtctgctgga 7394
QY 301 AGACCAACAAGGTGAAGGAGGAGCGAAGCAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7395 agaccaacaaggtagaaggagcaagtaagcactccgttaacctcaatgaagtcacatgtg 7454
QY 361 CCTCTGATCAATGATTGGCGGAGGAGGTGATGCGAGCCATCTGTATCCGCCATGAAGGT 420
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7455 cctttgatcaagtccttggctgaggaggtgatgctagcaacctatccgtcacgaaggt 7514
QY 421 CATCTGACCGTATATCGTGAGAGCAGACTTCGCCAAGGACCGCGGAGGTTCGGGACATG 480
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7515 caccctaccggtacacgtggaagcagacttcgcaagacgctggaaggttgggaact 7574
QY 481 CGCGCTCTCAACGGTTCGCGACGAGATCCTCAGCGCGGATCGGTTGCGGATTTTCGAT 540
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7575 cgtcgtctcaacggtgttcgtactcaaatccctcagcgtgatgcatcgtgattcgtat 7634
QY 541 CCGAAGTTCGCGATGCGTTTACCAAGGCGATTCCTTATAGAGAGAACGGTTCACAGATT 600
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7635 cctaaactgtctcaacgctttaccgaagggaatcccttatcgaagagagcgttcacacatc 7694
QY 601 AATCGCAAGGGCTCGTGACCCCTCTTGTTCGCGGTTTATCGCGAAGCGTGGCGAATT 660
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7695 aaccacaaaggctcgtcgtactcctctgttctcgtcgttaacgctgaacggttggaggttc 7754
QY 661 GTATCTGCGCGTGTATCGCGCTTTGAGACTGAAGGTAGGCGCGCTTAAAGGCAATTACAAC 720
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7755 gtgctcgtcgttctatcggttgcgactgaagtcgctcgtcctcaaggttatcaccacc 7814
QY 721 ACGAAGCGGTTCTGCGCGTTCGCGAGCGGTTGTCGAGCGCGGCGCACACTCGAATCA 780
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7815 accaaaggtgttcttctgtgtgatgcagctgtgtgtgcagctggtgcacactccaaagtct 7874
QY 781 CTGTGCTTAATTCGTAGGCGATGACATCCCGCTCGATACCGAAGCTGCGATATCATATCGTC 840
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7875 ctgtcactcctcttggtagacatcccatggataccgaacgtggatcaccacatcgtg 7934
QY 841 ATCGGCAATCCGGAAGCCGCTCCAGCATTCGAGACGACCGATCGCTCAGGAAAATTCATC 900
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7935 atcgcaaaccaagctgtctccacgtattccaactacagctctctctggaaggttcac 7994
QY 901 GCGACACCTATGGAATGGGGCTTCGCGTGGGGGTACGGTTGAGTTTCGTGGGCTCACA 960
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7995 gctactcctatgagatgggtctctgtgtgtgcgaaacggttgagttcgtggtcact 8054
QY 961 GCGGCTCCTTAAGTGGAAACGTGGCATGTGCTCTATACCGACGCTCGAAAACCTTCTTCCA 1020
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 8055 gctgctcctaaactggaagcgtgctcacgttctctacactcacgctcgtgaagttgctcca 8114
QY 1021 GCGCTCGCGCTCGGAGTTCTGAAGAACGATATTCAAAATGGATGGGTTCGGGCGGAGC 1080
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 8115 gctctcgtcctcgccagttctgaagaacgttactccaagtggatgggtttcgcgtccaaagc 8174
QY 1081 ATCCCGGATTCGCTCCCGCTGATTGGCCGGGCAACCCGACACCCGACGATTAATCTATGCT 1140
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 8175 atccagattctcctccagtgattggtcgtgctacccgtactccagacgttactacgt 8234
QY 1141 TTTCGCCACGGTTCATCTCGGCATGACAGGGGCGCCGATGACCGCAACGCTCGCTCTCAGAG 1200
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 8235 ttctgltcacggttcaactcgggtatgactggtctcaatgaccgcaacccctcttctgag 8294
QY 1201 CTCTTCGAGGGGAAAAGACCTCAATTCGACATTTGCGCCTTCGACCAACCGCTTTGCT 1260
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 8295 ctctcgtcaggtgagaagacctctctatcgaca tctctccattctgcacccaaaccttctcgt 8354
QY 1261 ATTTGCAAAATCCAAAGCAACGGGTCCGGCAAGTTAA 1296
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 8355 attgtaagtccaaagcaaaactggtcctcgtacactaa 8390

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Db 1414 cccctccagtgattggtgctaccggtactccgaagattatctacgcttccggtcagc 1473  
QY 1151 GTCACTCGCATGACAGGGGCGCGATGACCGCAACGCTCGTCTCAGAGCTCCCTCGCAG 1210  
Db 1474 gtccctcgtgatgactggtgctccaaatgacgcgaacccctcgtttctgagctccctcgca 1533  
QY 1211 GCGAAAGACCTCAATCGACATTTCCGCTTCCGACCAACCGCTTTGGTATTGGCAAT 1270  
Db 1534 gtgaaagacccctcctacatctcctcattcgacccaacccgtttccggtattgtaagt 1593  
QY 1271 CCAAGCAACGGGTCCGGCAAGTTAA 1296  
Db 1594 ccaagcaactggtcctgcactctaa 1619  
RESULT 8  
X57308  
ID X57308 standard; DNA; 8798 BP.  
AC X57308;  
XX  
XX  
DT 26-JUL-1999 (first entry)  
DE Sugar beet T-DNA containing cp4/epsps.  
DE  
DE  
KW Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plant;  
KW 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide;  
KW tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.  
OS Beta vulgaris.  
PN W0923232-AL.  
XX  
PD 14-MAY-1999.  
XX  
XX  
PF 29-OCT-1998; 98WO-EP06859.  
XX  
PR 31-OCT-1997; 97US-0112003.  
XX  
XX (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
PI Mannerloef M, Steen P, Tenning PP;  
XX  
XX WPI; 1999-313347/26.  
DR  
XX Glyphosate resistant transgenic sugar beet plants  
XX  
PS Claim 11; Page 31-36; 55pp; English.  
XX  
CC This invention describes a novel sugar beet plant, including its  
CC descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase  
CC (cp4/epsps) enzyme activity which is obtainable by Agrobacterium  
CC mediated transformation with a gene allowing expression of cp4/epsps  
CC in plants. Where the plant lacks both right and left T-DNA border  
CC sequences. The transgenic sugar beet plants of the invention are capable  
CC of tolerating herbicide treatment with glyphosate (also known as  
CC N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.  
XX  
SQ Sequence 8798 BP; 2346 A; 1999 C; 2032 G; 2421 T; 0 other;

Query Match 51.9%; Score 673; DB 20; Length 8798;  
Best Local Similarity 83.2%; Pred. No. 1.5e-204;  
Matches 766; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 1 ATCGGCTGAGAACCAAAAAGTAGCGTGGTGGAGCGGAATCGTGGCGGTATGACAG 60  
|||||  
Db 7205 atggtcgagaaacacaaagattggtatcgtgagctggaatcgttgggttgact 7264  
61 GGGCTGATGCTTACGCGCGCGGATTAAGTACACCTTGATTGACCCGACCTCTCTGCC 120  
|||||  
Db 7265 gcttggatgcttcaacgctgctgattcaaggcttacctgattgattccaaacccacaggt 7324

QY 121 GAAGGTGCATCGCTTTGGGAATCCCGATGCTTTCAACGGCTCAATCCGTCCTCCCTATGTCC 180  
|||||  
Db 7325 gaaggtgcttcttcggttaacgctggttgcttcaacggttctcctcggtgttccaaatgtcc 7384  
QY 181 ATGCCGGGAAACTTCACGAGCGTCCGAAGTGGCTTCCTTGACCCCGATGGGGCGCTTGTC 240  
Db 7385 atgcaggaacttgactagcgttccaaagtgtcttctgacccaatgggtccattgtcc 7444  
QY 241 ATCCGGTTGAGTATTTTCCAAACCATCATGCGCTGGTTCGTTGATTTCGTTCTGTTAGCCGA 300  
|||||  
Db 7445 atccgtttcagctactttccaaacctatgacctggttgattcgttctctgcttctgctgga 7504  
QY 301 AGACCAACAAGGTGAAGGAGCAGCGCAAGACATCCGCAATCTCATCAAGTCCACGGTG 360  
|||||  
Db 7505 agaccaacaaggtgaaggagcaagctaaagcactcctgtaacctcatcaagtcacaggt 7564  
QY 361 CCTCTGATCAAGTCAATTTGCCGAGGAGGCTGATGGAGGCCATCTGATCCGCCATGAAGGT 420  
Db 7565 ccttggatcaagctccttgctgaggtgctgtagcacccttatccgttcacaggt 7624  
QY 421 CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCGAAGCGCGGAGGTTGGGAACGTG 480  
Db 7625 cacttaccgtgtacogtggagaagcacttcgcgaaggacccgtggaggttgggaactt 7684  
QY 481 CGGCTCTCAACGGTGTTCGACGAGATCTTCACGCGCGATCGCTTCGGGATTTTCGAT 540  
Db 7685 cgtcgttcaacggtgttcgtactcaaatcctcagcgtgctgcatcgctgctgattcgtat 7744  
QY 541 CCGAATCTGTCGATCGCTTTACCAAGGGCATTTCTATAGAAGAACAGCGGTACACGATTT 600  
Db 7745 cctaaactgtctcagcgttttaccgaaggaaaccttatcgaagagaacggtcacacatc 7804  
QY 601 AATCGCAAGGGCTCGTGACCGCTCTGTTTCGGCGCTTTTATCGCAACGGTGGCGAATTT 660  
Db 7805 aaccacaaggtctcgtgactcctctgcttcgttcgttcgttcgttcgttcgttcgttcgttc 7864  
QY 661 GTATCTGCGCTGTCTCGGCTTTGAGACTGAAGGTAGGCGCTTTAAAGGCATTTACAACC 720  
Db 7865 gtgctgctcgttgcttcggttcgactgagactgaggtcgtgctcctcaagggtatccacc 7924  
QY 721 ACCAAGCGGCTTCGCGCTTTCATGACGCGGTTTCGACGCGCGGCGCACACCTCGAAATCA 780  
Db 7925 accaagcgtgttcctgctggtgctgagctgctgttgcagctggtgcacactccaagctc 7984  
QY 781 CTTGCTAATTCGCTAGGCGGTGACATCCGCTCGATACCGAACGTGGGATATCATCTGTC 840  
Db 7985 cttgctaaactccttgggtgagacatcccatcggataccgaacgtggatccacatcgtg 8044  
QY 841 ATCGGAATTCGGAAGCGCGCTCCACGCATTCGAGCACCGATCGCTCAGGAAATTTATC 900  
Db 8045 atcgccaaccagaagctcctccagctattccaaacctcagcttcctcggaaagtccgg 8104  
QY 901 GCGACACCTATGGAATGGG 921  
Db 8105 tccaaattgtttacattgtg 8125  
RESULT 9  
X57305  
ID X57305 standard; DNA; 8012 BP.  
AC X57305;  
XX  
XX  
DT 26-JUL-1999 (first entry)  
DE Sugar beet T-DNA containing cp4/epsps fragment.  
DE  
DE  
KW Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plant;  
KW 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide;  
KW tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.  
OS Beta vulgaris.

XX WO9923232-A1.  
XX 14-MAY-1999.  
XX 29-OCT-1998; 98WO-BP06859.  
XX 31-OCT-1997; 97US-0112003.  
XX (NOVS ) NOVARTIS AG.  
XX (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
XX Mannerloef M, Steen P, Tenning PP;  
XX WPI; 1999-313347/26.  
XX Glyphosate resistant transgenic sugar beet plants  
PS Claim 8; Page 24-29; 55pp; English.  
XX This invention describes a novel sugar beet plant, including its  
CC descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase  
CC (cp4/epsps) enzyme activity which is obtainable by Agrobacterium  
CC mediated transformation with a gene allowing expression of cp4/epsps  
CC in plants, where the plant lacks both right and left T-DNA border  
CC sequences. The transgenic sugar beet plants of the invention are capable  
CC of tolerating herbicide treatment with glyphosate (also known as  
CC N-phosphonomethyl-L-glycine) as the active ingredient, e.g. Roundup.  
XX Sequence 8012 BP; 2096 A; 1855 C; 1879 G; 2182 T; 0 other;  
SQ

Query Match 51.8%; Score 671.4; DB 20; Length 8012;  
Best Local Similarity 84.3%; Pred. No. 4.7e-204;  
Matches 756; Conservative 0; Mismatches 141; Indels 0; Gaps 0;  
QY 1 ATGGCTGACAAACACAAAAAGTAGGCTGCGTGGAGCGGAATCGTCGGCGTATGCACG 60  
DB 7116 ATGGCTGAGAACACAAAGAGTGTGATCGTGGAGTGGATCGTGTGTTGCACT 7175  
QY 61 GCGCTGATGCTTCAGCGCCGCGGATTCAAAGTCATCGTTCACCGCAACCGCTCTCGGC 120  
DB 7176 GCTTGTATGCTTCAACGCTGCTGATTCACCGCAACCGCTCTCGGC 7235  
QY 121 GAAGGTGCATCGTTTGGGAATCCGGATGCTTCAACGGCTCATCGTCCCTATGTCC 180  
DB 7236 GAAGGTGCTCTTCTGTAACGCTGCTGCTTCAACGGCTCTGCTTCAACGGCT 7295  
QY 181 ATCCCGGGAACTTGACGAGCGTGGCGAAGTGGCTCTTGAACCGGATGGGCGGTGTCA 240  
DB 7296 ATGCCAGGAACCTTGACTAGCGTTCACAAAGTGGCTCTTGACCAATGGTCCATGTCC 7355  
QY 241 ATCCGGTTCAGCTATTTTCCAAACATCATCGCTGCTGATTCGCTTTCTGTTAGCCGA 300  
DB 7356 ATCCGTTTCACTTCTTCCAAACATCACTGCTGCTGATTCGCTTTCTGTTAGCCGA 7415  
QY 301 AGACCAACAAAGGTGAAGGACGAGCGGCAAGCACTCCGCAATCTCATCAAGTCCACGGGT 360  
DB 7416 AGACCAACAAAGGTGAAGGACGAGCGGCAAGCACTCCGCAATCTCATCAAGTCCACGGGT 7475  
QY 361 CTTCTGATCAAGTTCATTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCGCCCATGAAGGT 420  
DB 7476 CATTGATCAAGTTCATTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCGCCCATGAAGGT 7535  
QY 421 CATCTGACCGTATATCGTGAAGACGAGACTTCGCCAAGGACCGCGAGGTGGGAACGTG 480  
DB 7536 CACCTTACCGTGTACCGTGAAGACGAGACTTCGCCAAGGACCGCGAGGTGGGAACGTG 7595  
QY 481 CGCGGTCTCAACGGTGTTCGACGAGGACCTCCACGCGCGGATCGTGTGGGGATTCGAT 540  
DB 7596 CGTCGTCACAGGTTGTCGTAAGTCAAACTCCACGCGCTGATGATCGTGTGATTCGAT 7655  
QY 541 CCGAACTTTCGATGCGGTTTACCAAGGCGATTCCTTATAGAGAGAACGGTTCACAGATT 600

DB 7656 CCTAAGTGTCTCAAGCGCTTTACCAAGGAGGAACTCCTTACGAAGGAGAAAGCGTCAACCATC 7715  
QY 601 AATCCGCAAGGCTCGTGACCTCTTGTTCGCGGCTTTTATCTCGCAACGGTGGCGAATTT 660  
DB 7716 AACCCACAAGGCTCGTGAAGTCTCTTGTTCGCTGCTTCTCACTCAAGGAGGAGGAGTTC 7775  
QY 661 GTATCTCGCGGTGTCATCGGCTTTGAGACTGAAGCTAGGCGCTTTAAAGGCAATTCACAAAC 720  
DB 7776 GTGTCTGCTGTTATCGGCTTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 7835  
QY 721 ACGAACGGGCTTCGCGGCTTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 780  
DB 7836 AACCAAGGCTGCTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 7895  
QY 781 CTTGCTAATTCGCTGAGGCTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 840  
DB 7896 CTTGCTAATTCGCTGAGGCTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 7955  
QY 841 ATCCGCAATCCGGAAGCGCTTCACGCTTCACGCTTCACGCTTCACGCTTCACGCTTCACGCTTC 897  
DB 7956 ATCCGCAATCCGGAAGCGCTTCACGCTTCACGCTTCACGCTTCACGCTTCACGCTTCACGCTTC 8012  
RESULT 10  
V30458/c  
ID V30458 standard; DNA: 534720 BP.  
XX  
AC V30458;  
XX  
DT 14-OCT-1998 (first entry)  
XX  
DE Rhizobium species plasmid pNGR234a.  
XX  
KW Symbiosis; open reading frame; ORF; plasmid; vector; transportation;  
KW degradation; metabolism; host range; nitrogen fixation; nodulation;  
XX  
OS Rhizobium sp.  
XX  
FH Key Location/Qualifiers  
FT CDS 417796..418671  
FT FT /\*tag= a  
FT FT /standard\_name= "ORF K1"  
FT FT /product= "oligopeptide permease"  
FT FT /note= "homologous to the OppC gene"  
FT CDS 418673..419680  
FT FT /\*tag= b  
FT FT /standard\_name= "ORF K2"  
FT FT /product= "oligopeptide permease"  
FT FT /note= "homologous to the OppD gene"  
FT CDS 419677..420738  
FT FT /\*tag= c  
FT FT /standard\_name= "ORF K3"  
FT FT /product= "oligopeptide permease"  
FT FT /note= "homologous to the OppF gene"  
FT CDS 420774..422159  
FT FT /\*tag= d  
FT FT /standard\_name= "ORF K4"  
FT FT /product= "encapsulation-like protein"  
FT FT /note= "homologous to the CapA gene"  
FT CDS 422628..424031  
FT FT /\*tag= e  
FT FT /standard\_name= "ORF K5"  
FT FT /product= "aminotransferase-like protein"  
FT FT /note= "homologous to the BioA gene"  
FT CDS 424056..425594  
FT FT /\*tag= f  
FT FT /standard\_name= "ORF K6"  
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FT CDS complement (426949..428028)  
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FT FT /standard\_name= "ORF K7"

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FT      /product= "transposase homologue"
FT      /note= "homologous to the Tnp gene"
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FT      /note= "homologous to the GUD1 gene"
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FT      /note= "homologous to the Tnp gene"
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FT      /product= "protein of unknown function"
FT      /note= "homologous to the FixU gene"
FT      complement (434107...434433)
FT      /*tag= l
FT      /standard_name= "ORF K12"
FT      /product= "protein of unknown function"
FT      complement (434517...434711)
FT      /*tag= m
FT      /standard_name= "ORF K13"
FT      /product= "ferrodoxin/ferrodoxin-like protein"
FT      /note= "homologous to the FdxN gene"
FT      complement (434753...436234)
FT      /*tag= n
FT      /standard_name= "ORF K14"
FT      /gene= "nifB"
FT      /product= "protein involved in FeMo co-factor
FT      biosynthesis"
FT      complement (436460...438130)
FT      /*tag= o
FT      /standard_name= "ORF K15"
FT      /gene= "nifA"
FT      /product= "positive regulator of nif, fix and other
FT      genes"
FT      complement (438297...438590)
FT      /*tag= p
FT      /standard_name= "ORF K16"
FT      /gene= "fixX"
FT      /product= "protein required for nitrogenase activity"
FT      complement (438605...439912)
FT      /*tag= q
FT      /standard_name= "ORF K17"
FT      /gene= "fixC"
FT      /product= "protein required for nitrogenase activity"
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FT      /standard_name= "ORF K18"
FT      /gene= "fixB"
FT      /product= "protein required for nitrogenase activity"
FT      complement (441042...441899)
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FT      /standard_name= "ORF K19"
FT      /gene= "fixA"
FT      /product= "protein required for nitrogenase activity"
FT      complement (442316...442636)
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FT      /standard_name= "ORF K20"
FT      /product= "protein of unknown function"
FT      complement (443313...443879)
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FT      /standard_name= "ORF K21"
FT      /product= "protein of unknown function"
FT      444337...445029
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FT      /standard_name= "ORF K22"

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FT      /product= "ferrodoxin-like protein"
FT      /note= "homologous to the NifQ gene"
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FT      /gene= "dctA"
FT      /product= "C4-dicarboxylate transport protein"
FT      /note= "homologous to the DctAI gene"
FT      446599...447843
FT      /*tag= x
FT      /standard_name= "ORF L1"
FT      /product= "cytochrome P450-like protein"
FT      /note= "homologous to the CamC gene"
FT      447844...448500
FT      /*tag= y
FT      /standard_name= "ORF L2"
FT      /product= "gamma-hexachlorocyclohexane-dechlorinase-like
FT      protein"
FT      /note= "homologous to the LinA gene"
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FT      /*tag= z
FT      /standard_name= "ORF L3"
FT      /product= "putative protein with degradative function"
FT      450341...451396
FT      /*tag= aa
FT      /standard_name= "ORF L4"
FT      /product= "luciferase alpha-subunit-like protein"
FT      /note= "homologous to the LuxA gene"
FT      452980...454494
FT      /*tag= ab
FT      /standard_name= "ORF L6"
FT      /gene= "nifD"
FT      /product= "alpha-subunit of FeMo protein of nitrogenase"
FT      454590...456131
FT      /*tag= ac
FT      /standard_name= "ORF L7"
FT      /gene= "nifK"
FT      /product= "beta-subunit of FeMo protein of nitrogenase"
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FT      /standard_name= "ORF L8"
FT      /product= "protein involved in FeMo co-factor
FT      biosynthesis"
FT      /note= "homologous to the NifB gene"
FT      457687...459096
FT      /*tag= ae
FT      /standard_name= "ORF L9"
FT      /product= "protein involved in FeMo co-factor
FT      biosynthesis"
FT      /note= "homologous to the FixF gene"
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FT      /*tag= af
FT      /standard_name= "ORF L10"
FT      /product= "protein of unknown function"
FT      /note= "homologous to the NifX gene"
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FT      /*tag= ag
FT      /standard_name= "ORF L11"
FT      /product= "protein of unknown function"
FT      460501...460920
FT      /*tag= ah
FT      /standard_name= "ORF L12"
FT      /product= "protein similar to part of the Fe protein
FT      of nitrogenase"
FT      /note= "homologous to the NifH gene"
FT      461228...461545
FT      /*tag= ai
FT      /standard_name= "ORF L13"
FT      /product= "protein of unknown function"
FT      463201...464739
FT      /*tag= aj
FT      /standard_name= "ORF L14"
FT      /product= "peptidase-like protein"

```



PT New isolated metalloprotease thrombospondin polypeptides, useful for  
PT treating hyperproliferative disorders, cancers or autoimmune disorders  
PT  
XX  
XX Disclosure: Page 296-321: 457pp: English.  
XX  
XX Z32000 and Z32001 encode, and Y49501 and Y49502 represent, human  
CC metalloprotease thrombospondin (METH) proteins METH1 and METH2  
CC respectively. METH1 and METH2 have been found to be potent inhibitors of  
CC angiogenesis both in vitro and in vivo. They can be used for treating  
CC cancer and other disorders related to angiogenesis including abnormal  
CC wound healing, inflammation, rheumatoid arthritis, psoriasis,  
CC endometrial bleeding disorders, diabetic retinopathy, some forms of  
CC macula degeneration, haemangiomas, and arterial-venous malformations.  
CC They may be useful in treating deficiencies or disorders of the immune  
CC system, by activating or inhibiting the proliferation, differentiation,  
CC or mobilisation (chemotaxis) of immune cells. The etiology of these  
CC immune deficiencies or disorders may be genetic, somatic, such as  
CC cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or  
CC toxins), or infectious. They can also be used to treat inflammatory  
CC conditions, both chronic and acute conditions. The products can also be  
CC used for detection and diagnosis. Z32002 to Z32080, and Y49503 to Y49511  
CC represent sequences given in the exemplification of the present  
CC invention.  
XX  
XX Sequence 38734 BP: 6142 A; 13140 C; 13585 G; 5867 T; 0 other:  
SQ

Query Match	2.7%	Score 35;	DB 20;	Length 38734;
Best Local Similarity	46.2%;	Pred. No. 2.1;		
Matches 116;	Conservative 0;	Mismatches 135;	Indels 0;	Gaps 0;
Qy 149	GCTTCAACGGCTCATCGTCGTCCTATGTCTCATGCGCGGAACATTGACGAGCGTGCGGA	208		
Db 38050	gcaacggcgtctgctccgacgccacgaggatcgctgctgcgcacacccacagacggtgcagcg	38109		
Qy 209	AGTCGCTCCTTGACCCGATGGGGCGGTGTCATATCCGGTTGAGCTATTTTCCAACCATCA	268		
Db 38110	cgaaggcagcgcagacagcggcagtcgcttggctcagcttgagcgcagcgccg999	38169		
Qy 269	TGCCCTCGTGTATTGCTGCTTTCTGTAGCCGGAAGACCAAGCTAAGGAGACGAGCGGA	328		
Db 38170	cgccctggatctcagctcgtgtagtgccacgctcgacgcgagggcgcggaattctgca	38229		
Qy 329	AAGCACTCCGCAARTCATCAAGTCCACGGTGCCTCTCATCAAGTCATTGGCGGAGGAGG	388		
Db 38230	gtgtggcgcgggaagtgtgcctgttgtagggcgtgcgcgctgttgagtcgactggagccgga	38289		
Qy 389	CTGATGCCAGC	399		
Db 38290	cgcactgcac	38300		

RESULT	13	
XX	X98168/c	
XX	ID	X98168 standard; DNA; 405 BP.
XX	AC	X98168;
XX	DT	25-OCR-1999 (first entry)
XX	DE	Nucleotide sequence of ORF33512 encoding a virulence factor.
XX	KW	Human pathogen; virulence polypeptide; virulence factor;
XX	KW	pathogenic infection; Pseudomonas aeruginosa infection; ss.
XX	OS	Pseudomonas aeruginosa.
XX	PN	WO9927129-A1.
XX	PD	03-JUN-1999.
XX	PF	25-NOV-1998; 98WO-US25247.

XX	25-NOV-1997; 97US-0066517.
PR	(GEHO ) GEN HOSPITAL CORP.
XX	
PA	Ausubel F, Cao H, Drenkard E, Goodman HM, Mahajan-Miklos S;
PI	Rahme LG, Tan M, Tsongalis J;
XX	WPI: 1999-357851/30.
DR	
XX	Virulence factors useful in developing disease treatments
PT	
XX	Disclosure; Fig 4; 228pp; English.
PS	
XX	The present sequence represents a Pseudomonas aeruginosa nucleic acid
CC	sequence. P. aeruginosa is an opportunistic human pathogen present in
CC	soil water and plants. The specification describes virulence polypeptides
CC	and nucleic acid sequence encoding such polypeptides. These sequences
CC	can be used to identify a compound which is capable of decreasing the
CC	expression of a pathogenic virulence factor. Compounds that inhibit
CC	the expression or activity of virulence factor polypeptides can be
CC	used to treat pathogenic infections, especially where the infection
CC	is a P. aeruginosa infection.
CC	note: the sequences given in the specification were poorly legible, and
CC	in some instances assumptions were made as to the identity of the base;
CC	it is therefore possible that the sequence given below is not entirely
CC	correct.
XX	
SQ	Sequence 405 BP; 98 A; 135 C; 97 G; 75 T; 0 other;
Query Match 2.6%; Score 34; DB 20; Length 405;	
Best Local Similarity 52.9%; Pred. No. 0.44;	
Matches 73; Conservative 0; Mismatches 65; Indels 0; Gaps 0	
Qy	16 AAAAAGTAGGATCGCTGGAGCCGGAATCGTGGCGGTATGCACGGCGTGATGCTTCAG 75
Db	146 AGAGATGTAGTAGTGTAGGCGCTGGCGCTCATCGGCCTGTTGACCGCCGGAGCTGGCG 87
Qy	76 GCCCGCGGATTCAAAGTCACCTTGATTGACCGGAACCTCCTCGGCGAAGGTGCATCGTTT 135
Db	86 CTCGCGGACATCGCGGTACCCCTGCTGGAGCGGCGGAGATGGCGGTGAGCATCTCTGG 27
Qy	136 GGGAAATCCGGATGCTTC 153
Db	26 GCGGGAGCGGGATCGTC 9
RESULT 14	
X98167/c	
ID	X98167 standard; DNA; 603 BP.
XX	
AC	X98167;
XX	
DT	25-OCT-1999 (first entry)
XX	
DE	Nucleotide sequence of ORF33205 encoding a virulence factor.
XX	
KW	Human pathogen; virulence polypeptide; virulence factor;
KW	pathogenic infection; Pseudomonas aeruginosa infection; ss.
XX	
OS	Pseudomonas aeruginosa.
XX	
FN	WO9927129-A1.
XX	
PD	03-JUN-1999.
XX	
PF	25-NOV-1998; 98WO-US25247.
XX	
PR	25-NOV-1997; 97US-0066517.
XX	
PA	(GEHO ) GEN HOSPITAL CORP.
XX	

PI Ausubel F, Cao H, Drenkard E, Goodman HM, Mahajan-Miklos S;  
PI Rahme LG, Tan M, Tsongalis J;  
XX  
DR WPI: 1999-357851/30.  
XX  
XX Virulence factors useful in developing disease treatments  
PT  
XX Disclosure; Fig 3; 228pp; English.  
PS  
XX

XX The present sequence represents a Pseudomonas aeruginosa nucleic acid  
CC sequence. P. aeruginosa is an opportunistic human pathogen present in  
CC soil water and plants. The specification describes virulence polypeptides  
CC and nucleic acid sequence encoding such polypeptides. These sequences  
CC can be used to identify a compound which is capable of decreasing the  
CC expression of a pathogenic virulence factor. Compounds that inhibit  
CC the expression or activity of virulence factor polypeptides can be  
CC used to treat pathogenic infections, especially where the infection  
CC is a P. aeruginosa infection.  
CC note: the sequences given in the specification were poorly legible, and  
CC in some instances assumptions were made as to the identity of the base;  
CC it is therefore possible that the sequence given below is not entirely  
CC correct.  
XX  
SQ Sequence 603 BP; 119 A; 219 C; 171 G; 94 T; 0 other;

Query Match 2.6%; Score 34; DB 20; Length 603;  
Best Local Similarity 52.9%; Pred. No. 0.54;  
Matches 73; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 16 AAAAAATAGGATCGGTGGAGCGGGAATCGTGGCGGTATGCGGCGGTGATGCTTTTCAG 75

Db 453 AGAGATGTAGTGTGTAGGCGGTGGCGGTATGCGGCGGTGATGCGGCGGTGATGCTTTTCAG 394

QY 76 CGCGCGGATTCAAAGTCACCTTGATTGACCGGAACCTCTCGCGAAGTGCATCTTT 135

Db 393 CTCCCCGACTGCGGTGACCCCTGGTGGGCGGCGGAGAGTGGCGGTGAGGCATCTCG 334

QY 136 GGGAAATCGCGGATGCTTC 153

Db 333 GCGGAGCGGGATCGTC 316

RESULT 15

VI5073/c

ID VI5073 standard; DNA; 922 BP.

XX

AC VI5073;

XX

DT 19-MAY-1998 (first entry)

XX

DE Hybrid DNA comprising a family 45 cellulase core region.

XX

XX Cellulase core region; isolation; microorganism; identification;

KW hybrid DNA; ss.

XX

OS Chimeric - Cylindrocarpus sp.

OS Chimeric - Humicola insolens.

XX

FH Key Location/Qualifiers

FT CDS 2..922

FT /\*tag= a

FT /product= "hybrid gene construct"

XX

XX WO9743409-A2.

XX

XX 20-NOV-1997.

PD

XX 12-MAY-1997; 97WO-DK00216.

XX

PR 10-MAY-1996; 96DK-0000562.

XX

PA (NOVO ) NOVO-NORDISK AS.

XX

XX

XX

XX

XX

XX

XX

XX Dalboge H, Diderichsen B, Kauppinen S, Sandal T;  
PI WPI: 1998-008878/01.  
XX P-PSDB; W44270.  
DR  
XX Isolating novel DNA sequences from microorganisms - without the need  
PT for culturing the microorganism  
PT  
XX Example 3; Page 53-54; 72pp; English.  
PS  
XX

XX The present sequence represents a novel hybrid gene construct  
CC from an example of the present invention. The present invention  
CC describes a novel method for providing a novel DNA sequence encoding a  
CC polypeptide from a microorganism with an activity of interest. The  
CC method comprises: (i) PCR amplification of the DNA with PCR primers with  
CC homology to (a) known gene(s) encoding a polypeptide with an activity of  
CC interest; (ii) linking the obtained PCR product of a 5' structural gene  
CC sequence and a 3' structural gene sequence; (iii) expressing the  
CC resulting hybrid DNA sequence; (iv) screening for hybrid DNA sequences  
CC encoding a polypeptide with the activity of interest or a related  
CC activity; and (v) isolating the hybrid DNA sequence identified in step  
CC (iv). This method provides for identification and isolation of sequences  
CC from microorganisms without having to cultivate and isolate the  
CC microorganism.  
XX

SQ Sequence 922 BP; 166 A; 325 C; 257 G; 174 T; 0 other;

Query Match 2.6%; Score 34; DB 19; Length 922;

Best Local Similarity 47.2%; Pred. No. 0.67;

Matches 103; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 553 CATCGCTTTACCAAGGCGCATCTTATAGAGAGAACGTCACACGATTAATCCCAAGGG 612

Db 373 CTTCGCCCTTCACGGGCGCAGTCGTAAGAGTGAGAGCGTAGCAACACACAGCAGCTGGA 314

QY 613 CTCTGTGACCTCTTTTTCGGCGTTTATCGCGAACGTCGCGAATTTGTATCTGCGCGT 672

Db 313 CTCGAGCCTCCAGAGAGCTTGTAGCGGCAAGCCATAGCGAGGTTGTCTTGACAGC 254

QY 673 GTCATCGGCTTTGAGACTGAAGGTAGGCGCTTAAAGGCATTTACAACACAGCGGCTT 732

Db 253 CCACGGGGAGTTGTTGTCTGAGGTGTAGGAAGTCCCGCGTTGCAACGCTCACCGGCTT 194

QY 733 CTGCGCGTTGATGCAGCGGTTGTGCGAGCGGCGCACA 770

Db 193 GCGTCGAGATGGGTTGTCTTGTCTCCAGCTCA 156

Search completed: January 1, 2001, 03:42:34

Job time: 20162 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 03:17:38 ; Search time 157.96 Seconds  
(without alignments)  
1240.873 Million cell updates/sec

Title: US-08-484-274-6  
Perfect score: 1296  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 262060 seqs, 75620496 residues

Total number of hits satisfying chosen parameters: 524120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/5C\_COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/5D\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/6\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/PCBUS\_COMB.seq.\*  
7: /cgn2\_6/ptodata/2/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1296	100.0	1296	1	US-08-391-339-6
2	1296	100.0	1296	2	US-08-484-274A-6
3	1291.2	99.6	1692	2	US-08-484-274A-3
4	1255.2	96.9	1293	1	US-08-391-339-4
5	1255.2	96.9	1293	2	US-08-484-274A-4
6	1255.2	96.9	1689	1	US-08-391-339-3
7	1201.6	92.7	1296	1	US-08-391-339-7
8	1201.6	92.7	1296	2	US-08-484-274A-7
9	961.6	74.2	1296	1	US-08-391-339-8
10	961.6	74.2	1296	2	US-08-484-274A-8
11	958.4	74.0	1296	1	US-08-391-339-17
12	958.4	74.0	1296	2	US-08-484-274A-17
13	56.2	4.3	69	1	US-08-391-339-30
14	56.2	4.3	69	1	US-08-391-339-33
15	56.2	4.3	69	2	US-08-484-274A-30
16	56.2	4.3	69	2	US-08-484-274A-33
17	50.6	3.9	65	1	US-08-391-339-28
18	50.6	3.9	65	2	US-08-484-274A-28
19	48.2	3.7	61	1	US-08-391-339-31
20	48.2	3.7	61	2	US-08-484-274A-31
21	47.6	3.7	62	1	US-08-391-339-27
22	47.6	3.7	62	2	US-08-484-274A-27
23	47.2	3.6	68	1	US-08-391-339-32
24	47.2	3.6	68	2	US-08-484-274A-32
25	33	2.5	41	1	US-08-391-339-29
26	33	2.5	41	2	US-08-484-274A-29

27	33	2.5	423	1	US-08-470-179-144	Sequence 144, Appl
c 28	32.4	2.5	1209	1	US-08-314-309A-5	Sequence 5, Appl
c 29	32.4	2.5	1513	1	US-08-314-309A-2	Sequence 2, Appl
c 30	32.4	2.5	1546	1	US-08-314-309A-3	Sequence 3, Appl
c 31	32.4	2.5	1722	1	US-08-314-309A-1	Sequence 1, Appl
c 32	31.4	2.4	2241	5	US-09-144-759-17	Sequence 17, Appl
c 33	31.4	2.4	2295	5	US-09-144-759-19	Sequence 19, Appl
c 34	31.4	2.4	2301	5	US-09-144-759-21	Sequence 21, Appl
c 35	31.2	2.4	3358	3	US-08-469-537A-104	Sequence 104, Appl
36	31	2.4	1531	2	US-08-449-986-1	Sequence 1, Appl
37	31	2.4	1531	3	US-08-756-855-1	Sequence 1, Appl
c 38	30.2	2.3	2880	1	US-08-462-484-3	Sequence 3, Appl
c 39	30.2	2.3	2880	2	US-08-441-147-3	Sequence 3, Appl
c 40	30.2	2.3	2880	6	PCT-US95-07536-3	Sequence 3, Appl
c 41	29.8	2.3	2970	6	PCT-US92-06391-1	Sequence 1, Appl
c 42	29.6	2.3	1300	4	US-08-440-845D-8	Sequence 8, Appl
c 43	29	2.2	1296	1	US-08-391-339-7	Sequence 7, Appl
c 44	29	2.2	1296	2	US-08-484-274A-7	Sequence 7, Appl
c 45	29	2.2	8931	5	US-09-028-934-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1  
US-08-391-339-6  
; Sequence 6, Application US/08391339  
; Patent No. 5463175  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dennis R. Hoerner, Jr.,  
; ADDRESSEE: Monsanto Co. B4F,  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391,339  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/156,968  
; FILING DATE:  
; APPLICATION NUMBER: US/07/17,370  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner, Dennis R., Jr.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10533)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1296 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (recombinant)  
US-08-391-339-6

Query Match 100.0%; Score 1296; DB 1; Length 1296;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	ATGGCTGAGAACCAAAAAGTAGGCATCGCTGAGCGGGAATCGTCGGCGTATGCACG	60
Db	1	ATGGCTGAGAACCAAAAAGTAGGCATCGCTGAGCGGGAATCGTCGGCGTATGCACG	60
QY	61	CGCGTATGCTTTCAGCGCGGGGATTCAAAGTCACCTTGGATGACCCGAAACCTCTCTGC	120
Db	61	CGCGTATGCTTTCAGCGCGGGGATTCAAAGTCACCTTGGATGACCCGAAACCTCTCTGC	120
QY	121	GAAGGTGCATCGTTTGGGAATGCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC	180
Db	121	GAAGGTGCATCGTTTGGGAATGCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC	180
QY	181	ATGCCGGAACATTCACGAGCGTCCGGAAGTGGCTCTTGACCGCATGGGCGCGTTGTCA	240
Db	181	ATGCCGGAACATTCACGAGCGTCCGGAAGTGGCTCTTGACCGCATGGGCGCGTTGTCA	240
QY	241	ATCGGCTTCAGCTATTTTCCAAACCATCATGCCCTGGTTGATTTCGCTTCTAGCCGGA	300
Db	241	ATCGGCTTCAGCTATTTTCCAAACCATCATGCCCTGGTTGATTTCGCTTCTAGCCGGA	300
QY	301	AGACCAACAAGGTGAAGGAGCAGCGGAAGCACTCCGCAATCTCATCAAGTCCACGGTG	360
Db	301	AGACCAACAAGGTGAAGGAGCAGCGGAAGCACTCCGCAATCTCATCAAGTCCACGGTG	360
QY	361	CCTGTGATCAAGTCATTTGGCGGAGAGGCTGATCGGAGCCATCTGATCCGCCATGAAGGT	420
Db	361	CCTGTGATCAAGTCATTTGGCGGAGAGGCTGATCGGAGCCATCTGATCCGCCATGAAGGT	420
QY	421	CATCTGACCGTATATCTGGAGAGCAGACATTCGCCAAGGACCGCGGAGTTGGAACTG	480
Db	421	CATCTGACCGTATATCTGGAGAGCAGACATTCGCCAAGGACCGCGGAGTTGGAACTG	480
QY	481	CGGCGTCTCAACCGTGTTCGCACCGATCCTCAGCGCGATGCGTTCGGGGATTTGAT	540
Db	481	CGGCGTCTCAACCGTGTTCGCACCGATCCTCAGCGCGATGCGTTCGGGGATTTGAT	540
QY	541	CCGAACTTGTGCGATGCGTTTACCAAGGCGATCTTATAGAAAGACGGTTCACAGATT	600
Db	541	CCGAACTTGTGCGATGCGTTTACCAAGGCGATCTTATAGAAAGACGGTTCACAGATT	600
QY	601	AATCCGCAAGGCTTCGTGACCTCTCTCTTTCGGGCTTTTATCGGGAACGGTGGCAATTT	660
Db	601	AATCCGCAAGGCTTCGTGACCTCTCTCTTTCGGGCTTTTATCGGGAACGGTGGCAATTT	660
QY	661	GTATCTCGCGGTGTATCGGGCTTTGAGACTGAAGGTAGGCGCTTAAAGGCATTACAACC	720
Db	661	GTATCTCGCGGTGTATCGGGCTTTGAGACTGAAGGTAGGCGCTTAAAGGCATTACAACC	720
QY	721	ACGAACGGCGTTCGCGCGTTGATGACGCGTTCGACGCGCGGCACACTCGAAATCA	780
Db	721	ACGAACGGCGTTCGCGCGTTGATGACGCGTTCGACGCGCGGCACACTCGAAATCA	780
QY	781	CTTTCCTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGCTGGATATCATATGTC	840
Db	781	CTTTCCTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGCTGGATATCATATGTC	840
QY	841	ATCGGGAATCCGAAGCGCTCCACCGCATTCGACGACCGCATGCGTCAGGAAATTCATC	900
Db	841	ATCGGGAATCCGAAGCGCTCCACCGCATTCGACGACCGCATGCGTCAGGAAATTCATC	900
QY	901	GCACACCTATGAAATGGGGCTTCGGGTGGGGGTACGGTTGAGTTTCGCTGGGCTCACA	960
Db	901	GCACACCTATGAAATGGGGCTTCGGGTGGGGGTACGGTTGAGTTTCGCTGGGCTCACA	960
QY	961	GCCGCTCCTAATCGAAACCTGGCGATGCTCTATACGCAACGCTCGAAACCTCTTCCA	1020
Db	961	GCCGCTCCTAATCGAAACCTGGCGATGCTCTATACGCAACGCTCGAAACCTCTTCCA	1020
QY	1021	GCCCTCGCGCTCGGATTTCTGAAGAACGATATTCGAAATGGATGGGTTCCGCGCGAGC	1080
Db	1021	GCCCTCGCGCTCGGATTTCTGAAGAACGATATTCGAAATGGATGGGTTCCGCGCGAGC	1080

QY	1081	ATCCCGGATTCGCTCCCGTGTATGGCCGGCAACCCGACACCCGACGTAATCTATGCT	1140
Db	1081	ATCCCGGATTCGCTCCCGTGTATGGCCGGCAACCCGACACCCGACGTAATCTATGCT	1140
QY	1141	TTCCGCCACGGTCATCTCGGCATGACAGGGGGCGGATGACCGCAACGCTTCGTCAGAG	1200
Db	1141	TTCCGCCACGGTCATCTCGGCATGACAGGGGGCGGATGACCGCAACGCTTCGTCAGAG	1200
QY	1201	CTCCTCGGAGGGAAGACCTCAATCGACATTTCCGCTTCGCAACCAACCGCTTTGCT	1260
Db	1201	CTCCTCGGAGGGAAGACCTCAATCGACATTTCCGCTTCGCAACCAACCGCTTTGCT	1260
QY	1261	ATTGCAAAATCCAAAGCAACGGTCCGGCAAGTTAA	1296
Db	1261	ATTGCAAAATCCAAAGCAACGGTCCGGCAAGTTAA	1296

RESULT 2  
US-08-484-274A-6  
; Sequence 6, Application US/08484274A  
; Patent No. 5776760  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,274A  
; FILING DATE: 07 June 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Patterson, Melinda L.  
; REGISTRATION NUMBER: 33,062  
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (713)789-2679  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1296 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (recombinant)  
; us-08-484-274A-6

Query Match	100.0%;	Score 1296;	DB 2;	Length 1296;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1296;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	ATGGCTGAGAACCAAAAAGTAGGCATCGCTGAGCGGGAATCGTCGGCGTATGCACG	60
Db	1	ATGGCTGAGAACCAAAAAGTAGGCATCGCTGAGCGGGAATCGTCGGCGTATGCACG	60
QY	61	GCCTGTATGCTTCAGCGCCCGCGGATTCAAAAGTCACCTTTGATTGACCGGAACCTCTCTGC	120
Db	61	GCCTGTATGCTTCAGCGCCCGCGGATTCAAAAGTCACCTTTGATTGACCGGAACCTCTCTGC	120
QY	121	GAAGGTGCATCGTTTGGGAATGCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC	180

Db 121 GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCGGTCCCTATGTCC 180  
Qy 181 ATGCCGGGAAACTTGACGAGCGTCCGGAAGTGGTCTCTTGACCCGATGGGCCGTTGTCA 240  
Db 181 ATGCCGGGAAACTTGACGAGCGTCCGGAAGTGGTCTCTTGACCCGATGGGCCGTTGTCA 240  
Qy 241 ATCCGGTTCAGCTATTTTCCAAACCATCATGCCCTGGTGTGATTCGCTTTCTGTAGCCGA 300  
Db 241 ATCCGGTTCAGCTATTTTCCAAACCATCATGCCCTGGTGTGATTCGCTTTCTGTAGCCGA 300  
Qy 301 AGACCAAAAGGTGAAGGACGAGCGGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360  
Db 301 AGACCAAAAGGTGAAGGACGAGCGGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360  
Qy 361 CTTCTGATCAAGTCAATTCGGCGAGGAGCTGATCGAGCCATCTCATCCGCCATGAAGGT 420  
Db 361 CTTCTGATCAAGTCAATTCGGCGAGGAGCTGATCGAGCCATCTCATCCGCCATGAAGGT 420  
Qy 421 CATCTGACCGTATATCTGTGGAGAGCAGACTTCGCCAAGGACCGGGAGGTGGGAAGTG 480  
Db 421 CATCTGACCGTATATCTGTGGAGAGCAGACTTCGCCAAGGACCGGGAGGTGGGAAGTG 480  
Qy 481 CGGCTCTCAACGGTGTTCGCACGCAGATCTTCAGCGCGGATGGTTCGGGGATTTTCGAT 540  
Db 481 CGGCTCTCAACGGTGTTCGCACGCAGATCTTCAGCGCGGATGGTTCGGGGATTTTCGAT 540  
Qy 541 CCGAACTTGTCCGATCGCTTTACCAAGGGCATTTCTATAGAGAGAACGGTCCACAGATT 600  
Db 541 CCGAACTTGTCCGATCGCTTTACCAAGGGCATTTCTATAGAGAGAACGGTCCACAGATT 600  
Qy 601 AATCCGAAGGGCTCGTGACCCCTTTTTCGGGGTTCGAGCGGATTTTCGAGCGGGAATTT 660  
Db 601 AATCCGAAGGGCTCGTGACCCCTTTTTCGGGGTTCGAGCGGATTTTCGAGCGGGAATTT 660  
Qy 661 GTATCTCGCGCTGTCATCGGCTTTGAGACTGAAGTACGGCGCTTAAAGGCATTACAACC 720  
Db 661 GTATCTCGCGCTGTCATCGGCTTTGAGACTGAAGTACGGCGCTTAAAGGCATTACAACC 720  
Qy 721 ACGAACGGCTTCTGGCGCTTCATCGACGGTTCGCGAGCGCGCGCACACTCGAAATCA 780  
Db 721 ACGAACGGCTTCTGGCGCTTCATCGACGGTTCGCGAGCGCGCGCACACTCGAAATCA 780  
Qy 781 CTTGCTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAAGTGGATATCATCGTC 840  
Db 781 CTTGCTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAAGTGGATATCATCGTC 840  
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Db 841 ATCCGGAATCCGGAAGCGCTCCAGCATTCGAGACCGATGGCTCAGGAAATTCATC 900  
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Db 901 CGCACACTATGGAATGGGCTTCGCGTGGCGGTTGAGTTGAGTTGCTGGCTCACA 960  
Qy 961 CGCGCTCTACTGGAACGTCGCGATGTCTATAGCGACGCTCGAANAATCTTCTCCA 1020  
Db 961 CGCGCTCTACTGGAACGTCGCGATGTCTATAGCGACGCTCGAANAATCTTCTCCA 1020  
Qy 1021 GCCCTCGCGCTCGGAGTTCTGAAGAAGCATATTCCAAATGGATGGGTTCCGGCCGAGC 1080  
Db 1021 GCCCTCGCGCTCGGAGTTCTGAAGAAGCATATTCCAAATGGATGGGTTCCGGCCGAGC 1080  
Qy 1081 ATCCCGGATTCGCTCCCGGTGATTTGGCGGCAACCCGACACCGACGCTAATCTATGCT 1140  
Db 1081 ATCCCGGATTCGCTCCCGGTGATTTGGCGGCAACCCGACACCGACGCTAATCTATGCT 1140  
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Qy 1201 CTCCTCGCAGCGGAAAGACCTCAATCGACATTTTCGCCCTTCGCAACCAACCGCTTGGT 1260  
Db 1201 CTCCTCGCAGCGGAAAGACCTCAATCGACATTTTCGCCCTTCGCAACCAACCGCTTGGT 1260

Qy 1261 ATTGCAAAATCAAGCAAAACGGGTCCGCAAGTTAA 1296  
Db 1261 ATTGCAAAATCAAGCAAAACGGGTCCGCAAGTTAA 1296  
RESULT 3  
US-08-484-274A-3  
; Sequence 3, Application US/08484274A  
; Patent No. 5776760  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,274A  
; FILING DATE: 07 June 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Patterson, Melinda L.  
; REGISTRATION NUMBER: 33,062  
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (713)789-2679  
; INFORMATION FOR SEQ ID NO: 3:  
; LENGTH: 1692 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-484-274A-3

Query Match 99.6%; Score 1291.2; DB 2; Length 1692;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1293; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 ATGCGTGAAGAACCAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGGTATGCACG 60  
Db 120 ATGCTGAGAACCAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGGTATGCACG 179  
Qy 61 CGCGTGTGCTTACGCGCGGGATTCAAAGTACCTTGTATGACCCGAACCCCTCTGCG 120  
Db 180 CGCGTGTGCTTACGCGCGGGATTCAAAGTACCTTGTATGACCCGAACCCCTCTGCG 239  
Qy 121 GAAGGTGCATCGTTTGGGAATCCGGATGCTTCAAGGCTCATCGCTCGCTATGTCC 180  
Db 240 GAAGGTGCATCGTTTGGGAATCCGGATGCTTCAAGGCTCATCGCTCGCTATGTCC 299  
Qy 181 ATGCCGGGAAACTTTCACGAGCGTCCGAAGTGGCTTCCTTGACCCGATGGGCCGTTGCA 240  
Db 300 ATGCCGGGAAACTTTCACGAGCGTCCGAAGTGGCTTCCTTGACCCGATGGGCCGTTGCA 359  
Qy 241 ATCCGGTTCAGCTATTTTCCAAACCATCATGCCCTGGTGTGATTCGCTTTCTGTAGCCGA 300  
Db 360 ATCCGGTTCAGCTATTTTCCAAACCATCATGCCCTGGTGTGATTCGCTTTCTGTAGCCGA 419  
Qy 301 AGACCAAAAGGTGAAGGACGAGCGGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360

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Db 420 AGACCAACAAGGTGAAGGAGCAGCGGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 479
Qy 361 CCTCTGATCAAGTCAATTCGGCGAGAGAGCTGATGGAGCCATCTGATCGGCATGAAGGT 420
Db 480 CCTCTGATCAAGTCAATTCGGCGAGAGAGCTGATGGAGCCATCTGATCGGCATGAAGGT 539
Qy 421 CATCTGACCGTATATCGTGGAGAACGACACTTCGCGCAAGGACCGGGAGGTTCGGCACTG 480
Db 540 CATCTGACCGTATATCGTGGAGAACGACACTTCGCGCAAGGACCGGGAGGTTCGGCACTG 599
Qy 481 CGGGCTCTCAACGGTGTTCGCGACGAGATCTCAGCGCGGATGCGTTCGGGGATTCGAT 540
Db 600 CGGGCTCTCAACGGTGTTCGCGACGAGATCTCAGCGCGGATGCGTTCGGGGATTCGAT 659
Qy 541 CCGAATCTGTCGCGATCGCTTACCAAGGCGATCTTATAGAGAGAGAGCGGTCAACGAT 600
Db 660 CCGAATCTGTCGCGATCGCTTACCAAGGCGATCTTATAGAGAGAGAGCGGTCAACGAT 719
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Db 720 AATCCGAAGGGCTCGTGACCGCTCTGTTTCGGCGTTCGCGAAGCGGTGGCAATTT 779
Qy 661 GTATCTGCGCGTGTATCGGCTTTGAGACTGAAGGTAGGGCGCTTAAAGGATTAACAAC 720
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Qy 721 ACGAAGCGGCTTCGCGGCTTGATGCGAGCGTTCGCGAGCGCGGCACACTCGAATCA 780
Db 840 ACGAAGCGGCTTCGCGGCTTGATGCGAGCGTTCGCGAGCGCGGCACACTCGAATCA 899
Qy 781 CTTGCTAAATCCGTTAGCGGATGACATCCCGCTCGATACCGAAGCGTGGATATCATATGTC 840
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Db 960 ATCCGGAATCCGGAAGCGGCTCCAGCATTCGCGACGCGATGCGTCAGGAAATTCATC 1019
Qy 901 GCGACACTATGGAATAGGGCTTCGCGTTCGCGGAGCGGTACGTTGAGTTCGCTGGGCTACA 960
Db 1020 GCGACACTATGGAATAGGGCTTCGCGTTCGCGGAGCGGTACGTTGAGTTCGCTGGGCTACA 1079
Qy 961 GCGCTCCTAACTGGAACGCTGCGCATGTCTATACGCGACGCTCGAAACCTCTTTCCA 1020
Db 1080 GCGCTCCTAACTGGAACGCTGCGCATGTCTATACGCGACGCTCGAAACCTCTTTCCA 1139
Qy 1021 GCGCTCCTGCGGCTCGGAGTCTGAAGAACGATATTCGCAATGATGGGTTCCGCGCGAGC 1080
Db 1140 GCGCTCCTGCGGCTCGGAGTCTGAAGAACGATATTCGCAATGATGGGTTCCGCGCGAGC 1199
Qy 1081 ATCCCGGATTCGCTCCCGCTGATGGCGGGCAACCGGACACCGCGATTAATCTATGCT 1140
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Qy 1141 TTCCGGCACCGTCTATCTCGGCATGACAGGGCGCGCGATACCGCAAGCTCGTCTCAGAG 1200
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Qy 1201 CTCTCTCGAGGGCAAGAACCTCAATCGACATTTTCGCGCTTCGCGACCAACCGGTTGGT 1260
Db 1320 CTCTCTCGAGGGCAAGAACCTCAATCGACATTTTCGCGCTTCGCGACCAACCGGTTGGT 1379
Qy 1261 ATTGGCAATCCAGCAACGGGTTCGGCAAGTTAA 1296
Db 1380 ATTGGCAATCCAGCAACGGGTTCGGCAAGTTAA 1415
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## RESULT 4

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US-08-391-339-4
; Sequence 4, Application US/08391339
; Patent No. 5463175
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
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; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr.,
; ADDRESS: Monsanto Co. B4F,
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,339
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/156,968
; FILING DATE:
; APPLICATION NUMBER: US/07/717,370
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1293 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1293
;
US-08-391-339-4
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Query Match 96.9%; Score 1255.2; DB 1; Length 1293;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 1290; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

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Qy 1 ATGCTGAGAACCAACAAAAAGTAGGCATCGCTGGAGCCGGAATCGTGGCGGTATGCACG 60
Db 1 ATGCTGAGAACCAACAAAAAGTAGGCATCGCTGGAGCCGGAATCGTGGCGGTATGCACG 60
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Db 61 GCGCTGATGCTTCAGCCGCGGGATTCAAAAGTCACCTTGATTGACCCGAACCCCTCTGGC 120
Qy 121 GAAGGTGCATCGTTTGGGAATGCGCGATGCTTCAACGGCTCATCCGTCGTCCTATATGCC 180
Db 121 GAAGGTGCATCGTTTGGGAATGCGCGATGCTTCAACGGCTCATCCGTCGTCCTATATGCC 180
Qy 181 ATCCCGGAACTTTCAGCAGCGTCCGGAAGTGGCTCCCTGACCCGATGGGCGCCCTTGTCA 240
Db 181 ATCCCGGAACTTTCAGCAGCGTCCGGAAGTGGCTCCCTGACCCGATGGGCGCCCTTGTCA 239
Qy 241 ATCCGTTTACGCTATTTTCCAAACCATCATCGCTGGTGGTTCGCTTCTGTAGCCCGGA 300
Db 240 ATCCGTTTACGCTA-TTTCCAAACCATCATG-CCTGGTTGATTGCTTCTGTAGCCCGGA 297
Qy 301 AGACCAACAAGGTGAAGGAGCAGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360
Db 298 AGACCAACAAGGTGAAGGAGCAGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 357
Qy 361 CCTCTGATCAAGTCAATTCGGCGAGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT 420
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Db 358 CCTCTGATCAAGTCATGTCGGGAGGAGGCTGATGCGAGCCATCTCTATCGCCCATGAAGGT 417
Qy 421 CATCTGACCGGTATATCGTGGAGAAGCAGACTTCGCGCAGGAGCCGGGAGGTTGGGAACGTG 480
Db 418 CATCTGACCGGTATATCGTGGAGAAGCAGACTTCGCGCAGGAGCCGGGAGGTTGGGAACGTG 477
Qy 481 CGGCGTCTCAACGGTGTTCGCGACCGAGATCTCTACGCGCGATGCGTTCGGGGATTTCCGAT 540
Db 478 CGGCGTCTCAACGGTGTTCGCGACCGAGATCTCTACGCGCGATGCGTTCGGGGATTTCCGAT 537
Qy 541 CGGAACCTGTCGCATGCGCTTTACCAAGGCGATTTATAGAGAGAGAACGGTTCACACGATT 600
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Qy 601 NATCGCAAGGCGTCTGACCGCTCTTGTTCGGCGCTTTTATCGCAACGGTTCGCGAATTT 660
Db 598 NATCGCAAGGCGTCTGACCGCTCTTGTTCGGCGCTTTTATCGCAACGGTTCGCGAATTT 657
Qy 661 GTATCTGGCGGTGTCTATCGGCTTTGAGACTGAAGGTAGGGCGCTTTAAAGGCAATTACAACC 720
Db 658 GTATCTGGCGGTGTCTATCGGCTTTGAGACTGAAGGTAGGGCGCTTTAAAGGCAATTACAACC 717
Qy 721 ACGAACGGGTCTGCGCGTTCATCGAGGGTTCGCGAGCGCGCACACTCGAAATCA 780
Db 718 ACGAACGGGTCTGCGCGTTCATCGAGGGTTCGCGAGCGCGCACACTCGAAATCA 777
Qy 781 CTTGCTAATTCGCTAGGCGATGACATCCGCTCGATACCGAAGTGGATATCATATCGTTC 840
Db 778 CTTGCTAATTCGCTAGGCGATGACATCCGCTCGATACCGAAGTGGATATCATATCGTTC 837
Qy 841 ATCCGGAATCCGGAAGCGCTCCAGCGATTCGCGAGCGAGTTCGCGAGAAATTTTCATC 900
Db 838 ATCCGGAATCCGGAAGCGCTCCAGCGATTCGCGAGCGAGTTCGCGAGAAATTTTCATC 897
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Db 898 GCGACACCTATGGAATGGGCTTCGCGTGGCGGTACGCTTGAGTTCGCTGGGCTCACA 957
Qy 961 GCGGCTCCTAATCGGAAGTGGCATGTGCTCTATACGACGCTCGAANAACCTTCTTCCA 1020
Db 958 GCGGCTCCTAATCGGAAGTGGCATGTGCTCTATACGACGCTCGAANAACCTTCTTCCA 1017
Qy 1021 GCGGCTCCTAATCGGAAGTGGCATGTGCTCTATACGACGCTCGAANAACCTTCTTCCA 1080
Db 1018 GCGGCTCCTAATCGGAAGTGGCATGTGCTCTATACGACGCTCGAANAACCTTCTTCCA 1077
Qy 1081 ATCCGGAATCCGGAAGCGCTCCAGCGATTCGCGAGCGAGTTCGCGAGAAATTTTCATC 1140
Db 1078 ATCCGGAATCCGGAAGCGCTCCAGCGATTCGCGAGCGAGTTCGCGAGAAATTTTCATC 1137
Qy 1141 TTCCGCGCATGCTCATCTCGGCGATGACAGGGCGCGGATGACCGCAACGCTCGTCTCAGAG 1200
Db 1138 TTCCGCGCATGCTCATCTCGGCGATGACAGGGCGCGGATGACCGCAACGCTCGTCTCAGAG 1197
Qy 1201 CTCCTCGAGCGGAAAGACCTCAATGACATTTCCGCTTCGCGCAACCGCTTTGGT 1260
Db 1198 CTCCTCGAGCGGAAAGACCTCAATGACATTTCCGCTTCGCGCAACCGCTTTGGT 1257
Qy 1261 ATTTGCAATCCAAAGCAACGGTTCGCGCAAGTTAA 1296
Db 1258 ATTTGCAATCCAAAGCAACGGTTCGCGCAAGTTAA 1293
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RESULT 5
US-08-484-274A-4
; Sequence 4, Application US/08484274A
; Patent No. 5776760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,274A
; FILING DATE: 07 June 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Mellinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)789-2679
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1293 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1293
; US-08-484-274A-4
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Query Match 96.9%; Score 1255.2; DB 2; Length 1293;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1290; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

Qy 1 ATGCGCTGAGAACCACAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGGTATGCACG 60
Db 1 ATGCTGAGAACCACAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGGTATGCACG 60
Qy 61 GCGCTGATGCTTCAGCGCGCGGATTCAAAGTACCTTGATTGACCCGAACCCCTCTGCG 120
Db 61 GCGCTGATGCTTCAGCGCGCGGATTCAAAGTACCTTGATTGACCCGAACCCCTCTGCG 120
Qy 121 GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCGTCCCTATGTCC 180
Db 121 GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCGTCCCTATGTCC 180
Qy 181 ATGCGCGGAAACTTGACGAGCGTGCGGAAGTGGCTCCTTGACCCGATGGGCGGTGTCA 240
Db 181 ATGCGCGGAAACTTGACGAGCGTGCGGAAGTGGCTCCTTGACCCGATGGGCGGTGTCA 239
Qy 241 ATCCGCTTCAGCTATTTTCCAAACCATCATGCGCTGGTGGTTCGCTTCGTTAGCCGA 300
Db 240 ATCCGCTTCAGCTA-TTTCCAAACCATCATG-CCTGGTTGATTGCTTCTCTGTAGCCGA 297
Qy 301 AGACCAAAACAGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
Db 298 AGACCAAAACAGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 357
Qy 361 CCTCTGATCAAGTTCATTGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Db 358 CCTCTGATCAAGTTCATTGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 417
Qy 421 CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCGCAGGAGCCGCGAGGAGTTCGGGA 480
Db 418 CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCGCAGGAGCCGCGAGGAGTTCGGGA 477
Qy 481 GCGCGTCTCAACGGTGTTCGCGAGCGAGATTCGCGAGCGCGAGTTCGCGGAGTTCGAT 540
Db 481 GCGCGTCTCAACGGTGTTCGCGAGCGAGATTCGCGAGCGCGAGTTCGCGGAGTTCGAT
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Db 478 CGCGCTCTCAACGGTGTTCGACGACGATCTCAGCGCGGATGCGTTCCGGGATTTTCGAT 537  
Qy 541 CCGAACTTGTCCGATGCGTTTACCAAGGGCATCTTATAGAGAGAACGGTTCACACGATT 600  
Db 538 CCGAACTTGTCCGATGCGTTTACCAAGGGCATCTTATAGAGAGAACGGTTCACACGATT 597  
Qy 601 AATCCGAGGGCTCGTGACCCCTCTTGTTCGGGCTTTTATCGGAGACGGTGGGGAATTT 660  
Db 598 AATCCGAAGGGCTCGTGACCCCTCTTGTTCGGGCTTTTATCGGAGACGGTGGGGAATTT 657  
Qy 661 GTATCTCGCGCTGTATCGCGCTTTGAGACTGAAGTAGGGGCTTAAAGGCATTTACAAACC 720  
Db 658 GTATCTCGCGCTGTATCGCGCTTTGAGACTGAAGTAGGGGCTTAAAGGCATTTACAAACC 717  
Qy 721 ACGAACGGCTTCTGGCGTTTGATCGACGGTGTTCGACGGCGGCGACACTCGAAATCA 780  
Db 718 ACGAACGGCTTCTGGCGTTTGATCGACGGTGTTCGACGGCGGCGACACTCGAAATCA 777  
Qy 781 CTTGCTTAATTCGCTAGGGGATGACATCCCGCTCGATACCGAACGTGGATATCATATCGTC 840  
Db 778 CTTGCTTAATTCGCTAGGGGATGACATCCCGCTCGATACCGAACGTGGATATCATATCGTC 837  
Qy 841 ATCCGGAATCCGGAAGCGCTCCACGGATTCGACGACCGATGCTCAGGAAATTCATC 900  
Db 838 ATCCGGAATCCGGAAGCGCTCCACGGATTCGACGACCGATGCTCAGGAAATTCATC 897  
Qy 901 GCGACACTATGGAATGGGGTTCGCGGTGGCGGTACGGTTGAGTTTCGCTGGGCTCACA 960  
Db 898 GCGACACTATGGAATGGGGTTCGCGGTGGCGGTACGGTTGAGTTTCGCTGGGCTCACA 957  
Qy 961 GCCGCTCTAATCGAAGCTGGCGATGCTCTATAGCAGCTCGAAGACTTCTTCCA 1020  
Db 958 GCCGCTCTAATCGAAGCTGGCGATGCTCTATAGCAGCTCGAAGACTTCTTCCA 1017  
Qy 1021 GCCCTCGCGCTCGAGTCTTGAAGACGATATTCGAAATGGATGGGTTCCGCGCGGAGC 1080  
Db 1018 GCCCTCGCGCTCGAGTCTTGAAGACGATATTCGAAATGGATGGGTTCCGCGCGGAGC 1077  
Qy 1081 ATCCCGGATTCGCTCCCGCTGATTTGGCGGCAACCGGACACCGCTGCTATGCT 1140  
Db 1078 ATCCCGGATTCGCTCCCGCTGATTTGGCGGCAACCGGACACCGCTGCTATGCT 1137  
Qy 1141 TTCCGCGACGGTCTATCGCGATGACAGGGCGCGGATGACCGAACGCTGCTCTAGAG 1200  
Db 1138 TTCCGCGATGCTATCGCGATGACAGGGCGCGGATGACCGAACGCTGCTCTAGAG 1197  
Qy 1201 CTCTCGCAGCGGAAAGACCTCAATCGACATTTTCGCCCTTCGACCAAAACCGCTTTGGT 1260  
Db 1198 CTCTCGCAGCGGAAAGACCTCAATCGACATTTTCGCCCTTCGACCAAAACCGCTTTGGT 1257  
Qy 1261 ATTGGCAATCCAAAGCAACGGGTTCGGCAAGTTAA 1296  
Db 1258 ATTGGCAATCCAAAGCAACGGGTTCGGCAAGTTAA 1293

RESULT 6

US-08-391-339-3  
; Sequence 3, Application US/08391339  
; Patent No. 5463175  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glycosylase Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dennis R. Hoerner, Jr.,  
; ADDRESS: Monsanto Co. B44F  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391,339  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/156,968  
; FILING DATE:  
; APPLICATION NUMBER: US/07/717,370  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner, Dennis R., Jr.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10533)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1689 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-391-339-3

Query Match 96.9%; Score 1255.2; DB 1; Length 1689;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1290; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

Qy 1 ATGCTGAGAACCAACAAAAAGTAGGCATCGCTGAGCGCGGAATCGTCGGGATGTCACG 60  
Db 120 ATGCTGAGAACCAACAAAAAGTAGGCATCGCTGAGCGCGGAATCGTCGGGATGTCACG 179  
Qy 61 GCGCTGATGCTTTCAGCGCGCGGATTCACAGTCACTTGTGACCCGACCCCTCTGTCG 120  
Db 180 GCGCTGATGCTTTCAGCGCGCGGATTCACAGTCACTTGTGACCCGACCCCTCTGTCG 239  
Qy 121 GAAGGTGATGCTTTGGGATGCGGATGCTTCAACGGCTCATCGCTGCTCCCTATGTCC 180  
Db 240 GAAGGTGATGCTTTGGGATGCGGATGCTTCAACGGCTCATCGCTGCTCCCTATGTCC 299  
Qy 181 ATGCCGGGAAACTTTCAGCAGCGTCCGAAAGTGGCTTCCTTACCCGAT-TGGCCCGTTGTCA 240  
Db 300 ATGCCGGGAAACTTTCAGCAGCGTCCGAAAGTGGCTTCCTTACCCGAT-TGGCCCGTTGTCA 358  
Qy 241 ATCCGGTTTCACTATTTTCCAAACCATCATGCCCTGGTTGATTCGCTTCTGTTAGCCGGA 300  
Db 359 ATCCGGTTTCACTA-TTTTCCAAACCATCATG-CTTGGTTGATTCGCTTCTGTTAGCCGGA 416  
Qy 301 AGACCAACAAAGGTGAAGGAGCAGCGGAAAGCACTCCGCATCTCATCAAGTCCACGGTG 360  
Db 417 AGACCAACAAAGGTGAAGGAGCAGCGGAAAGCACTCCGCATCTCATCAAGTCCACGGTG 476  
Qy 361 CCTCTGATCAAGTTCATTTGGGAGGAGGCTCATGCGAGCCCATCTGATCCGCCATGAAGGT 420  
Db 477 CCTCTGATCAAGTTCATTTGGGAGGAGGCTCATGCGAGCCCATCTGATCCGCCATGAAGGT 536  
Qy 421 CATCTGACCGTATATCGTGGAGAGCAGACTTCCCAAGGACCGCGGAGGTGGGAAGT 480  
Db 537 CATCTGACCGTATATCGTGGAGAGCAGACTTCCCAAGGACCGCGGAGGTGGGAAGT 596  
Qy 481 CGGCGTCTCAACGGTGTTCGCACCCAGATCTCAGCGCGGATGCTGCGGGATTTTCGAT 540  
Db 597 CGGCGTCTCAACGGTGTTCGCACCCAGATCTCAGCGCGGATGCTGCGGGATTTTCGAT 656  
Qy 541 CCGAACTTGTCCGATGCGTTTACCAAGGGCATCTTATAGAGAGAACGGTTCACACGATT 600  
Db 657 CCGAACTTGTCCGATGCGTTTACCAAGGGCATCTTATAGAGAGAACGGTTCACACGATT 716

QY 601 AATCCGCAAGGGCTCGTACCCCTCTGTTCGGCGTTTATCCGCAACGGTGGCAATTT 660  
Db 717 AATCCGCAAGGGCTCGTACCCCTCTGTTCGGCGTTTATCCGCAACGGTGGCAATTC 776  
QY 661 GTATCTGGCGCTGTATCGGCTTTGAGACTGAAGGTAGGGCGCTTAAAGGCATTAACAAC 720  
Db 777 GTATCTGGCGCTGTATCGGCTTTGAGACTGAAGGTAGGGCGCTTAAAGGCATTAACAAC 836  
QY 721 ACGAACGGGTTCTCGCGCTTGATCGACGGTGTGCGAGCGCGGCACACTCGAAATCA 780  
Db 837 ACGAACGGGTTCTCGCGCTTGATCGACGGTGTGCGAGCGCGGCACACTCGAAATCA 896  
QY 781 CTTGCTAATTCCTAGGGCATGACATCCGCTCGATACCGACGTGGATATCATATCGTC 840  
Db 897 CTTGCTAATTCCTAGGGCATGACATCCGCTCGATACCGACGTGGATATCATATCGTC 956  
QY 841 ATCCGCAATCCGGAAGCGCTCCAGCGATTCGAGACCGATGCGTTCAGGAAATTCATC 900  
Db 957 ATCCGCAATCCGGAAGCGCTCCAGCGATTCGAGACCGATGCGTTCAGGAAATTCATC 1016  
QY 901 GCGACACCTATGGAATGGGGTTCGCGTGGCGGGTACGGTTGAGTTCGCTGGGCTCACA 960  
Db 1017 GCGACACCTATGGAATGGGGTTCGCGTGGCGGGTACGGTTGAGTTCGCTGGGCTCACA 1076  
QY 961 GCGGCTCTTAAGTGAAGAGTGGCGATGCTCTATAGCAGCGCTCGAAACCTTCTTCCA 1020  
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QY 1021 GCGCTCGCGCTCGAGTTCCTCAAGAACGATATCCAAATGATGGGTTCGGCGCGAGC 1080  
Db 1137 GCGCTCGCGCTCGAGTTCCTCAAGAACGATATTCAAATGATGGGTTCGGCGCGAGC 1196  
QY 1081 ATCCGGGATTCGCTCCCGTGTATGGCGGGCAACCGGACACCGAGCTAATCTATGCT 1140  
Db 1197 ATCCGGGATTCGCTCCCGTGTATGGCGGGCAACCGGACACCGAGCTAATCTATGCT 1256  
QY 1141 TTCGGCAGGTCATCTCGGATGACAGGGGGCGGATGACCGGAACGCTGCTCTCAGAG 1200  
Db 1257 TTCGGCAGGTCATCTCGGATGACAGGGGGCGGATGACCGGAACGCTGCTCTCAGAG 1316  
QY 1201 CTCCTCGCAGGGAAGAACCTCAATCGACATTCGCGCTTCGCAACCGCTTTTGGT 1260  
Db 1317 CTCCTCGCAGGGAAGAACCTCAATCGACATTCGCGCTTCGCAACCGCTTTTGGT 1376  
QY 1261 ATTGGCAATCCAAAGCAACGGGTCCGGCAAGTTAA 1296  
Db 1377 ATTGGCAATCCAAAGCAACGGGTCCGGCAAGTTAA 1412

RESULT 7

US-08-391-339-7  
: Sequence 7, Application US/08391339  
: Patent No. 5463175  
: GENERAL INFORMATION:  
: APPLICANT: Kishore, Ganesh M.  
: APPLICANT: Barry, Gerard F.  
: TITLE OF INVENTION: Glyphosate Tolerant Plants  
: NUMBER OF SEQUENCES: 33  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Dennis R. Hoerner, Jr.,  
: ADDRESSEE: Monsanto Co. B4F  
: STREET: 700 Chesterfield Village Parkway  
: CITY: St. Louis  
: STATE: Missouri  
: COUNTRY: USA  
: ZIP: 63198  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/391.339

; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/156.968  
; FILING DATE:  
; APPLICATION NUMBER: US/07/717.370  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner, Dennis R., Jr.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10533)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1296 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (recombinant)  
US-08-391-339-7

Query Match 92.7%; Score 1201.6; DB 1; Length 1296;  
Best Local Similarity 95.4%; Pred. No. 0;  
Matches 1237; Conservative 0; Mismatches 59; Indels 0; Gaps 0;  
QY 1 ATGGCTGAGAACCAAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGTATGSCAG 60  
Db 1 ATGGCTGAGAACCAAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCAT 60  
QY 61 GCGCTGATGCTTCAGCGCGCGGATTCAAAGTCACTTTGATTGACCCGAACCTCTCTGCG 120  
Db 61 GCTTTGATGCTTCAGCGCTCGTGGATTCAAAGTCACTTTGATTGACCCGAACCTCTCTGCG 120  
QY 121 GAAGTGCATCGTTTGGGATGCGCGATGCTTCACGGGCTCATCGTCTGCTATGTGC 180  
Db 121 GAAGTGCATCGTTTGGGATGCGCGATGCTTCACGGGCTCATCGTCTGCTATGTGC 180  
QY 181 ATCCCGGGAAACTTCACGAGCGTGGCGAAGTGGCTTCCTTACCCGATGGGCGGTGTCA 240  
Db 181 ATCCCGGGAAACTTCACGAGCGTGGCGAAGTGGCTTCCTTACCCGATGGGCGGTGTCA 240  
QY 241 ATCCGGTTCAGTATTTTCCAAACCATCATGATGCTGCTGTTGATTGCTGCTTCTGTAGCCGA 300  
Db 241 ATCCGGTTCAGTATTTTCCAAACCATCATGATGCTGCTGTTGATTGCTGCTTCTGTAGCCGA 300  
QY 301 AGACCAACAAGGTGAAGAGCAGGCGGAAGCACTCCGCAATCTCATCAAGTCCAGGGTG 360  
Db 301 AGACCAACAAGGTGAAGAGCAGGCGGAAGCACTCCGCAATCTCATCAAGTCCAGGGTG 360  
QY 361 CCTCTGATCAAGTCAATGGCGGAGGAGGCTGATGGAGGCATCTGATCCGCCATGAAGCT 420  
Db 361 CCTCTGATCAAGTCAATGGCGGAGGAGGCTGATGGAGGCATCTGATCCGCCATGAAGCT 420  
QY 421 CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAGGACCGGGAGGTTGGGAATCG 480  
Db 421 CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAGGACCGGGAGGTTGGGAATCG 480  
QY 481 CGGCGCTCAACGGTGTTCGCAACGAGATCTCTCAGCGCGGATGCGTTCGCGGATTCGAT 540  
Db 481 CGGCGCTCAACGGTGTTCGCAACGAGATCTCTCAGCGCGGATGCGTTCGCGGATTCGAT 540  
QY 541 CCGAACTTCTCGCATCGCTTTTACCAAGGCGATCTTATAGAAGAGACCGGTACACGATT 600  
Db 541 CCTAACTTCTCGCATCGCTTTTACCAAGGCGATCTTATAGAAGAGACCGGTACACGATT 600  
QY 601 AATCCGCAAGGGCTCGTGACCCCTCTTGTTCGGCGTTTATCCGCAACGGTGGCAATTT 660  
Db 601 AATCCGCAAGGGCTCGTGACCCCTCTTGTTCGGCGTTTATCCGCAACGGTGGCAATTT 660  
QY 661 GTATCTGGCGCTGTATCGGCTTTGAGACTGAAGGTAGGGCGCTTAAAGGCATTAACAAC 720

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Qy	721	ACGAACGGCTTCTTGGCCGTTGATGCAGCGGTTGTGCAGCGCGGCACACTCGAAATCA	780
Db	721	ACTAACGGTGTCTTGGCTGTGATGCAGCTGTTGTGCAGCTGGTGACACTCTAAATCA	780
Qy	781	CTTGTCTAATTTCGTAGCGGATGACATCCCGGTCGATACCGAAGCTGGATATCATATCGTC	840
Db	781	CTTGTCTAATTTCGTAGCGGATGACATCCCGGTCGATACCGAAGCTGGATATCATATCGTC	840
Qy	841	ATCGCAATCCGGAAGCCGCTCACGCATTTCCGACGACCGGATGGCTCAGGAAAATTCACTC	900
Db	841	ATCGCGAATCCGGAAGCCGCTCACGCATTTCCGACGACCGGATGGCTCAGGAAAATTCACTC	900
Qy	901	GCACACCTATGGAATGGGGCTTCGCGTGGCGGATACGGTTCGCTGGGCTCACAC	960
Db	901	GCACACCTATGGAATGGGGCTTCGCGTGGCGGATACGGTTCGCTGGGCTCACAC	960
Qy	961	GCAGCTCTTAATCTGGAACGCTGGGATGTGCTCTATACGCACGCTCGAANAATCTTCTTCCA	1020
Db	961	GCTGCTCTTAATCTGGAACGCTGGGATGTGCTCTATACGCACGCTCGAANAATCTTCTTCCA	1020
Qy	1021	GCCTTCGCGCTCGCAGTTCGAAGAACGATATTCCAATGGATGGGGTTCGCGCCGAGC	1080
Db	1021	GCCTTCGCGCTCGCAGTTCGAAGAACGATATTCCAATGGATGGGGTTCGCGCCGAGC	1080
Qy	1081	ATCCCGGATTCGCTCCCTCGATTTGCCGGGCAACCCGGACACCCGACGTAATCTATGCT	1140
Db	1081	ATTCTCTGATTCCTTCCAGTGTGCTGCAACTCGTACACCGGACGTAATCTATGCT	1140
Qy	1141	TTGGGCCACGGTCATCTCGGCATGACAGGGGCGCGATGACCGCAACGCTGCTCTCAGAG	1200
Db	1141	TTTGGTCAAGGTCATCTCGGTATGACAGGTGCTCCAAATGACTGCAACTCTGCTCTCAGAG	1200
Qy	1201	CTCCTCGCAGGCGAAAAGACCTCAATTCGACATTTTCGCCCTTCGCAACCAACCGCTTTGGT	1260
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Qy	1261	ATTGGCAAAATCCAAGCAAAACGGGTCGGGCAAGTTAA	1296
Db	1261	ATTGGCAAAATCCAAGCAAAACGGGTCGGGCAAGTTAA	1296

## RESULT

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US-08-484-274A-7
; Sequence 7, Application US/08484274A
; Patent No. 5776760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,274A
; FILING DATE: 07 June 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Mellinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: M08T130 38-21(13560)A
; TELECOMMUNICATION INFORMATION:

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Db 841 ATCCGGAATCCGGAACCGCTCCACCGCATTCGACGACGATGCGTCAGGAAAAATTCATC 900  
Qy 901 GCGACACCTATGGAATGGGCTTCGCGTGGCGGTACGGTTGAGTTGCGTGGGCTCACA 960  
Db 901 GCGACACCTATGGAATGGGCTTCGCGTGGCGGTACGGTTGAGTTGCGTGGGCTCACA 960  
Qy 961 CCCGCTCTTAAGTGAACGTCGCGATGCTGCTATAGCAGCGCTCGAAAACCTTCCTTCCA 1020  
Db 961 GCTGCTCTTAAGTGAACGTCGCGATGCTGCTATAGCAGCGCTCGAAAACCTTCCTTCCA 1020  
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Db 1021 GCGCTCGCGCTCGAGTCTGAAGAAGCATATCCAAATGATGGGTTCGCTCCTAGC 1080  
Qy 1081 ATCCCGGATTCGCTCCCGCTGATTCGCGGGCAACCCGACACCGAGTAACTATGCT 1140  
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Qy 1141 TTCGCGCAGGTCATCTCGGCATGACAGGGGCGCGATGACCGCAACGCTCGCTCTCAGAG 1200  
Db 1141 TTGTGTACGGTCATCTCGGTATGACAGGTGCTCCAAATGACTGCAACTCTCGTCTCAGAG 1200  
Qy 1201 CTCCTCGCAGGCGAAAAGACCTCAATCGACATTTCCGCCCTTCGCACCAACCGCTTTGGT 1260  
Db 1201 CTCCTCGCAGGCGAAAAGACCTCAATCGACATTTCCGCCCTTCGCACCAACCGCTTTGGT 1260  
Qy 1261 ATTGCAATCCAGCAACGCGGTCCGCAAGTTAA 1296  
Db 1261 ATTGCAATCCAGCAACGCGGTCCGCAAGTTAA 1296

RESULT 9

US-08-391-339-8  
; Sequence 8, Application US/08391339  
; Patent No. 5463175  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dennis R. Hoerner, Jr.,  
; ADDRESSEE: Monsanto Co. B4F,  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391,339  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/156,968  
; FILING DATE:  
; APPLICATION NUMBER: US/07/17,370  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner, Dennis R., Jr.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10533)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1296 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double

; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (synthetic)  
US-08-391-339-8  
  
Query Match 74.2%; Score 961.6; DB 1; Length 1296;  
Best Local Similarity 83.9%; Pred. No. 0;  
Matches 1087; Conservative 0; Mismatches 209; Indels 0; Gaps 0;  
  
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Db 1 ATGGCTGAGAACACAAAAGTAGGCATCGCTGAGCGGGAATCGTCGGCGCTATGSCAG 60  
Qy 61 GCGCTGATGCTTCAGCGCGCGGATTCAAAGTACCTTTGATTTGACCCGAAACCTTCCTGCG 120  
Db 61 GCTTTGATGCTTCAAAGTACCTTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 120  
Qy 121 GAAGGTGCAATCGTTTGGGAATCCCGGATGCTTCAAGGCTCATCGTTCCTCTATGTC 180  
Db 121 GAAGGTGCTTCTTTCGGTAACGCTGCTTCAACGGTTCTCTCGTTCTTCAATGTCC 180  
Qy 181 ATCCCGGGAACCTTCAGGAGCGTCCGAAAGTGGCTCCTTGACCCGATGGCGCGTGTGTC 240  
Db 181 ATCCCGGGAACCTTCAGGAGCGTCCGAAAGTGGCTCCTTGACCCGATGGCGCGTGTGTC 240  
Qy 241 ATCCCGTTCAGCTATTTTCCAAACCATCATGCTTGGTGGTTCGCTTCTGTTAGCCGGA 300  
Db 241 ATCCCGTTCAGCTATTTTCCAAACCATCATGCTTGGTGGTTCGCTTCTGTTAGCCGGA 300  
Qy 301 AGACCAACAAAGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360  
Db 301 AGACCAACAAAGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360  
Qy 361 CCTCTGATCAAGTCAATGGCGAGGAGGCTGATGCGAGGCACTGATCGCGCATGAAGT 420  
Db 361 CCTTTGATCAAGTCCCTTGGCTGAGGAGGCTGATGCGAGGCACTGATCGCGCATGAAGT 420  
Qy 421 CATCTCACCGTATATCGTGGAGAACAGACTTCGCCAAGGAGCGGAGGAGGAGGAGGAGG 480  
Db 421 CACCTTACCGTGTACCGTGGAGAACAGACTTCGCCAAGGAGCGGAGGAGGAGGAGGAGG 480  
Qy 481 GCGCGTCTCAACGGTGTTCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540  
Db 481 CGTCTCTCAACGGTGTTCGCTACTCAAACTCCTCAGCGCTGATGCGATTCGATTCGAT 540  
Qy 541 CGAACTTGTGCTGATGCTTACCAAGGCACTTCTATAGAAGAGAACGCTCACAGATT 600  
Db 541 CCTAATTTGCTCAGCGCTTTTACCAAGGCACTTCTATAGAAGAGAACGCTCACAGATT 600  
Qy 601 AATCCGGAAGGCTCGTGACCTCTTGTTCGGCGCTTTTATCCGGAACGCTGCGCAATTT 660  
Db 601 AACCACAAAGGCTCGTGACTCTTGTTCGTCTTTCATCGCTAACGCTGGAGAGTTTC 660  
Qy 661 GTATCTGCGCGTGTATCGGCTTCAGACTGAAGGTAGGCGGCTTAAAGGCAATTAACA 720  
Db 661 GTGTCTGCTGTATCGGATTCGAGACTGAAGGTGCTGCTTCAAGGCTATCAACCC 720  
Qy 721 AGGAACGCGGTTCTGCGCGTTCATGACGAGGTTGTCGACGCGGCGCACACTCGAAATCA 780  
Db 721 ACCAAGGCTGTTCTTGTGCTGTTGATGACGCTGTTGTTGACGCTGCTGACACTCCA 780  
Qy 781 CTTCCTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAAGCTGGATATCATATGCT 840  
Db 781 CTTCCTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAAGCTGGATATCAACCT 840  
Qy 841 ATCCGGAATCCGGAAGCGCTCCAGCATTTCCGAGACCGATGCGCTCAGGAAATTCATC 900  
Db 841 ATCCGGAATCCGGAAGCGCTCCAGCATTTCCGAGACCGATGCGCTCAGGAAATTCATC 900  
Qy 901 GCGACACCTATGGAATGGGCTTCGCGTGGCGGTACGGTTGAGTTGCTTCCGCTCACA 960  
Db 901 GCTACTCTATGGAGATGGGTCTTCGTGTGTAACCGTTTGAAGTTCGCTGCTGCTCACT 960

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Qy 961 GCCGCTCCTAACTGGAACAGTGGCATGTGCTATAGGCAAGCTCGAANAACCTCTCTCCA 1020
Db 961 GCTGCTCCTAACTGGAACAGTGGCATGTGCTATAGGCAAGCTCGAANAACCTCTCTCCA 1020
Qy 1021 GCCCTCGCGCTCGGAGTCTTGAAGAAGATATCCAAATGGATGGGTTCCGCCCGAGC 1080
Db 1021 GCTCTCGCTCGGAGTCTTGAAGAAGATATCCAAATGGATGGGTTCCGCCCGAGC 1080
Qy 1081 ATCCCGGATTCGCTCCCGGTGATTCGGCGGCAACCCGGACACCCGACGCTAATCTATGCT 1140
Db 1081 ATCCCGGATTCGCTCCCGGTGATTCGGCGGCAACCCGGACACCCGACGCTAATCTATGCT 1140
Qy 1141 TTCGGCCAGGTATCTCGGCATGACAGGGCGCGCGATGACCGAAGCTGCTCAGAG 1200
Db 1141 TTCGGTCAAGGTACCTCGGTATGACTGCTCCAATGACCGAAGCCTGTTCTGAG 1200
Qy 1201 CTCCTCCAGCGCAAGACCTCAATGCATTTTCGCCCTTCGCAACCAACCGCTTTGGT 1260
Db 1201 CTCCTCCAGGTGAGAAGCCTCTATGCATCTCTCCATTCGCACCAACCGCTTTGGT 1260
Qy 1261 ATTGGCAATCCAAAGCAACCGGTCGGCGCAAGTTAA 1296
Db 1261 ATTGGTAAGTCCAAAGCAACCGTGGTCTGCATCCTAA 1296

RESULT 10
US-08-484-274A-8
; Sequence 8, Application US/08484274A
; Patent No. 5776760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,274A
; FILING DATE: 07 June 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)789-2679
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
US-08-484-274A-8

Query Match 74.2%; Score 961.6; DB 2; Length 1296;
Best Local Similarity 83.9%; Pred. No. 0;
Matches 1087; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

Qy 1 ATGGCTGAGAACCAAAAAAGTAGGATCGCTGGAGCGGAATCGTCGGCGTATGCACG 60
Db 1 ATGGCTGAGAACCAACAGAGGTGGTATCGCTGGAGCTGGAATCGTTGGTGTTCGCACT 60
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Qy 61 CGCGTGATGCTTCAGCGCCGCGGATTCAAAGTCACTTGTATTGACCCGCAACCCCTCTGCG 120
Db 61 GCTTTGATGCTTCAACGTCGTTGATTCAGGTTACCTTGTATTGATCCAAACCCACCAGGT 120
Qy 121 GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTGGTCCCTATGTC 180
Db 121 GAAGGTGCTTCTTCGGTAACGCTGGTTGCTTCAACGGTCTCTCCGTGTGTTCCAAATGTC 180
Qy 181 ATGCCGGGAAACTTGCACGAGCGTCCCGAAGTCTCTTCCCTTTCCTTTCAGCCGATGGGCGCTGTGCA 240
Db 181 ATGCCGAGAACTTGCAGTAGCGTTCCAAAGTGGGTCTCTTGACCCCAANTGGGTCCATTTGTC 240
Qy 241 ATCCGGTTCAGCTATTTTCCAAACCATCATGCCCTGGTGTGATTTCGTTCTCTTAGCCGGA 300
Db 241 ATCCGGTTCAGCTACTTTCCAACCATCATGCTTGGTGTGATTTCGTTCTCTTAGCCGGA 300
Qy 301 AGACCAACAAAGTGAAGGAGCAGCGGAAAGCACTCCGCAATCTCATCAAGTCCACCGTG 360
Db 301 AGACCAACAAAGTGAAGGAGCAAGCTAAGCACTCCGTAACCTCATCAAGTCCACGTGTG 360
Qy 361 CCTCTGATCAAGTCAATTCGGCGGAGGAGCTCATGGAGCCCATCTCATCCGCCCATGAAGGT 420
Db 361 CCTTGATCAAGTCTCTGGCTGAGGAGCTCATGCTAGCCACCTTATCCGTCACGNAAGGT 420
Qy 421 CATCTGACCGCTATATCGTGGAGAAGCAGACTTCGCCAAGGACCCGCGAGGTTCGGAACTG 480
Db 421 CACCTTACCGCTGTACCGTGGAGAAGCAGACTTCGCCAAGGACCGTGGAGGTTCGGAACTT 480
Qy 481 CGCGCTCTCAACGGTGTTCGACGACGATCCTCAGCGCGGATGCGTTCGCGGATTTGAT 540
Db 481 CGTCTCTCAACGGTGTTCGCTACTCAAACTCAGCGCTGATGATTCGCTGATTTGAT 540
Qy 541 CCGAACTTGTGCGATCGCTTTACCAAGGGCATCTTATAGAAAGAGACGGTCACACCATTT 600
Db 541 CTTAACTTGTCTACGCTTTTACCAAGGAAATCCTATFCGAAGAGAACGGTCACACCATC 600
Qy 601 AATCCGAAGGGCTCGTGACCCCTCTTGTTCGGCGTTTTATTCGCGAACGGTGGCGAATTT 660
Db 601 AACCCACAAGGCTCTGCTGACTCTCTTGTTCGTCGTTTCATCGCTAACGGTGGAGAGTTC 660
Qy 661 GTATCTCGCGGTGTCATCGGCTTTGAGACTGNAAGTTCAGGCGGCTTAAAGGATTTACAA 720
Db 661 GTGTCGCTCGTGTATTCGGAATTCGAGACTGAAGTTCGCTCTCAAGGGTATCACCACC 720
Qy 721 ACGAACGGGTTTCGCGCTGTGATGCAAGCGTTCGCAAGCGCGGACACCTCCAAATCA 780
Db 721 ACCAAGCGTGTCTTGTGCTGTGATGCAAGCTGTTTGCAGCTGTGCAACACTCCAAAGTCT 780
Qy 781 CTTGCTAATTTCGCTAGCGATGACATCCCGCTCGATACCGAACGCTGGATATCATATGCTC 840
Db 781 CTTGCTAATTCCTTCGCTGATGACATCCCATTCGATACCGAACGCTGGATACCATCATG 840
Qy 841 ATCCGGAATCCGGNAGCGCTCCAGCATTCGAGACGACCGATGCGTCAGGAAATTCATC 900
Db 841 ATCCGCAACCCAGAAAGCTGCTCCACGTATTCCAACTACCGATGCTTCTGGAAGATTCATC 900
Qy 901 CGGACACTATGGAATGGGCTTTCGCGTGGCGGTACGGTTGAGTTCGCTGGGCTCACA 960
Db 901 GCTACTCCTATGAGATGGGTCTTCGTTGCTGGAACCGTTGAGTTCGCTGGTCTCAGT 960
Qy 961 GCGGCTCCTAACTGGAAACGTCGTCATCTATACGACGCTCGAANAACCTTCTTCCA 1020
Db 961 GCTGCTCCTAACTGGAAGCGTGTCTACGTTCTCTACACTCAGCGCTCGTAAAGTTCCTTCCA 1020
Qy 1021 GCCCTCGCGCTCGGAGTTCGGAAGAAGATATTCAAATGGATGGGTTCCGCCCGAGC 1080
Db 1021 GCTCTCGCTCCTGCCAGTTCCTGAAGAAGCTTACTTCCAAAGTGGATGGGTTTCGCTCAAGC 1080
Qy 1081 ATCCCGGATTCGCTCCCGGTGATTCGGCGGCAACCCGGACACCCGACGCTAATCTATGCT 1140
Db 1081 ATCCAGATTCCTTCAGTGATGGTGTGCTGCTACCCGTACTCCAGACGTTATCTACGCT 1140
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QY 1141 TTCGCCACGGTCATCTCGGCATGACAGGGGGCCGATGACCGCAACGGTCGTCACAG 1200  
Db 1141 TTCGGTCAACGGTCACCTCGGTATGACTGGTCTCCAATGACCGCAACCCCTCTTTCTGAG 1200  
QY 1201 CTCCTCGCAGGCGAAAGACCTCAATCGACATTTCCGCCCTTCGCCACCAACCGCTTTGGCT 1260  
Db 1201 CTCCTCGCAGGCGAAGACCTCTATGACATCTCTCCATTCGCACCAACCGTTTCGGT 1260  
QY 1261 ATTGCAATCCAAACCAACCGGTCGCCCAAGTTAA 1296  
Db 1261 ATTGCTAAGTCCAAGCAAACTGGTCTGCATCCTAA 1296

RESULT 11

US-08-391-339-17  
; Sequence 17, Application US/08391339  
; Patent No. 5463175  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dennis R. Hoerner, Jr.,  
; ADDRESSEE: Monsanto Co. B4F  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/391,339  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/156,968  
; FILING DATE:  
; APPLICATION NUMBER: US/07/17,370  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner, Dennis R., Jr.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10533)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1296 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (recombinant)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1296  
US-08-391-339-17

Query Match 74.0%; Score 958.4; DB 1; Length 1296;  
Best Local Similarity 83.7%; Pred No. 0;  
Matches 1085; Conservative 0; Mismatches 211; Indels 0; Gaps 0;

QY 1 ATGGCTGAGAACCAACCAAGTAGCGATCGCTGGAGCGGAATCGTCGGCGTATGCAG 60  
Db 1 ATGGCTGAGAACCAACCAAGATTGGTATCGCTGGAGCTGGAATCGTTGGTCTTTGCACT 60  
QY 61 GCGCTGATGCTTCACGGCGCGGATTCAAATGACCTTGATGACCGCAACCCCTCTGGC 120

Db 61 GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTGATTGATCCAAACCCACAGGT 120  
QY 121 GAAGGTGCAATCGTTTGGGAATGCCGATCGTTCAACGGCTCATCCGTCGTCCTCATATGTCC 180  
Db 121 GAAGGTGCTCTTTCCGTAAACGCTGGTTCGTTCAACGGTTCTCTCCGTTGTTCCAAATGTCC 180  
QY 181 ATGCCGGGAAATCTGACGAGCGTGCGGAAGTGGCTCCTTTGACCCCGATGGGGCGTTGTCA 240  
Db 181 ATGCCAGGAATTTGACTAGCGTTCCAAAGTGGCTTCTTTGACCCAATGGGTCTCATTTGTCC 240  
QY 241 ATCCGGTTCCAGCTATTTTCCAAACCATCATGCCCTGGTTGATTTCGGTTTGTGTAGCCGGA 300  
Db 241 ATCCGTTTCGGCTACTTTCCAAACCATCATGCCCTGGTTGATTTCGGTTTGTGTGGA 300  
QY 301 AGACCAAAACAGGTGAAGGAGGAGCGCAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360  
Db 301 AGACCAAAACAGGTGAAGGAGGAGCAAGCTAAGGCACATCCGTAACTCATCAAGTCCACGTG 360  
QY 361 CCTCTGATCAAGTCAATTTGGCGAGGAGGTGATGCGAGCCATCTGATCCGCCCATGAAGGT 420  
Db 361 CCTTTGATCAAGTCTTGGCTGAGGAGGCTGATGCTTAGCCACCTTATCCGTCACGAAGT 420  
QY 421 CATCTCACCGTATATCGTCGAGAGCAGACTTCGCCAAAGACCGCGGAGGTTGGGAACTC 480  
Db 421 CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAGGAGCGGTGGAGGTTGGGAACCT 480  
QY 481 CCGCGTCTCAACGGTTCGCCACGAGATCTCAGCGCCGATCGCTTGGGGATTTTCGAT 540  
Db 481 CGTCGCTCAACGGTGTTCGTACTCAAATCTCAGCGCTGATGCAATTTGGATTTTCGAT 540  
QY 541 CGGAATCTGTCGATCGCTTTACCAAGGCAATTTATAGAAGAGAACGGTCTCACAGNTT 600  
Db 541 CCTAACTTGTCTCACGCCCTTTACCAAGGAACTCTTATCGAAGAGAAGCGGTACACCATC 600  
QY 601 AATCCGCAAGGGCTCGTGACCTCTTTGTTTCGGCGTTTATCCGCAACGGTGGCGAATTT 660  
Db 601 AACCCACAAGGTCGTGTAATCTCTTTGTTTCGGTCTCATCGCTAAGCGTGGAGAGTT 660  
QY 661 GTATCTGCCGCTCTCATCGGCTTTGAGACTGAAGGTAGGGCGCTTAAAGGCATTTACAACC 720  
Db 661 GTGCTGCTCGTGTATTCGGATTCGAGACTGAAGGTCTGCTCTCAAGGCTATCACCAACC 720  
QY 721 AGAAGCGGCTTCTGGCCGTTGATGACGCGGTTGTCGACGCGGCGCACACTCGAANTCA 780  
Db 721 ACCAAGCGTGTCTGCTGTTGATGACGCTGTGTTGACAGCTGGTGCACACTCCAAGTCT 780  
QY 781 CTTGCTAATTCGCTAGCGCATGACATCCCGCTCGATACCGAAGCTGATATCATATCGTC 840  
Db 781 CTTGCTAATCTCCCTTGGTGTATGACATCCCATTTGGATACCGAAGCTGGATACCATCTG 840  
QY 841 ATCGCAATCCGGAAGCCGCTCCACGCATTTCCGACACCGATCGCTCAGAAAAATTCATC 900  
Db 841 ATCGCAACCCAGAGCTGCTCCACGATTTCCAACTACCGATGCTTCTGTGAAAGTTCAATC 900  
QY 901 GCGACACCTATGAAATGGGCTTCGCGTGGCGGTACGGTTGAGTTGCTGCGGTGCACA 960  
Db 901 GCTACTCCTATGAGATGGGTCTTCTGTTGCTGGAACCGTTGAGTTGCTGCTCTCACT 960  
QY 961 GCGGCTCCTAACTGGAAACGTCGGCATGTCTATACGCACGCTCGAAAAATTCCTTCCA 1020  
Db 961 GCTGCTCCTAACTGGAAAGCGTCTCACGCTCTCTACACTCGCGCTCGTAAGTTGCTTCCA 1020  
QY 1021 GCGCTCGCGCTCGGAGTTCTGAAGAACGATATTTCCAAATGGATGGGTTTCCGCGCGAG 1080  
Db 1021 GCTCTCGCTTCGCGCATTTCTGAAGAACGTTACTCCAAGTGGATGGGTTTCCGCTCCAAGC 1080  
QY 1081 ATCCCGGATTTCCTCCCGTGTATGGCCGGGCAACCCGGACACCCGACGCTTAATCTATGCT 1140  
Db 1081 ATCCCGGATTTCCTCCAGTGTGTTGCTGCTGCTACCGGTACTCCAGACGCTTATCTACGCT 1140  
QY 1141 TTCGGCCACGGTCATCTCGGCATGACAGGGGGCCCGATGACCGCAACCGCTCTGCTCAGAG 1200  
Db 1141 TTCGGTCACGGTCACCTCGGTATGACTGGTGTCTCAATGACCGCAACCCCTCTTCTGAG 1200

Qy 1201 CTCCTCGAGCGAANAAGACCTCAATCGACATTTTCGCCCTTCGACCAAAACCGGTTTGGT 1260  
Dbb 1201 CTCCTCGAGGTGAGAAGACCTCTATCGACATCTCTCCATTCGACCAAAACCGGTTTCGGT 1260  
Qy 1261 ATTGGCAATCCAGCAAAACCGGTCGCGCAAGTTAA 1296  
Dbb 1261 ATTGGTAAGTCCAAAGCAAACTGGCTGCATCCCTAA 1296

RESULT 12

US-08-484-274A-17  
: Sequence 17, Application US/08484274A  
: Patent No. 5776760  
: GENERAL INFORMATION:  
: APPLICANT: Kishore, Ganesh M.  
: APPLICANT: Barry, Gerard F.  
: TITLE OF INVENTION: Glyphosate Tolerant Plants  
: NUMBER OF SEQUENCES: 33  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Arnold, White & Durkee  
: STREET: P.O. Box 4433  
: CITY: Houston  
: STATE: Texas  
: COUNTRY: USA  
: ZIP: 77210-4433  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patentin Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: FILING DATE: 07 June 1996  
: CLASSIFICATION: 435  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Patterson, Melinda L.  
: REGISTRATION NUMBER: 33,062  
: REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (713)789-2679  
: INFORMATION FOR SEQ ID NO: 17:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 1296 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: double  
: TOPOLOGY: linear  
: MOLECULE TYPE: DNA (recombinant)  
: FEATURE:  
: NAME/KEY: CDS  
: LOCATION: 1..1296  
US-08-484-274A-17

Query Match 74.08; Score 958.4; DB 2; Length 1296;  
Best Local Similarity 83.7%; Pred. No. 0;  
Matches 1085; Conservative 0; Mismatches 211; Indels 0; Gaps 0;

Qy 1 ATGGCTCAGAACCAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGGGTATGCACG 60  
Dbb 1 ATGGCTCAGAACCAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGGGTATGCACG 60  
Qy 61 CGCGTGATGCTTCAGCGCCCGGATTCAAAAGTCACCTTGATTGACCGCAACCCCTCCCTGGC 120  
Dbb 61 GCTTTGATGCTTCAACGCTCGTGATTCAGGTTACCTTGATTGATCCAAACCCACAGGT 120  
Qy 121 GAAGGTGCATCGTTGGGATGCGGGATGCTTCAACGGCTCATCCGCTGCTCCCTATGTCC 180  
Dbb 121 GAAGGTGCCCTCTTTCGGTAAACGCTGGTTGCTTCAACGGTTCTCCGCTGTTTCCAAATGTCC 180  
Qy 181 ATGCCCGGAAACTTGACGAGCTGCCGAAGTGGCTCTTGACCCGATGGGCGCGTGTGCA 240  
Dbb 181 ATGCCAGGAACCTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCCAATGGGTCCATTGTCC 240

Qy 241 ATCCGGTTACGTATTTTCCAAACCATCATGCCCTGGTTGATTCGCTTCTTGTAGCCGA 300  
Dbb 241 ATCCGGTTTCGGCTACTTTTCCAAACCATCATGCCCTGGTTGATTCGCTTCTTGTAGCCGA 300  
Qy 301 AGACCAAAAGGTGAAGGAGCAGCGAAGACTCCGCAATCTCATCAAGTCCACAGGTG 360  
Dbb 301 AGACCAAAAGGTGAAGGAGCAGCTAAGCACTCCGCTAACTCATCAAGTCCACAGGTG 360  
Qy 361 CCTGTGATCAAGTCAATTCGGCGAGGAGCTGATCGAGCCCATCTCATCCGCATCAAGGT 420  
Dbb 361 CCTTTGATCAAGTCTTGGCTGAGGAGCTGATGTAGCCACCTTATCCGTCACCAAGGT 420  
Qy 421 CATCTGACCGGTATATCGTGGAGAGCAGACTTCGCAAGAGCAGCGGAGGTGGGAATCG 480  
Dbb 421 CACCTTACCGGTACCGTGGAGAGCAGACTTCGCCAGGACCGTGGAGGTGGGAATCT 480  
Qy 481 CGGGGTCTCAACGGTGTTCGACGAGATCTCAGCGCGGATGCTTCGCGGATTTTCGAT 540  
Dbb 481 CGTCGCTCTCAACGGTGTTCGTAATACTCAGCGCTGATGATTCGCTGATTTTCGAT 540  
Qy 541 CCGAACTTGTCCGATCGCTTTACCAAGGGCACTCTTATAGAGAGAACGCTCACAGATT 600  
Dbb 541 CCTAACTTGTCTACGCTTTACCAAGGGCACTCTTATAGAGAGAACGCTCACAGATT 600  
Qy 601 AATCCGAAAGGCTCGTGACCTCTTGTTCGGGCTTTTATCGCGAACGCTGGCGAATTT 660  
Dbb 601 AACCACAAAGGTCTCGTGACTCTCTTGTTCGCTGCTTTCATCGCTACCGTGGAGAGTTC 660  
Qy 661 GTATCTGGCGGTCTATCGGCTTTGAGACTGAAGGTAGGGCGCTTAAAGGATTAACAAC 720  
Dbb 661 GTGCTGCTGCTGTTATCGGATTCGAGACTGAAGGTCTGCTCTCAAGGGTATCACACC 720  
Qy 721 ACGAACGCGTTCGGCGTTCGACGCTGTCGAGCGGTGTCGAGCGCGCGCACACTCGAAATCA 780  
Dbb 721 ACCAACGCTGTTCTGCTGTTGATGACGCTGTTGTCAGCTGGTGCACACTCCAAAGTCT 780  
Qy 781 CTTGCTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAACGCTGGGATATCATATCTC 840  
Dbb 781 CTTGCTAATTCCTTTCGTTGATGACATCCCATTTGGATACCGAACGCTGGATACCATCTG 840  
Qy 841 ATCGCGAATCCGGAAGCGGCTCCAGCATTCGAGGACCGATGGGTACAGAAAATTCATC 900  
Dbb 841 ATCGCAACCCAGAGGCTGCTCCAGTATTCGAACCTACCGATGCTTCTGGAAGTTTATC 900  
Qy 901 GCGACACTATGGAATGGGGCTTCGCGTGGGGTACGGTTGAGTTCGCTGGGCTCACA 960  
Dbb 901 GCTACTCTATGGAGATGGGCTTCGCTGTTGTCGAACCGTTGAGTTCGCTGGTCTCACT 960  
Qy 961 GCCGCTCCTAACTGGAACGTCGCGCATGTCTATAGCACGCTCGAAAACTTCTTCCA 1020  
Dbb 961 GCTGCTCCTAACTGGAAGCGTCTCACGTTCTCTACACTCGCGCTCGTAAGTTCCTTCCA 1020  
Qy 1021 GCCCTCGGCTCGGAGTTCTGAAGACGATATTCGAATGGATGGGTTCCGGCGGAGC 1080  
Dbb 1021 GCTCTCGCTCTCGCAGCTTCTGAAGACGTTACTCCAAAGTGGATGGGTTTCGCTCAAAG 1080  
Qy 1081 ATCCCGATTCGCTCCCGCTGATTTGGCGGCAACCCGACACCGAGCTATCTATGCT 1140  
Dbb 1081 ATCCCGATTCCTTCAGATGTTGGTCTACCCGCTACTCCAGAGCTTATCTACGCT 1140  
Qy 1141 TTCGGCCACGCTCATCTCGGCATGACAGGGCGCGGATGACCGCAACCGCTCTCTCAGAG 1200  
Dbb 1141 TTCGGTCAGGTCACCTCGGTATGACTGGTCTCCAAATGACCGCAACCGCTCTCTCAG 1200  
Qy 1201 CTCCTCGAGCGCAAAAGACCTCAATCGACATTTTCGCCCTTCGACCAAAACCGGTTTGGT 1260  
Dbb 1201 CTCCTCGAGGTGAGAAGACCTCTATCGACATCTCTCCATTCGACCAAAACCGGTTTCCGT 1260  
Qy 1261 ATTGGCAATCCAGCAAAACCGGTCGCGCAAGTTAA 1296  
Dbb 1261 ATTGGTAAGTCCAAAGCAAACTGGCTGCATCCCTAA 1296

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RESULT 13
US-08-391-339-30
: Sequence 30, Application US/08391339
: Patent No. 5463175
: GENERAL INFORMATION:
: APPLICANT: Kishore, Ganesh M.
: APPLICANT: Barry, Gerard F.
: TITLE OF INVENTION: Glyphosate Tolerant Plants
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dennis R. Hoerner, Jr.,
: ADDRESSEE: Monsanto Co. BB4F
: STREET: 700 Chesterfield Village Parkway
: CITY: St. Louis
: STATE: Missouri
: COUNTRY: USA
: ZIP: 63198
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/391,339
: FILING DATE:
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/156,968
: FILING DATE:
: APPLICATION NUMBER: US/07/717,370
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Hoerner, Dennis R., Jr.
: REGISTRATION NUMBER: 30,914
: REFERENCE/DOCKET NUMBER: 38-21(10533)
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (314)537-6099
: INFORMATION FOR SEQ ID NO: 30:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 69 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (synthetic)
: US-08-391-339-30

Query Match 4.3%; Score 56.2; DB 1; Length 69;
Best Local Similarity 88.4%; Pred. No. 1.3e-09;
Matches 61; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 714 TACAAACCAAGCGGCTTCTGGCGTTGATGACAGCGGTGTCGACGCGGCACACTC 773
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Db 1 TACAAACCACTAACCGTCTTCTGGCTGTGATGACAGCTGTGTTCCAGCTGTGTCACACTC 60
|||||
QY 774 GAATCACT 782
|||||
Db 61 TAATCACT 69

RESULT 14
US-08-391-339-33
: Sequence 33, Application US/08391339
: Patent No. 5463175
: GENERAL INFORMATION:
: APPLICANT: Kishore, Ganesh M.
: APPLICANT: Barry, Gerard F.
: TITLE OF INVENTION: Glyphosate Tolerant Plants
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dennis R. Hoerner, Jr.,
: ADDRESSEE: Monsanto Co. BB4F
: STREET: 700 Chesterfield Village Parkway
: CITY: St. Louis
: STATE: Missouri
: COUNTRY: USA
: ZIP: 63198
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/391,339
: FILING DATE:
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/156,968
: FILING DATE:
: APPLICATION NUMBER: US/07/717,370
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Hoerner, Dennis R., Jr.
: REGISTRATION NUMBER: 30,914
: REFERENCE/DOCKET NUMBER: 38-21(10533)
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (314)537-6099
: INFORMATION FOR SEQ ID NO: 30:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 69 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (synthetic)
: US-08-391-339-33

Query Match 4.3%; Score 56.2; DB 1; Length 69;
Best Local Similarity 88.4%; Pred. No. 1.3e-09;
Matches 61; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 714 TACAAACCAAGCGGCTTCTGGCGTTGATGACAGCGGTGTCGACGCGGCACACTC 773
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 TACAAACCACTAACCGTCTTCTGGCTGTGATGACAGCTGTGTTCCAGCTGTGTCACACTC 60
|||||
QY 774 GAATCACT 782
|||||
Db 61 TAATCACT 69

RESULT 15
US-08-484-274A-30
: Sequence 30, Application US/08484274A
: Patent No. 5776760
: GENERAL INFORMATION:
: APPLICANT: Kishore, Ganesh M.
: APPLICANT: Barry, Gerard F.
: TITLE OF INVENTION: Glyphosate Tolerant Plants
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/484,274A
: FILING DATE: 07 June 1996
: CLASSIFICATION: 435

STREET: 700 Chesterfield Village Parkway
:
CITY: St. Louis
:
STATE: Missouri
:
COUNTRY: USA
:
ZIP: 63198
:
COMPUTER READABLE FORM:
:
MEDIUM TYPE: Floppy disk
:
COMPUTER: IBM PC compatible
:
OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.25
:
CURRENT APPLICATION DATA:
:
APPLICATION NUMBER: US/08/391,339
:
FILING DATE:
:
CLASSIFICATION: 800
:
PRIOR APPLICATION DATA:
:
APPLICATION NUMBER: US/08/156,968
:
FILING DATE:
:
APPLICATION NUMBER: US/07/717,370
:
FILING DATE:
:
ATTORNEY/AGENT INFORMATION:
:
NAME: Hoerner, Dennis R., Jr.
:
REGISTRATION NUMBER: 30,914
:
REFERENCE/DOCKET NUMBER: 38-21(10533)
:
TELECOMMUNICATION INFORMATION:
:
TELEPHONE: (314)537-6099
:
INFORMATION FOR SEQ ID NO: 33:
:
SEQUENCE CHARACTERISTICS:
:
LENGTH: 69 base pairs
:
TYPE: nucleic acid
:
STRANDEDNESS: single
:
TOPOLOGY: linear
:
MOLECULE TYPE: DNA (synthetic)
:
US-08-391-339-33

Query Match 4.3%; Score 56.2; DB 1; Length 69;
Best Local Similarity 88.4%; Pred. No. 1.3e-09;
Matches 61; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1128 CGTAATCTATGCTTTCGGCCACGGTCATCTCGCATGACAGGGCGCGGATGACCGCAAC 1187
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Db 1 CGTAATCTATGCTTTCGGTCACGGTCATCTCGGTATGACAGGTGCTCCATGACTGCAAC 60
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QY 1188 GCTCGTCTC 1196
|||||
Db 61 TCTCGTCTC 69
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ATTORNEY/AGENT INFORMATION:  
NAME: Patterson, Melinda L.  
REGISTRATION NUMBER: 33,062  
REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (713)789-2679  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 69 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (synthetic)  
US-08-484-274A-30

Query Match 4.3%; Score 56.2; DB 2; Length 69;  
Best Local Similarity 88.4%; Pred. No. 1.3e-09;  
Matches 61; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
QY 714 TACAACACGAGCGGTTCTGGCCGTTGATGCAGCGGTTGTCGACGCGGCGCACACTC 773  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 1 TACAACCACTAAGCGTGTCTGGCTGTGATGCAGCTGTGTTGCACGCTGGTGCACACTC 60  
QY 774 GAAATCACT 782  
|||||||  
Db 61 TAAATCACT 69

Search completed: January 1, 2001, 03:17:58  
Job time: 29302 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 01:12:42 ; Search time 3327.86 Seconds  
(without alignments)  
2407.829 Million cell updates/sec

Title: US-08-484-274-6  
Perfect score: 1296  
Sequence: 1 ATGCGTGAGACCAACAAAAA.....AAACGGGTCCGCCAAGTTAA 1296

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues  
Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*  
12: gb\_est12:\*  
13: gb\_est13:\*  
14: gb\_est14:\*  
15: gb\_est15:\*  
16: gb\_est16:\*  
17: gb\_est17:\*  
18: gb\_est18:\*  
19: gb\_est19:\*  
20: gb\_est20:\*  
21: gb\_est21:\*  
22: gb\_est22:\*  
23: gb\_est23:\*  
24: gb\_est24:\*  
25: gb\_est25:\*  
26: gb\_est26:\*  
27: gb\_est27:\*  
28: gb\_est28:\*  
29: gb\_est29:\*  
30: gb\_est30:\*  
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42: em\_estfun:\*  
43: em\_esthum1:\*

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46: em\_esthum4:\*  
47: em\_esthum5:\*  
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65: em\_estin3:\*  
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70: em\_estpl1:\*  
71: em\_estpl2:\*  
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73: em\_estpl4:\*  
74: em\_estpl5:\*  
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87: em\_estrol3:\*  
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90: gb\_gss3:\*  
91: gb\_gss4:\*  
92: em\_gss1:\*  
93: em\_gss2:\*  
94: em\_gss3:\*  
95: em\_gss4:\*  
96: gb\_gss5:\*  
97: gb\_gss6:\*  
98: gb\_gss7:\*  
99: gb\_gss8:\*  
100: gb\_gss9:\*  
101: em\_gss5:\*  
102: em\_gss6:\*  
103: em\_gss7:\*  
104: em\_gss8:\*  
105: em\_gss9:\*  
106: em\_gss10:\*  
107: em\_gss11:\*  
108: gb\_gss10:\*  
109: gb\_gss11:\*  
110: gb\_gss12:\*  
111: gb\_gss13:\*  
112: gb\_gss14:\*  
113: gb\_gss15:\*  
114: gb\_gss16:\*  
115: gb\_gss17:\*  
116: gb\_gss18:\*

117: gb\_gss18:\*  
118: gb\_gss19:\*  
119: em\_gss13:\*  
120: gb\_gss20:\*  
121: gb\_gss21:\*  
122: gb\_gss22:\*  
123: gb\_gss23:\*  
124: gb\_gss24:\*  
125: em\_gss14:\*  
126: em\_gss15:\*  
127: em\_gss16:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	44.4	3.4	434	124	P149R	AL160534 Leishmania
C 2	37.4	2.9	702	96	AQ328054	AQ328054 nbx0042I
C 3	36.8	2.8	922	121	CNS015Y8	AL108058 Drosophil
C 4	36	2.8	380	22	AW500960	AW500960 UI-HF-BP0
C 5	36	2.8	389	22	AW501280	AW501280 UI-HF-BP0
C 6	36	2.8	895	123	CNS04UDT	AL307658 Tetraodon
C 7	35.6	2.7	614	21	AW254765	AW254765 ML105 pep
C 8	35	2.7	360	16	AV190084	AV190084 AV190084
C 9	35	2.7	382	36	C47876	C47876 C47876 Yuj1
C 10	35	2.7	517	17	AV386799	AV386799 AV386799
C 11	34.8	2.7	171	17	AV316270	AV316270 AV316270
C 12	34.8	2.7	494	14	AL387587	AL387587 MtBC43E07
C 13	34.8	2.7	634	19	AW097371	AW097371 ts43a11.y
C 14	34.6	2.7	676	34	BE248875	BE248875 NF023D11D
C 15	34.6	2.7	205	18	AV413471	AV413471 AV413471
C 16	34.6	2.7	251	18	AV418303	AV418303 AV418303
C 17	34.6	2.7	271	24	AW19954	AW19954 LjNEST12e
C 18	34.6	2.7	273	18	AV427698	AV427698 AV427698
C 19	34.6	2.7	300	18	AV406977	AV406977 AV406977
C 20	34.6	2.7	349	18	AV412853	AV412853 AV412853
C 21	34.6	2.7	416	18	AV425451	AV425451 AV425451
C 22	34.6	2.7	423	18	AV407852	AV407852 AV407852
C 23	34.6	2.7	429	18	AV408636	AV408636 AV408636
C 24	34.6	2.7	429	18	AV415123	AV415123 AV415123
C 25	34.6	2.7	452	18	AV423367	AV423367 AV423367
C 26	34.4	2.7	460	35	BE357122	BE357122 DGL_146.B
C 27	34.4	2.7	474	25	AW925090	AW925090 WS1_75.CO
C 28	34.4	2.7	586	35	BE357121	BE357121 DGL_146.B
C 29	34.4	2.7	652	35	BE362682	BE362682 DGL_88.H0
C 30	34.4	2.7	974	121	CNS002K5	AL097775 Drosophil
C 31	34.2	2.6	699	118	B07704	B07704 318H1F05706
C 32	34.2	2.6	1009	123	CNS03ZOP	AL267874 Tetraodon
C 33	34	2.6	258	39	W09527	W09527 ma01b07.r1
C 34	34	2.6	261	36	DA0242	DA0242 RICS2075A.R
C 35	34	2.6	425	7	AA871231	AA871231 vq32g02.r
C 36	34	2.6	433	4	AA542047	AA542047 vk43d01.r
C 37	34	2.6	636	97	AQ447252	AQ447252 mgx00006C
C 38	33.8	2.6	222	19	AV536254	AV536254 AV536254
C 39	33.8	2.6	226	5	AA644181	AA644181 ab63a02.s
C 40	33.8	2.6	360	36	C41677	C41677 C41677 Yuj1
C 41	33.8	2.6	935	123	CNS03IPN	AL245876 Tetraodon
C 42	33.6	2.6	409	35	BE411304	BE411304 ISC004.B1
C 43	33.6	2.6	452	35	BE356986	BE356986 DGL_146.B
C 44	33.6	2.6	460	15	AU088715	AU088715 AU088715
C 45	33.6	2.6	500	36	BE517838	BE517838 WHE0803.C

ALIGNMENTS

RESULT 1  
P149R/c

LOCUS DEFINITION	P149R	434 bp	DNA	GSS	16-MAR-2000
ACCESSION	Leishmania major Friedlin PAC P149	right end-sequence, genomic survey sequence.			
VERSION	AL160534				
KEYWORDS	AL160534.1	GI:7258935			
SOURCE	GSS.				
ORGANISM	Leishmania major.				
REFERENCE	Leishmania major.				
AUTHORS	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania				
TITLE	1 (bases 1 to 434)				
MEDLINE	Ivens,A.C., Lewis,S.M., Bagherzadeh,A., Zhang,L., Chan,H.M. and Smith,D.F.				
AUTHORS	A physical map of the Leishmania major Friedlin genome				
TITLE	Genome Res. 8 (2), 135-145 (1998)				
JOURNAL	98146435				
COMMENT	2 (bases 1 to 41)				
FEATURES	Taylor,R.G., Huckle,E.E.J., Ivens,A.C., Rajandream,M.A. and Barrell,B.G.				
BASE COUNT	Submitted (14-MAR-2000) Leishmania major Friedlin genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and alicats@sanger.ac.uk				
ORIGIN	see http://www.ebi.ac.uk/parasites/leish.html				
QUERY MATCH	Details of Leishmania sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/projects/Lmajor/				
LOCUS DEFINITION	The primer sequence can be obtained from alicats@sanger.ac.uk.				
ACCESSION	Location/Qualifiers				
VERSION	1..434				
KEYWORDS	/organism="Leishmania major"				
ORGANISM	/strain="Friedlin"				
REFERENCE	/db_xref="taxon:5664"				
AUTHORS	/clone="PAC P149"				
TITLE	76 a 131 c 157 g 70 t				
JOURNAL					
COMMENT					
FEATURES					
BASE COUNT					
ORIGIN					
QUERY MATCH					
LOCUS DEFINITION	Query Match	3.4%	Score 44.4	DB 124	Length 434
ACCESSION	Best Local Similarity	54.2%	Pred. No. 0.022		
VERSION	Matches	90	Conservative	0	Mismatches 76
KEYWORDS					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
COMMENT					





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FEATURES
source
Seq primer: M13 Forward.
Location/Qualifiers
1. .380
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3073464"
/clone_lib="NIH_MGC_51"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LT1)"
/note="Vector: pT7f3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(4.4-7.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      62 a 115 c 133 g 70 t
ORIGIN
Query Match      2.8%; Score 36; DB 22; Length 380;
Best Local Similarity 50.0%; Pred. No. 6.6;
Matches 90; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
QY 364 CTGATCAAGTCATTGGCGGAGGAGGTGATGCGGAGGCATCTGATCGCCCATGAAGTTCAT 423
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 378 CGGGTGCATCGCTTCGCCGACCGGACGCGATCGGATCGGATGAATGCCGCGAGGAGTG 319
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 424 CTGACCGTATATCGTGAGAGCAGACTTCGCCAAGGACCGCGAGGTTGGGAATCGCGG 483
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 318 GCGATCGACGACCGCGCGAGGCGGAACTCGCCAAGTCGCGCTGATCGCGCATCTGCGAC 259
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 484 CGTCTCAACGGTGTTCGACGCGAGATCCTCAGCGCGGATCGTGTGGGGATTTTCGATCCG 543
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 258 CGCAAGAACAACATGATCGCGGCGCTTCATCGCGGCCCATTCGCTGCAGGACGACGACG 199
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 5
AWS01280/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
Location/Qualifiers
1. .389
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3073186"
/clone_lib="NIH_MGC_51"
/tissue_type="lymph"
/cell_type="germinal center B cells"
FEATURES
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Seq primer: M13 Forward.
Location/Qualifiers
1. .380
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3073464"
/clone_lib="NIH_MGC_51"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LT1)"
/note="Vector: pT7f3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(4.4-7.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      65 a 115 c 137 g 72 t
ORIGIN
Query Match      2.8%; Score 36; DB 22; Length 389;
Best Local Similarity 50.0%; Pred. No. 6.7;
Matches 90; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
QY 364 CTGATCAAGTCATTGGCGGAGGAGGTGATGCGGAGGCATCTGATCGCCCATGAAGTTCAT 423
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 378 CGGGTGCATCGCTTTCGCCGACCGGACGCGATCGGATGAATGCCGCGAGGAGTG 319
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 424 CTGACCGTATATCGTGAGAGCAGACTTCGCCAAGGACCGCGAGGTTGGGAATCGCGG 483
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 318 GCGATCGACGACCGCGCGAGGCGGAACTCGCCAAGTCGCGCTGATCGCGCATCTGCGAC 259
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 484 CGTCTCAACGGTGTTCGACGCGAGATCCTCAGCGCGGATCGTGTGGGGATTTTCGATCCG 543
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 258 CGCAAGAACAACATGATCGCGGCGCTTCATCGCGGCCCATTCGCTGCAGGACGACGACG 199
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
CNS040UDT
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
1. .895
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="027A06"
/clone_lib="B"
/note="Genoscope sequence ID : C0A8027BA03B2-end : Sp6"
FEATURES
source
Location/Qualifiers
1. .895
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
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/clone_lib="B"
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	Query Match	2.7%	Score 35.6;	DB 21;	Length 614;
	Best Local Similarity	47.1%;	Pred. No. 9.8;	Mismatches 0;	Gaps 0;
	Matches 107;	Conservative			
Qy	443	AACGAGACTTCGCCAAGCAGCGCGAGGTGGGAACATGC GCGCTCAACGGTGTTCCGCA	502		
Dd	435	ANTCGGAATCCCCAAGGGCGAAGGCTTCTTCAGANTCTCTCGATGTTCTTCGAG	376		
Qy	503	CGCAGATCCTCAGCGCGATGCGTTGGCGGANITTCGATCCGAAC TTCTCGCATGCGTTTTA	562		
Dd	375	ATCAGCCCGGCGACGTCTTTCAGGAGGTGGAAGGTGAGGCCACGCTCCCGGAGTGCCCG	316		
Qy	563	CMAAGGCCATTCTTATAGAAGAAAGCTCACACGATTTAATCCGACAAGGCTCGTAGACC	622		
Dd	315	TGATAGCGGTGATGTTAGGTTCTCCTTCAGGTACTCTCCCGTCAATGCATGTA CTT	256		
Qy	623	TCITTGTTTCGGCGTTTTCATCCGCAACGGTGGCGAATTTGATC TCGC	669		
Dd	255	TTCTTTTATCATCATGATTCTCGCACATCGCGTTGAATTTCTCTTTGAG	209		

REFERENCE  
AUTHORS

C47876  
C47876.1 GI:3384129  
EST.  
Caenorhabditis elegans.  
Caenorhabditis elegans.  
Caenorhabditis elegans.  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea  
; Rhabditidae; Peloderinae; Caenorhabditis.  
1 (bases 1 to 382)  
Kohara,Y., Mochizashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano  
M., Miyata,A. and Nishigaki,A.

TITLE Expression map of the C.elegans genome  
JOURNAL Unpublished (1996)  
COMMENT Contact: Yuji Kohara  
Gene Library Lab  
National Institute of Genetics  
Yata 1111, Mishima, Shizuoka 411, Japan  
Tel: 81-559-81-6854  
Fax: 81-559-81-6855  
Email: ykohara@lab.nig.ac.jp.  
Location/Qualifiers

FEATURES  
Source 1..382  
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QY 1233 TTGCGCCCTTCCGACCAAC 1251  
DB 294 CTCAATCCAGAGCCCGCAGC 312

RESULT 10  
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LOCUS AV386799 517 bp mRNA EST 21-JAN-2000  
DEFINITION AV386799 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii  
cDNA clone CM007a05\_r, mRNA sequence.  
ACCESSION AV386799  
VERSION AV386799.1 GI:6541015  
KEYWORDS EST.  
SOURCE Chlamydomonas reinhardtii.  
ORGANISM Chlamydomonas reinhardtii  
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
Chlamydomonadaceae; Chlamydomonas.  
REFERENCE 1 (bases 1 to 517)  
Asamizu,E., Nakamura,Y., Sato,S., Fukuzawa,H. and Tabata,S.  
A Large Scale Structural Analysis of cDNAs in a Unicellular Green  
Alga, Chlamydomonas reinhardtii. I. Generation of 3433  
Non-redundant Expressed Sequence Tags  
DNA Res. 6, 369-373 (1999)  
Contact: Yasukazu Nakamura  
The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
Email: ynakamu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>.  
Location/Qualifiers  
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/note="Vector: pBluescriptII SK-; Site\_1: EcoRI; Site\_2:  
XhoI"

TITLE Expression map of the C.elegans genome  
JOURNAL Unpublished (1996)  
COMMENT Contact: Yuji Kohara  
Gene Library Lab  
National Institute of Genetics  
Yata 1111, Mishima, Shizuoka 411, Japan  
Tel: 81-559-81-6854  
Fax: 81-559-81-6855  
Email: ykohara@lab.nig.ac.jp.  
Location/Qualifiers

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QY 1113 AACCCGGACACCGCAGCTATCTATCTGTTTCGGCCGCGGTCTCGGCATGACAGGGGC 1172  
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QY 1173 GCCGATGACCGCAACGCTCGTCTCAGAGCTCTCGCAGGCGGAAAGACCTCAATCGACAT 1232  
DB 234 GACCGAGGTTCTCCNTCTGCGTGAAGAGCCCCCGCCGCGGAGAGAGCGCGCTCACCAT 293  
QY 1233 TTGCGCCCTTCCGACCAAC 1251  
DB 294 CTCAATCCAGAGCCCGCAGC 312

RESULT 10  
AV386799  
LOCUS AV386799 517 bp mRNA EST 21-JAN-2000  
DEFINITION AV386799 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii  
cDNA clone CM007a05\_r, mRNA sequence.  
ACCESSION AV386799  
VERSION AV386799.1 GI:6541015  
KEYWORDS EST.  
SOURCE Chlamydomonas reinhardtii.  
ORGANISM Chlamydomonas reinhardtii  
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
Chlamydomonadaceae; Chlamydomonas.  
REFERENCE 1 (bases 1 to 517)  
Asamizu,E., Nakamura,Y., Sato,S., Fukuzawa,H. and Tabata,S.  
A Large Scale Structural Analysis of cDNAs in a Unicellular Green  
Alga, Chlamydomonas reinhardtii. I. Generation of 3433  
Non-redundant Expressed Sequence Tags  
DNA Res. 6, 369-373 (1999)  
Contact: Yasukazu Nakamura  
The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
Email: ynakamu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>.  
Location/Qualifiers  
1..517  
/organism="Chlamydomonas reinhardtii"  
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Best Local Similarity 47.1%; Pred. No. 14;  
Matches 107; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 321 GCAGGGCAAGAGCACTCGCAATCTCATCAAGTCCACGGTGCTCTGATCAAGTCATTGGC 380  
DB 175 GCTGACGAGCGTGTGCGGAGATCATCAAGCCGAGGCCCCCAGCAGCAACTTCAAGCG 234  
QY 381 GGAGAGGCTGATCGGAGCCATCTGATCGGCATGAAGGTCTATCGCTATATCTGCG 440  
DB 235 CATGGGACGACGACCTTCCGAGACCCACCGACGAGGAGGGTGCACGACGATGA 294  
QY 441 AGAAGCAGACTTCGCCAAGGACCCGAGGTTGGGAACTGGGGCTCTCAACGGGTGTCG 500  
DB 295 CGACGAGGAGGAGGAGGAGGCCAAAGTAAACGGCATCGTTGCCTACTCGCGGTACTTG 354  
QY 501 CACGCAGATCTCAGCGCCGATCGTTGCGGATTTTCGATCCGAACT 547  
DB 355 GGGACACGACAGAGCGGGGCTAAGCTGCGGGTTGTTGGTGGGACT 401

RESULT 11  
AV316270/c  
LOCUS AV316270 171 bp mRNA EST 08-NOV-1999  
DEFINITION AV316270 RIKEN full-length enriched, adult male thymus Mus musculus  
cDNA clone 5830435F07 3', mRNA sequence.  
ACCESSION AV316270  
VERSION AV316270.1 GI:6281688  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 171)  
Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,  
Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,E.,  
Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai  
C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,  
Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,  
Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata  
Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H.,  
Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N., Tsunoda,Y.,  
Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T.,  
Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.  
RIKEN Mouse ESTs (Konno,H., et al. 1999)  
Unpublished (1999)  
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The Institute of Physical and Chemical Research (RIKEN), Genomic  
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Fax: +81-298-36-9098  
Email: genome-res@tc.riken.go.jp,  
URL: <http://genome.rtc.riken.go.jp/>  
Transcriptional sequencing: A method for DNA sequencing using RNA  
polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)  
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,  
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki  
Y., and Hayashizaki,Y.  
Automated filtration-based high-throughput plasmid preparation  
system. Genome Res. 9 (5), 463-470 (1999)  
Carninci,P. and Hayashizaki,Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
19-44 (1999)

please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

#### FEATURES

source  
1. .171  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/tissue\_type="thymus"  
/dev\_stage="adult"  
/lab\_host="DH108"  
/note="Site\_1: Sali; Site\_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGATCCAGAGCTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot -10.0 and subtraction to Rot -100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTTAATTAATATCCCTCCCTCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sali; 3' end: BamHI."

BASE COUNT 45 a 41 c 33 g 51 t 1 others  
ORIGIN

Query Match 2.78; Score 34.8; DB 17; Length 171;  
Best Local Similarity 65.48; Pred. No. 12; Mismatches 0; Gaps 0;  
Matches 51; Conservative 0; Indels 27; Indels 0; Gaps 0;  
Qy 888 AGGAAATTCACGACACCTATGGAATGGGCTTCGGTGGGGTACGGTTGAGTT 947  
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Db 84 AGGATTTTGATCAAAATCAATGGAATGGGCGAGTGTGTGGTCCAGTTGATTT 25  
Qy 948 CGCTGGGCTCACACCCG 965  
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Db 24 CTCAGTCCCTCTTCG 7

#### RESULT 12

AL387587 494 bp mRNA EST 03-AUG-2000  
LOCUS MtBC43E07F1 MtBC Medicago truncatula cDNA clone MtBC43E07 T3, mRNA  
DEFINITION  
ACCESSION AL387587  
VERSION AL387587.1 GI:9687338  
KEYWORDS EST.  
SOURCE barrel medic.  
ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Medicago.  
1 (bases 1 to 494)  
Journet,E.P., Crespeau,H., van-Tuinen,D., Gouzy,J., Jaillon,O., Niebel,A., Carreau,V., Chatagnier,O., Kahn,D., Glaninazzi-Pearson,V. and Gamas,P.  
Medicago truncatula ESTs from endomycorrhizal roots  
Unpublished (2000)

#### REFERENCE

AUTHORS  
CONTACT: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr)  
Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de Biologie Molculaire des Relations Plantes-Microorganismes,

CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email : [mt-est@toulouse.inra.fr](mailto:mt-est@toulouse.inra.fr) website : <http://sequence.toulouse.inra.fr/Mtruncatula.html>).

#### FEATURES

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/tissue\_type="arbuscular mycorrhiza"  
/dev\_stage="harvested 3 weeks post inoculation with Glomus intraradices"  
/note="vector: pBluescript PSK; Site\_1: EcoRI; Site\_2: XhoI; M. truncatula sterilised seeds were germinated for 72h at 25 C, before transplanting into a 1/3 Epilissea soil : 2/3 calcined Terragreen mix in the presence of onion root fragments colonized by the arbuscular mycorrhizal fungus Glomus intraradices (Schenck & Smith, isolate LP48 ). The plants were watered every day and twice a week with a modified nutrient Long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zap XR vector from Stratagene and packaged using Gigapack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using Exaest helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France). Note : EST may be of fungal origin."

BASE COUNT 131 a 97 c 128 g 138 t  
ORIGIN

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Best Local Similarity 54.88; Pred. No. 16; Mismatches 69; Conservative 0; Mismatches 57; Indels 0; Gaps 0;  
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Db 359 TCATGTGCGCTGTGTGGAAAGAGGGTGGCACAGGATTTTGTATTGGGGTCCCACTGCT 418  
Qy 683 TTGACACTGAAGGTAGGGCGCTTAAAGGCATTACACCAACGAGCGCTTCTGGCCGTTG 742  
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Db 419 ATGAGAGGCAACTGTAGCCAGTGCAGAGATAAAATTCAGGCAGCGCTTCTCCCGGTG 478  
Qy 743 ATGCAG 748  
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Db 479 ATGGAG 484

#### RESULT 13

AL387371 634 bp mRNA EST 19-OCT-1999  
LOCUS rs43all.y1 Sommer Pristionchus Pristionchus pacificus cDNA 5', similar to WP:Y61A9LA\_74.D CE22688 ;, mRNA sequence.  
DEFINITION  
ACCESSION AL387371  
VERSION AL387371.1 GI:6067682  
KEYWORDS EST.  
SOURCE Pristionchus pacificus.  
ORGANISM Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.  
1 (bases 1 to 634)

#### REFERENCE

AUTHORS  
McCartner,J., Clifton,S., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)  
Contact: McCarter JP



/note="Vector: pBluescriptII SK-; Site\_1: EcoRI; Site\_2:

XhoI; Isolate=Miyakojima MG-20"

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ORIGIN

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## ORIGIN

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Qy	69	CTTTTCAGCGCCCGGANTCAAAGTCACCTTTCATTGAC	105		
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100

Qy 69 GCTTCAGCGCGCGGATTCAAAGTCACCTTGATTGAC 105

Db 158 GCTTCTCCATGACGGCTTCCATGCTCCATCATCGAC 194

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Job time: 25785 sec

Job time: 25785 sec

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 03:15:19 ; Search time 7299.04 Seconds  
(without alignments)  
775.497 Million cell updates/sec

Title: us-08-484-274-7  
Perfect score: 1296  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues 2067340  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 89: gb\_sts1:\*
- 90: gb\_sts2:\*
- 91: gb\_sy:\*
- 92: gb\_un:\*
- 93: gb\_vil:\*
- 94: gb\_vil2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1296	100.0	1296	5	I15327	I15327 Sequence 7
3	1201.6	92.7	1296	5	AR016593	AR016593 Sequence
4	1201.6	92.7	1296	5	I15326	I15326 Sequence 6
5	1196.8	92.3	1692	5	AR016591	AR016591 Sequence
6	1160.8	89.6	1293	5	AR016592	AR016592 Sequence 4
7	1160.8	89.6	1293	5	I15325	I15325 Sequence 4
8	1160.8	89.6	1689	5	I15324	I15324 Sequence 3
9	1011.2	78.0	1296	5	AR016595	AR016595 Sequence
10	1011.2	78.0	1296	5	I15328	I15328 Sequence 8
11	1006.4	77.7	1296	5	AR016604	AR016604 Sequence
12	1006.4	77.7	1296	5	I15337	I15337 Sequence 17

13	926.8	71.5	1631	5	A59869	A59869 Sequence 1
14	87.4	6.7	3430	2	PSEKSD	M69158 Pseudomonas
15	69.2	5.3	2289	2	PSEKSDA	M69159 Pseudomonas
16	69	5.3	69	5	AR016616	AR016616 Sequence
17	69	5.3	69	5	AR016619	AR016619 Sequence
18	69	5.3	69	5	I15349	I15349 Sequence 30
19	69	5.3	69	5	I15352	I15352 Sequence 33
20	68	5.2	68	5	AR016618	AR016618 Sequence
21	68	5.2	68	5	I15351	I15351 Sequence 32
22	63.4	4.9	65	5	AR016614	AR016614 Sequence
23	63.4	4.9	65	5	I15347	I15347 Sequence 28
24	62	4.8	62	5	AR016613	AR016613 Sequence
25	62	4.8	62	5	I15346	I15346 Sequence 27
26	61	4.7	61	5	AR016617	AR016617 Sequence
27	61	4.7	61	5	I15350	I15350 Sequence 31
28	42.8	3.3	196999	57	AC073946	AC073946 Mus muscu
29	42.6	3.3	1586	88	MMU70653	U70653 Mus muscu
30	42.6	3.3	1598	88	MMU70654	U70654 Mus muscu
31	42	3.2	31202	37	AC013022	AC013022 Drosophil
32	42	3.2	302357	29	AE003443	AE003443 Drosophil
33	41	3.2	41	5	AR016615	AR016615 Sequence
34	41	3.2	41	5	I15348	I15348 Sequence 29
35	40.4	3.1	186935	48	AC022322	AC022322 Homo sapi
36	40.2	3.1	840	89	CNS01EDB	AL140400 Anopheles
37	40.2	3.1	38914	2	MSGB937CS	L78820 Mycobacteri
38	40.2	3.1	179553	49	AC024253	AC024253 Homo sapi
39	39.8	3.1	223469	56	AC069019	AC069019 Mus muscu
40	39.4	3.0	767	54	ETIMAX	M30933 E.tenella a
41	39.4	3.0	1612	88	MMU70652	U70652 Mus muscu
42	39.2	3.0	47268	40	AC020414	AC020414 Drosophil
43	39	3.0	34220	38	AC014160	AC014160 Drosophil
44	39	3.0	235414	29	AE003708	AE003708 Drosophil
45	38.8	3.0	1558	88	MMU70646	U70646 Mus muscu

ALIGNMENTS

RESULT 1						
LOCUS	AR016594	1296 bp	DNA	PAT	05-DEC-1998	
DEFINITION	Sequence 7 from patent US 5776760.					
ACCESSION	AR016594					
VERSION	AR016594.1	GI:3972871				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 1296)					
AUTHORS	Barry,G.Francis and Kishore,G.Murthy.					
TITLE	Glyphosate tolerant plants					
JOURNAL	Patent: US 5776760-A 7 07-JUL-1998;					
FEATURES	Location/Qualifiers					
source	1..1296					
BASE COUNT	287 a	344 c	332 g	333 t		
ORIGIN						
Query Match	100.0%; Score 1296; DB 5; Length 1296;					
Best Local Similarity	100.0%; Pred. No. 0;					
Matches 1296;	Conservative	0;	Mismatches	0;	Indels	0; Gaps
QY	1	ATGGCTGAGAACCAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCAC	60			
DB	1	ATGGCTGAGAACCAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCAC	60			
QY	61	GCTTTGATGCTTCAACGTCGTGGATTCAAAGTCACCTTGATTGACCCGCAACCCCTCTGGC	120			
DB	61	GCTTTGATGCTTCAACGTCGTGGATTCAAAGTCACCTTGATTGACCCGCAACCCCTCTGGC	120			
QY	121	CAAGTTCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC	180			
DB	121	CAAGTTCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC	180			

Db	121	GAAGGTGCATCGTTTGGGAATCCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC	180
QY	181	ATGCCGGAAACTTGACGAGCTGCCGCAAGTGGCTCTTGACCGGATGGGCGCTTCTCA	240
Db	181	ATGCCGGAAACTTGACGAGCTGCCGCAAGTGGCTCTTGACCGGATGGGCGCTTCTCA	240
QY	241	ATCCGGTTCAGCTATTCTTCCAAACCATCATGCCCTGGTGTATCGCTTCTGTTAGCCGA	300
Db	241	ATCCGGTTCAGCTATTCTTCCAAACCATCATGCCCTGGTGTATCGCTTCTGTTAGCCGA	300
QY	301	AGACCAACAAGGTGAAGGAGCAGCGGAAGACACTCGGCAATCTCATCAAGTCACGGTG	360
Db	301	AGACCAACAAGGTGAAGGAGCAGCGGAAGACACTCGGCAATCTCATCAAGTCACGGTG	360
QY	361	CTCTGTATCAAGTCATTGGCGGAGGAGCTGATGCGAGCCATCTGATCGCCCATGAAGGT	420
Db	361	CTCTGTATCAAGTCATTGGCGGAGGAGCTGATGCGAGCCATCTGATCGCCCATGAAGGT	420
QY	421	CATCTGACCCGTATATCGTGGAAGCAGACTTCCCAAGGACCGCGAGGTTGGGAATG	480
Db	421	CATCTGACCCGTATATCGTGGAAGCAGACTTCCCAAGGACCGCGAGGTTGGGAATG	480
QY	481	CGCGCTCTCAACGGTGTTCGACGCGAGATCCTCTCTGCTGATGCTTTCGCTGATTTCCGAT	540
Db	481	CGCGCTCTCAACGGTGTTCGACGCGAGATCCTCTCTGCTGATGCTTTCGCTGATTTCCGAT	540
QY	541	CCTAACTTGTGCGATGCTTTTACCAAGGGCATCTTATAGAAGAACCGGTCAACGATT	600
Db	541	CCTAACTTGTGCGATGCTTTTACCAAGGGCATCTTATAGAAGAACCGGTCAACGATT	600
QY	601	AATCCGCAAGGGTCGTGACCCCTCTTGTTCGCGGTTTATCGCGAACCGGTGGCGAATTT	660
Db	601	AATCCGCAAGGGTCGTGACCCCTCTTGTTCGCGGTTTATCGCGAACCGGTGGCGAATTT	660
QY	661	GTATCTCGCGCTCATCGGTTTTTGAGACTGAAGGTGCTCTCTCAAGGCATATACACC	720
Db	661	GTATCTCGCGCTGTATCGGTTTTTGAGACTGAAGGTGCTCTCTCAAGGCATATACACC	720
QY	721	ACTAAGGTTGCTTGGCTGTGATGACAGCTGTTGTTGCAGCTGCTGCACACTCTAAATCA	780
Db	721	ACTAAGGTTGCTTGGCTGTGATGACAGCTGTTGTTGCAGCTGCTGCACACTCTAAATCA	780
QY	781	CTTGCTTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAACGTTGGATATCATATGTC	840
Db	781	CTTGCTTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAACGTTGGATATCATATGTC	840
QY	841	ATCGGAAATCCGGAACCGCTCCACGATTCGCGACGATCCGTCAGGAAATTCATC	900
Db	841	ATCGGAAATCCGGAACCGCTCCACGATTCGCGACGATCCGTCAGGAAATTCATC	900
QY	901	GGACACCTATGGAATGGGCTTTCGTTGCTGGTACTGTTGAGTTTGGTCTCTCACCA	960
Db	901	GGACACCTATGGAATGGGCTTTCGTTGCTGGTACTGTTGAGTTTGGTCTCTCACCA	960
QY	961	GCTGCTCTAACTGGAACCGTGGCATGTCTATACGCAACGCTCGAAAACCTCTTCCA	1020
Db	961	GCTGCTCTAACTGGAACCGTGGCATGTCTATACGCAACGCTCGAAAACCTCTTCCA	1020
QY	1021	GGCCTCGCGCTCGAGTTCTGAAGAACGATATTCCAAATGGATGGGTTTCGTCCTAGC	1080
Db	1021	GGCCTCGCGCTCGAGTTCTGAAGAACGATATTCCAAATGGATGGGTTTCGTCCTAGC	1080
QY	1081	ATTCCTGATTTCTTCCAGTGATTGGTGTGCAACTCGTACACCCGACGTAATCTATGCT	1140
Db	1081	ATTCCTGATTTCTTCCAGTGATTGGTGTGCAACTCGTACACCCGACGTAATCTATGCT	1140
QY	1141	TTTGGTCACGGTCATCTCGGTATGACAGGTGCTCCAATGACTGCAACTCTCGTCTCAGAG	1200
Db	1141	TTTGGTCACGGTCATCTCGGTATGACAGGTGCTCCAATGACTGCAACTCTCGTCTCAGAG	1200
QY	1201	CTCCTCGCAGGCGAAAGACCTCAATCGACATTTTCGCCCTTCGCACCAACCCGCTTGGT	1260
Db	1201	CTCCTCGCAGGCGAAAGACCTCAATCGACATTTTCGCCCTTCGCACCAACCCGCTTGGT	1260



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Db 1 ATGGCTGAGAACACAAAAAGTAGGCATCGCTGGAGCCGGAATCGTGGCGGTATGCACG 60  
QY 61 GCTTTGATGCTTCAACCTCGCTGGATTCAAAAGTCACCTTTGATTGACCCGGAACCCCTCTCTGGC 120  
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Db 61 GCCTGATGCTTCAGCGCCGCGGATTCAAAAGTCACCTTTGATTGACCCGGAACCCCTCTCTGGC 120  
QY 121 GAAGGTGCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGCTGCTCCCTATGTCC 180  
Db 121 GAAGGTGCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGCTGCTCCCTATGTCC 180  
QY 181 ATCGCGGGAACCTGAGAGCGCTGCGCAAGTGCCTCTTGACCCGATGGGCGCGTGTCTCA 240  
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Db 181 ATCGCGGGAACCTGAGAGCGCTGCGCAAGTGCCTCTTGACCCGATGGGCGCGTGTGTCA 240  
QY 241 ATCCGGTTACGCTATTTTCCAAACCATCATGCCCTGGTTGATTGCTTTCTGTTAGCCGGA 300  
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Db 241 ATCCGGTTACGCTATTTTCCAAACCATCATGCCCTGGTTGATTGCTTTCTGTTAGCCGGA 300  
QY 301 AGACCAAAACGAGTGAAGGAGCAGGCGAAAGCACTCCGCAAGACCCGCGAGGTTGGGAACCTG 360  
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Db 301 AGACCAAAACGAGTGAAGGAGCAGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360  
QY 361 CCTCTGATCAAGTCATTTGGCGGAGGAGGCTGATGCCAGCCATCTGATCCGCCATGAAGT 420  
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Db 361 CCTCTGATCAAGTCATTTGGCGGAGGAGGCTGATGCCAGCCATCTGATCCGCCATGAAGT 420  
QY 421 CATCTGACCCGTATATCGTGAGAGCAGACCTTCCCAAGGACCCGCGAGGTTGGGAACCTG 480  
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Db 421 CATCTGACCCGTATATCGTGAGAGCAGACCTTCCCAAGGACCCGCGAGGTTGGGAACCTG 480  
QY 481 CGGCGTCTCAACGGTGTTCGCACGACATCCTCTCTGCTGATGCTTTGGCTGATTTTCGAT 540  
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Db 481 CGGCGTCTCAACGGTGTTCGCACGACATCCTCTCAGCGCCGATCGCTTGGCGGATTTTCGAT 540  
QY 541 CTTAACTTGTGCGATGCTTTTACCAAGGCGATTTTATAGAGAGACGCTCACAGATT 600  
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Db 541 CCGAATCTGTCGATCGCTTTACCAAGGCGATTTTATAGAGAGACGCTCACAGATT 600  
QY 601 AATCCGCAAGGCGTCTGACCCCTTTGTTTCGGCGTTTATCCGCAACGCTGGCGAATTT 660  
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Db 601 AATCCGCAAGGCGTCTGACCCCTTTGTTTCGGCGTTTATCCGCAACGCTGGCGAATTT 660  
QY 661 GTATCTGCGGCTGTATCAGGCTTTGAGACTGAAGGTGCTCTCAAGAGCATTACAACC 720  
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Db 661 GTATCTGCGGCTGTATCAGGCTTTGAGACTGAAGGTGCTCTCAAGAGCATTACAACC 720  
QY 721 ACTAAGGCTGCTTGGCTGTTGATGACGCTGTTGTTGCAGCTGGTGCACACTCTAATCA 780  
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Db 721 ACTAAGGCTGCTTGGCTGTTGATGACGCTGTTGTTGCAGCTGGTGCACACTCTAATCA 780  
QY 781 CTTTGTCTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGCCTGGATATCATATCGTC 840  
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Db 781 CTTTGTCTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGCCTGGATATCATATCGTC 840  
QY 841 ATCGGAATCCCGAAGCCGCTCCACGATTCGCAAGCAGCAGTGCCTCAGGAAAATTCATC 900  
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Db 841 ATCGGAATCCCGAAGCCGCTCCACGATTCGCAAGCAGCAGTGCCTCAGGAAAATTCATC 900  
QY 901 GCGACACCTATGGAATGGGCTCTCGTGTGCTGGTACTGTTGAGTTTCTGCTCTCACA 960  
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QY 961 GCTGCTCTAATTCGGAAGCTGCGCATGTCTCTATACGACACGCTCGAAAATTCCTTCCA 1020  
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Db 1021 GCGCTCGGCTGCGAGTTCTGAAGAACGATATTCGCAATGGATGGGTTTTCGCGCGGAGC 1080  
QY 1081 ATTCTCTGATTTCTTCCAGTGATGCTCGTGCACACTCTGACCCGACCTAATCTATGCT 1140  
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Db 1081 ATCCCGGATTGCTCCCGGTGATTGGCGGGCAACCCGGGACACCCGACGTAATCTATGCT 1140  
QY 1141 TTTGGTCCACGCTCATCTCGGTATGACAGGTGCTTCCAAATGACTGCAACTCTCGTCTCAGAG 1200  
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Db 1141 TTTGGTCCACGCTCATCTCGGTATGACAGGTGCTTCCAAATGACTGCAACTCTCGTCTCAGAG 1200  
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Db 1201 CTCTCTCGAGGCGAAAGACCTCAATGCGACATTTGCGCCCTTCGCAACAAACCGCTTTGGT 1260  
QY 1261 ATTGGCAAAATCCAAGCAAAACCGGTTCGGCAAGTTAA 1296  
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Db 1261 ATTGGCAAAATCCAAGCAAAACCGGTTCGGCAAGTTAA 1296  
RESULT 4  
LOCUS I15326 115326 1296 bp DNA PAT 02-APR-1996  
DEFINITION Sequence 6 from patent US 5463175.  
ACCESSION I15326  
VERSION I15326.1 GI:1250234  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1296)  
AUTHORS Barry,G.F. and Kishore,G.M.  
TITLE Glyphosate tolerant plants  
JOURNAL Patent: US 5463175-A 6 31-OCT-1995;  
FEATURES Location/Qualifiers  
source  
1..1296  
BASE COUNT 286 a 368 c 361 g 281 t  
ORIGIN  
Query Match 92.7%; Score 1201.6; DB 5; Length 1296;  
Best Local Similarity 95.4%; Pred. No. 0;  
Matches 1237; Conservative 0; Mismatches 59; Indels 0; Gaps 0;  
QY 1 ATGGCTGAGAACACAAAAAGTAGGCATCGCTGGAGCTGGGAATCGTTGGTGTATGCAC 60  
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Db 1 ATGGCTGAGAACACAAAAAGTAGGCATCGCTGGAGCGCGGAATCGTGGCGGTATGCACG 60  
QY 61 GCTTTGATGCTTCAACGCTCGTGATTCAAAGTCACCTTTGATTGACCCGGAACCCCTCTCTGGC 120  
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Db 61 GCCTGATGCTTCAGCGCCGCGGATTCAAAGTCACCTTTGATTGACCCGGAACCCCTCTCTGGC 120  
QY 121 GAAGGTGCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGCTGCTCCCTATGTCC 180  
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Db 121 GAAGGTGCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGCTGCTCCCTATGTCC 180  
QY 181 ATCGCGGGAACCTGAGAGCGCTGCGCAAGTGCCTCTTGACCCGATGGGCGCGTGTCTCA 240  
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Db 181 ATCGCGGGAACCTGAGAGCGCTGCGCAAGTGCCTCTTGACCCGATGGGCGCGTGTGTCA 240  
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QY 301 AGACCAAAACGAGTGAAGGAGCAGGCGAAAGCACTCCGCAAGACCCGCGAGGTTGGGAACCTG 360  
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Db 301 AGACCAAAACGAGTGAAGGAGCAGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360  
QY 361 CCTCTGATCAAGTCATTTGGCGGAGGAGGCTGATGCCAGCCATCTGATCCGCCATGAAGT 420  
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Db 361 CCTCTGATCAAGTCATTTGGCGGAGGAGGCTGATGCCAGCCATCTGATCCGCCATGAAGT 420  
QY 421 CATCTGACCCGTATATCGTGAGAGCAGACCTTCCCAAGGACCCGCGAGGTTGGGAACCTG 480  
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Db 421 CATCTGACCCGTATATCGTGAGAGCAGACCTTCCCAAGGACCCGCGAGGTTGGGAACCTG 480  
QY 481 CGGCGTCTCAACGGTGTTCGCACGACATCCTCTCTGCTGATGCTTTGGCTGATTTTCGAT 540

Db 481 CGGGCTCTCAACGGTGTTCGCACACGATCCTCAGCCCGCATGCGTTTCGGGATTTCCGAT 540  
Qy 541 CCTAACTTTGTCGCATGCTTTTACCAGGGCATCTTATAGAGAGAACGGTTCACACGATT 600  
Db 541 CCGAACTTGTGCGATGCGTTTACCAGGGCATCTTATAGAGAGAACGGTTCACACGATT 600  
Qy 601 AATCCGAAGGGCTCGTGACCCCTCTTGTTCGGCGTTTATTCGCGAAGTTCGCGAATT 660  
Db 601 AATCCGAAGGGCTCGTGACCCCTCTTGTTCGGCGTTTATTCGCGAAGTTCGCGAATT 660  
Qy 661 GTATCTCGCGCTGTCATCGGTTTTCAGACTCAAGGTGCTCTCAAGAGCATTTACAAACC 720  
Db 661 GTATCTCGCGCTGTCATCGGTTTTCAGACTCAAGGTGAGGCTAGGCGCTTTAAAGGCATTTACAAACC 720  
Qy 721 ACTAACGGTGTTCGGCTGTGATGCGAGCTGTGTCAGCTGGTGCACACTCTAAATCA 780  
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Qy 781 CTTGCTTAATTCGCTTAGCGGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC 840  
Db 781 CTTGCTTAATTCGCTTAGCGGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC 840  
Qy 841 ATCCGGAATCCGGAAGCGCTCCACGCATTCGCGACGCCGATCGTTCAGGAAATTCATC 900  
Db 841 ATCCGGAATCCGGAAGCGCTCCACGCATTCGCGACGCCGATCGTTCAGGAAATTCATC 900  
Qy 901 CGGACACTATGGAATGGGTCTTCTGTTGCTGCTACTGTTGAGTTTGTGCTCTCACA 960  
Db 901 CGGACACTATGGAATGGGTCTTCTGTTGCTGCTACTGTTGAGTTTGTGCTCTCACA 960  
Qy 961 GCTGCTCTTAAGTGGAAAGCTGCGCATGTGCTCTATACGACAGCTCGAAGAACTTCTTCCA 1020  
Db 961 GCGCTCTTAAGTGGAAAGCTGCGCATGTGCTCTATACGACAGCTCGAAGAACTTCTTCCA 1020  
Qy 1021 GCGCTCGCGCTCGAGTCTGAGAAAGCATATTCCAAATGGATGGGTTCGTTCTCTAGC 1080  
Db 1021 GCGCTCGCGCTCGAGTCTGAGAAAGCATATTCCAAATGGATGGGTTCGTTCTCTAGC 1080  
Qy 1081 ATTCCTGATCTCTTCCAGTGATTTGGTGTGCAACTCGTACACCCGAGCGTAATCTATGCT 1140  
Db 1081 ATCCCGGATTCGCTCCCGCTGATTTGGCGGCAACCCGACACCCGAGCTAATCTATGCT 1140  
Qy 1141 TTTGGTCAGGTCATCTCGGTATGACAGTGCTCTCAATGAGCTGCAACTCTGCTCTCAGAG 1200  
Db 1141 TTTGGTCAGGTCATCTCGGTATGACAGTGCTCTCAATGAGCTGCAACTCTGCTCTCAGAG 1200  
Qy 1201 CTCTTCGAGCGGAAAGACCTCAATCGACATTTTCGCCCTTCGACCAAAACCGCTTTGGT 1260  
Db 1201 CTCTTCGAGCGGAAAGACCTCAATCGACATTTTCGCCCTTCGACCAAAACCGCTTTGGT 1260  
Qy 1261 ATTCGAAATCCAAAGCAACGGTTCGGCAAGTTAA 1296  
Db 1261 ATTCGAAATCCAAAGCAACGGTTCGGCAAGTTAA 1296

RESULT 5

AR016591  
LOCUS AR016591 1692 bp DNA PAT 05-DEC-1998  
DEFINITION Sequence 3 from patent US 5776760.  
ACCESSION AR016591  
VERSION AR016591.1 GI:3972868  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1692)  
AUTHORS Barry.G.Francis and Kishore,G.Murthy.  
TITLE Glyphosate tolerant plants  
JOURNAL Patent: us 5776760-A 3 07-JUL-1998;  
FEATURES Location/Qualifiers  
source 1..1692  
/organism="unknown"

BASE COUNT 381 a 480 c 469 g 361 t 1 others  
ORIGIN  
Query Match 92.38; Score 1196.8; DB 5; Length 1692;  
Best Local Similarity 95.2%; Pred. NO. 0;  
Matches 1234; Conservative 0; Mismatches 62; Indels 0; Gaps 0;  
Qy 1 ATGCTGAGAACACAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCACT 60  
Db 120 ATGCTGAGAACACAAAAAGTAGGCATCGCTGGAGCCGAATCGTCGGCGTATGCAG 179  
Qy 61 GCTTTGATGCTTCAACGTGCTGGATTCAAAAGTCACCTTGAATTGACCCGAACCCCTCTGCG 120  
Db 180 GCGCTGATGCTTCAAGCGCGGATTCAAAGTCACCTTGAATTGACCCGAACCCCTCTGCG 239  
Qy 121 GAAGGTGCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCGCTGCTCCCTATGTCC 180  
Db 240 GAAGGTGCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCGCTGCTCCCTATGTCC 299  
Qy 181 ATGCGCGGAAACTTTGACGAGCGTCCGAAAGTGGCTCTTGACCCGATGGGCGCTTGTCA 240  
Db 300 ATGCGCGGAAACTTTGACGAGCGTCCGAAAGTGGCTCTTGACCCGATGGGCGCTTGTCA 359  
Qy 241 ATCGCGTTTCAAGCTATTTTCAACCATCATGCCCTGGTGTGAATTTCGCTTTCGTTAGCCGGA 300  
Db 360 ATCGCGTTTCAAGCTATTTTCAACCATCATGCCCTGGTGTGAATTTCGCTTTCGTTAGCCGGA 419  
Qy 301 AGACCAACAGGTGAAGGAGCAGCGGAAAGCACTCCGCAATCTCANTCAAGTCCACGGTG 360  
Db 420 AGACCAACAGGTGAAGGAGCAGCGGAAAGCACTCCGCAATCTCANTCAAGTCCACGGTG 479  
Qy 361 CCTCTGATCAAGTCATTTGGCGAGGAGCTGATCGAGCCCATCTGATCCGCCATGAAGGT 420  
Db 480 CCTCTGATCAAGTCATTTGGCGAGGAGCTGATCGAGCCCATCTGATCCGCCATGAAGGT 539  
Qy 421 CATCTGACCGTATATCTGTTGAGAGACAGACTTCGCCAAGAGCAGCGGAGTTGGGAAGT 480  
Db 540 CATCTGACCGTATATCTGTTGAGAGAGAGACTTCGCCAAGAGCAGCGGAGTTGGGAAGT 599  
Qy 481 CGGCGTCTCAACGGTGTTCGCACGCAGATCCTCTCTGCTGATGCTTTTCGCTGATTTCCGAT 540  
Db 600 CGGCGTCTCAACGGTGTTCGCACGCAGATCCTCTAGCCCGGATGCGTTTCGCGGATTTCCGAT 659  
Qy 541 CCTAACTTGTGCGATGCTTTTACCAAGGGCATCTTATAGAGAGAGACGGTTCACACGATT 600  
Db 660 CCGAACTTGTGCGATGCTTTTACCAAGGGCATCTTATAGAGAGAGACGGTTCACACGATT 719  
Qy 601 AATCCGAAGGGCTCGTGACCCCTCTTGTTCGGCGTTTATTCGCGAAGCGTGGCGAATTT 660  
Db 720 AATCCGAAGGGCTCGTGACCCCTCTTGTTCGGCGTTTATTCGCGAAGCGTGGCGAATTT 779  
Qy 661 GTATCTCGCGCTGTCATCGGTTTTCAGACTCAAGGTGCTGCTCTCAAGAGCATTTACAAACC 720  
Db 780 GTATCTCGCGCTGTCATCGGCTTTGAGACTGAAGGTAGGCGCTTTAAAGGCATTTACAAACC 839  
Qy 721 ACTAACGGTGTTCGGCTGTGATGCGAGCTGTGTTGAGCTGGTTCACACTCTAAATCA 780  
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Qy 781 CTTGCTTAATTCGCTTAGCGGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC 840  
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Qy 841 ATCCGGAATCCGGAAGCGCTCCACGCATTCGCGACGCCGATCGCTCAGGAAATTCATC 900  
Db 960 ATCCGGAATCCGGAAGCGCTCCACGCATTCGCGACGCCGATCGCTCAGGAAATTCATC 1019  
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Db 1020 GCGACACCTATGGAATGGGTCTTCTGCTGTGCTGGGTGAGTTGAGTTTCGCTGGGTCTACA 1079  
Qy 961 GCTGCTCTTAAGTGGAAACGTCGCAATGCTGCTATACGCGACGCTCGAAGAACTTCTTCCA 1020

Db	1080	GC	CGCTCCCTTA	CTGGAACGTCGCGATGTGCTCTATACGCACGCTCGAAAACTCTTCTCCA	1139
QY	1021	GC	CTTCGCGCCTCCG	AGTTTCTTGAAGAAGCATATTTCCAAATGGATGGTGGTTCGTCTTAGC	1080
Db	1140	GC	CTTCGCGCCTCGG	AGTTTCTTGAAGAAGCATATTTCCAAATGGATGGTGGTTCGCGCGCAGC	1199
QY	1081	ATT	CTCGATTTCTTCTC	CAAGTGAATGGTCGTCGAACCTCGTACACCCGACGTAATCTATGCT	1140
Db	1200	AT	CCCGGATTCGCTCC	CGCGTGAATGGCGGGCAACCCGACACCCGACGTAATCTATGCT	1259
QY	1141	TTT	TGTCACGTCATCT	CGGTATGACAGGTGCTCCAATGACTCGCACTCTGCTCTCAGAG	1200
Db	1260	TT	CGGCCATTGGTCAT	CTCGGCATGACAGGGCGCGGATGACCGCAACGCTCGTCTCAGAG	1319
QY	1201	CT	CCTCCGAGGCGAAA	AGACCTCAATCGACATTTTCGCCCTTCGCACCAAAACCGCTTTGGT	1260
Db	1320	CT	CCTCGCAGGCGAAA	AGACCTCAATCGACATTTTCGCCCTTCGCACCAAAACCGCTTTGGT	1379
QY	1261	ATT	GGCAAAATCCAA	GCAACGGGTCCGGCAAGTTAA	1296
Db	1380	ATT	GGCAAAATCCAA	GCAACGGGTCCGGCAAGTTAA	1415
RESULT 6					
LOCUS	AR016592	1293 bp	DNA	PAT	05-DEC-1998
DEFINITION	Sequence 4 from patent US 5776760.				
ACCESSION	AR016592				
VERSION	AR016592.1 GI:3972869				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 1293)				
AUTHORS	Barry, G. Francis and Kishore, G. Murthy.				
TITLE	Glyphosate tolerant plants				
JOURNAL	Patent: US 5776760-A 4 07-JUL-1998;				
FEATURES	Location/Qualifiers				
source	1..1293				
BASE COUNT	286 a	367 c	359 g	281 t	
ORIGIN					
Query Match 89.6%; Score 1160.8; DB 5; Length 1293;					
Best Local Similarity 95.0%; Pred. No. 0;					
Matches 1231; Conservative 0; Mismatches 62; Indels 3; Gaps 3;					
QY	1	AT	GGCTGAGAACCA	CAAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCAC	60
Db	1	AT	CTCTGAGAACCA	CAAAAAAGTAGGCATCGCTGGAGCGGAATCGTGGCGGTATGCACG	60
QY	61	GC	TTTGTATCTTCA	ACGTCGTGTGATTCAAAGTCACCTTGATTCACCGCAACCTCTCTGGC	120
Db	61	GC	CTGTATCTTCA	ACGTCGTGTGATTCAAAGTCACCTTGATTCACCGCAACCTCTCTGGC	120
QY	121	GA	AGTGCATCGTTT	GGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC	180
Db	121	GA	AGTGCATCGTTT	GGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC	180
QY	181	AT	GCCGGGAAACTT	GACGAGCGTGCCGAAGTGCGTCTTTGACCCGATGGGCGGTTGTCA	240
Db	181	AT	GCCGGGAAACTT	GACGAGCGTGCCGAAGTGCGTCTTTGACCCGATGGGCGGTTGTCA	239
QY	241	AT	CCGGTTCAGCTA	TTTTCCTCAACCATCATGCCCTGGTTGATTCGCTTTCTGTTAGCCGA	300
Db	240	AT	CCGGTTCAGCTA	-TTTTCCTCAACCATCATG-CCTGGTTGATTCGCTTTCTGTTAGCCGA	297
QY	301	AG	ACCAAAACAA	AGGTGAAGGAGCAGGCAAGCACTCCGCAATCTCATCAAGTCCACGGTG	360
Db	298	AG	ACCAAAACAA	AGGTGAAGGAGCAGGCAAGCACTCCGCAATCTCATCAAGTCCACGGTG	357

Qy	361	CTCTTGATCAAGTCATTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT	420	
Db	358	CTCTTGATCAAGTCATTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT	417	
Qy	421	CATCTGACCGCTATATCGTGGAGAGCAGACTTTCGCCAAGAGCAGCGGAGGTTGGGAACGTG	480	
Db	418	CATCTGACCGCTATATCGTGGAGAGCAGACTTTCGCCAAGAGCAGCGGAGGTTGGGAACGTG	477	
Qy	481	CGGCGTCTCAACCGGTGTTCCACGCCAGATCTCTCTCTGCTGATGCTTTTGGCTGATTTCCGAT	540	
Db	478	CGGCGTCTCAACCGGTGTTCCACGCCAGATCTCTCTCTGCTGATGCTTTTGGCTGATTTCCGAT	537	
Qy	541	CCTAACTTGTGCGATGCTTTTACCAAGGCACTTCTTATAGAAGAGAACGGTTCACACGATT	600	
Db	538	CCGAACCTGTGCGATGCGTTTACCAAGGCACTTCTTATAGAAGAGAACGGTTCACACGATT	597	
Qy	601	AATCCGCAAGGCGTCTGTGACCCCTCTTGTTCGGCGTTTTTATCCGGAACGGTGGCGAATTT	660	
Db	598	AATCCGCAAGGCGTCTGTGACCCCTCTTGTTCGGCGTTTTTATCCGGAACGGTGGCGAATTT	657	
Qy	661	GTATCTCGCGGTGCTCATCGGTTTTGAGACTGAAGGTGCTGCTCTCAAGAGCATTTACAACC	720	
Db	658	GTATCTCGCGGTGCTCATCGGTTTTGAGACTGAAGGTGAGGGCGCTTTAAGAGCATTTACAACC	717	
Qy	721	ACTAACGCGTGTCTTGGCTGTGATGACAGCTGTTGTTGACAGCTGGTGCACACTCTAAATCA	780	
Db	718	ACGAACGCGTGTCTTGGCGGTTGATGACAGCGTTGTTCGACGCGCGCGCACACTCGAAATCA	777	
Qy	781	CTTTGCTTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAACGTTGGATATCATATCGTC	840	
Db	778	CTTTGCTTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAACGTTGGATATCATATCGTC	837	
Qy	841	ATCCGCAATCCGGAAGCGCTCCACGCACTTCGACGACCGGATGCGCTCAGGAAATTTTCATC	900	
Db	838	ATCCGCAATCCGGAAGCGCTCCACGCACTTCGACGACCGGATGCGCTCAGGAAATTTTCATC	897	
Qy	901	GCACACCTATGGAATGGGCTTTCGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCT	960	
Db	898	GCACACCTATGGAATGGGCTTTCGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCT	957	
Qy	961	GCTGCTCTTAACCTGGAACGCTGGCGCATGCTCTATACCGACGCTCGAATACTTCTTCCA	1020	
Db	958	GCGGCTCTTAACCTGGAACGCTGGCGCATGCTCTATACCGACGCTCGAATACTTCTTCCA	1017	
Qy	1021	GCCTTCGCGCTCGGATCTGGAAGAACCATATTCCAAATGGATGGGTTTTTCGCTCTTAGC	1080	
Db	1018	GCCTTCGCGCTCGGATCTGGAAGAACCATATTCCAAATGGATGGGTTTTTCGCGCCGAGC	1077	
Qy	1081	ATTCTCGATTCTCTTCCAGTGTATGCTGCTGCAACTCGTACACCCGACGTAATCTATGCT	1140	
Db	1078	ATCCGGATTTTCGCTTCCCGGTGATTGGCCGGCAACCCGGACACCCGACGTAATCTATGCT	1137	
Qy	1141	TTTGGTTCACGGTCTATCTCGGTATGACAGGTGCTCCAAATGACTGCAACTCTCGTCTCAGAG	1200	
Db	1138	TTTGGGCGATGGTCTATCTCGGCATGACAGGGGCGCGATGACCGCAACCTCGTCTCAGAG	1197	
Qy	1201	CTCCTTCGACGCGCAAAAGACCTCAATCGACATTTTCGCGCTTCGCACCAACCCGCTTTGGT	1260	
Db	1198	CTCCTTCGACGCGCAAAAGACCTCAATCGACATTTTCGCGCTTCGCACCAACCCGCTTTGGT	1257	
Qy	1261	ATTGGCAAAATCCAAAGCAACGGGTCCGGCAAGTTAA	1296	
Db	1258	ATTGGCAAAATCCAAAGCAACGGGTCCGGCAAGTTAA	1293	
RESULT	7			
LOCUS	I15325	1293 bp	DNA	PAT 02-APR-1996
DEFINITION	Sequence 4 from patent US 5463175.			
ACCESSION	I15325			
VERSION	I15325.1 GI:1250233			
KEYWORDS	Unknown.			
SOURCE				

[illegible]

QY 241 ATCCGGTTCAGCTATTTTCCAAACCATCATCCCTGGTGTGATTCGCTTTCGTAGCCGGA 300  
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Db 359 ATCCGGTTCAGCTA-TTTTCCAAACCATCATG-CCTGGTGTGATTCGCTTTCGTAGCCGGA 416  
QY 301 AGACCAACAAGGTGAAGGAGCAGCGGAAGAGCACTCCGCAATCTCATCAAGTCCACGGTG 360  
Db 417 AGACCAACAAGGTGAAGGAGCAGCGGAAGAGCACTCCGCAATCTCATCAAGTCCACGGTG 476  
QY 361 CCTCTGATCAAGTCATTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT 420  
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Db 477 CCTCTGATCAAGTCATTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT 536  
QY 421 CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAGACCCGCGAGGTGGGAAGTG 480  
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Db 537 CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAGACCCGCGAGGTGGGAAGTG 596  
QY 481 CGCGCTCAACGGTGTTCGACGCGCAGATCCTCTCTGCTGATGCTTTGGCTGATTTCCGAT 540  
Db 597 CGCGCTCAACGGTGTTCGACGCGCAGATCCTCTAGCGCCGATCGCTTGGCGGATTTCCGAT 656  
QY 541 CCTAACTGTGCGATGCTTTTACCAGGGCATCTTATAGAAGAGAACGGTTCACACGATT 600  
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Db 657 CCGAACTGTTCGATGCGTTCCTTACCAGGGCATCTTATAGAAGAGAACGGTTCACACGATT 716  
QY 601 AATCCGCAAGGGTCTGTGACCCCTCTTTTTCGGCGTTTATCCGGAACGGTGGCGAAATTT 660  
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Db 717 AATCCGCAAGGGTCTGTGACCCCTCTTTTTCGGCGTTTATCCGGAACGGTGGCGAAATTC 776  
QY 661 GTATCTCGCGGTGTATCGGTGTTGAGACGTGAAGTGGTCTCTCAAGAGCATTTACAACC 720  
Db 777 GTATCTCGCGGTGTATCGGTGTTGAGACGTGAAGTGGTCTCTCAAGAGCATTTACAACC 836  
QY 721 ACTAAACGGTCTCTGGCGTGTGATGAGCTGTTGTTGTCAGCTGTGCACACTCTAAATCA 780  
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Db 837 ACCAAGCGGCTTCTGGCGTGTGATGACGCGTGTGTCGACCCGCGGCACACTCGAAATCA 896  
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QY 841 ATCCGGAATCCGGAAGCGCTCCACCATTTCCGACGACCGATCGGTCAAGAAAATTCATC 900  
Db 957 ATCCGGAATCCGGAAGCGCTCCACCATTTCCGACGACCGATCGGTCAAGAAAATTCATC 1016  
QY 901 GCGACACACTATGGAATGGGTCTTCGTGTGCTGCTACTGTTGAGTTTGTGCTCTCACCA 960  
Db 1017 GCGACACACTATGGAATGGGTCTTCGCTGCGGGTACGGTTGAGTTCTGCTGGGCTCACCA 1076  
QY 961 GCTGCTCCTAACTGGAAACGTGGCGATGTGCTCTATACGACGCTCGAAAACCTCTTTCCA 1020  
Db 1077 GCGGCTCCTAACTGGAAACGTGGCGATGTGCTCTATACGACGCTCGAAAACCTCTTTCCA 1136  
QY 1021 GCGCTCGCGCTCGGAGTCTGAAGAAGCATATTCAAAATGGATGGTTCGTCCTTAGC 1080  
Db 1137 GCGCTCGCGCTCGGAGTCTGAAGAAGCATATTCAAAATGGATGGTTCGCGCGCGAGC 1196  
QY 1081 ATTCCTGATTCTCTCCAGTGTATGGTCGTCGCAACTCGTACACCCGACGTAATCTATGCT 1140  
Db 1197 ATCCCGGATTCGCTCCCGCTGATTTGGCCGGCAACCCGGACACCCGACGTAATCTATGCT 1256  
QY 1141 TTTTGGTACAGGTCACTTCGGTATGACAGGTGCTTCCAAATGACTGCAACTCTCTGCTCAGAG 1200  
Db 1257 TTCGGCATGGTTCATCTCGGCAATGACAGGGCGCGCATGACCCGAACGCTCGTCTCAGAG 1316  
QY 1201 CTCCTCGCAGGCGCAAGACCTCAATCGACATTTTCGCCCTTCGCCACCAACCGCTTTGGT 1260  
Db 1317 CTCCTCGCAGGCGCAAGACCTCAATCGACATTTTCGCCCTTCGCCACCAACCGCTTTGGT 1376  
QY 1261 ATTTGGAAAATCCAAAGCAACGGGTCCGGCAAGTTAA 1296  
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Db 1377 ATTTGGAAAATCCAAAGCAACGGGTCCGGCAAGTTAA 1412

RESULT 9  
AR016595  
LOCUS AR016595 1296 bp DNA PAT 05-DEC-1998  
DEFINITION Sequence 8 from patent US 5776760.  
ACCESSION AR016595  
VERSION AR016595.1 GI:3972872  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 1296)  
AUTHORS Barry,G.Francis and Kishore,G.Murthy.  
TITLE Glyphosate tolerant plants  
JOURNAL Patent: US 5776760-A 8 07-JUL-1998;  
FEATURES Location/Qualifiers  
source 1..1296  
/organism="unknown"  
BASE COUNT 271 a 359 c 305 g 361 t  
ORIGIN  
  
Query Match 78.0%; Score 1011.2; DB 5; Length 1296;  
Best Local Similarity 86.3%; Pred. No. 2.8e-277;  
Matches 1118; Conservative 0; Mismatches 178; Indels 0; Gaps 0;  
  
QY 1 ATGGCTCAGAACCAACAAAAGTAGCATCGCTGGAGCTGGAATCGTTGGTGTATGCACT 60  
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Db 1 ATGGCTCAGAACCAACACAGAAGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTATGCACT 60  
QY 61 GCTTTGATGCTTCAACGCTCGTGGATTCAAAAGTCAACCTTTGATTGACCGAAGCCCTTCCTGGC 120  
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Db 61 GCTTTGATGCTTCAACGCTCGTGGATTCAAGGTTACCTTTGATTGATCCAAACCCACCAAGT 120  
QY 121 GAAGGTGCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC 180  
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Db 121 GAAGGTGCTTCTTCGGTAAACGGTGGTTGCTTCAACGGTTCTCCGTTGTTCCTCAATGTCC 180  
QY 181 ATCCCGGAAACTTGACGAGCGTCCGAAGTGGCTCTTGACCGGATGGGGCCCTTTGTCA 240  
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Db 181 ATCCAGGAAACTTGACTAGCGTTCACAAAGTGGCTTCTTGACCCAAATGGGTTCATTTGCC 240  
QY 241 ATCCGGTTCAGCTATTTTCCAAACCATCATGCCCTGGTGTGATTCGCTTTCTGTTAGCCGGA 300  
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Db 241 ATCCGTTTCAAGTACTTTCCAAACCATCATGCCCTGGTGTGATTCGCTTTCTGCTTGTCTGGA 300  
QY 301 AGACCAACAAGGTGAAGGAGCAGCGCAAGAGCACTCCGCAATCTCATCAAGTCCACCGTG 360  
Db 301 AGACCAACAAGGTGAAGGAGCAGCGTAAAGCAAGCTAAGGCATCCGTAACCTCATCAAGTCCAC 360  
QY 361 CCTCTGATCAAGTCATTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT 420  
Db 361 CCTTTGATCAAGTCCCTTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGT 420  
QY 421 CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAGGACCCGCGAGGTGGGAAGTG 480  
Db 421 CACCTTACCGCTGATACCGTGGAGAAGCAGACTTCGCCAAGGACCCGCGAGGTGGGAAGT 480  
QY 481 CGCGCTCAACGGTGTTCGCACGCGATCCTCTCTGCTGATGCTTTTCGCTGATTTTCGAT 540  
Db 481 CGTGGTCTCAACGGTGTTCGTAAGTCTCAAACTCTCAGCGCTGATGCAATTCGCTGATTTTCGAT 540  
QY 541 CCTAACTGTTCGATGCTTTTACCAGGGCATCTTATAGAAGAGAACGGTTCACACGATT 600  
Db 541 CCTAACTGTCTCAGCGCTTTACCAGGGATCCTTATCGAAGAGAACGGTTCACACGATC 600  
QY 601 AATCCGCAAGGGTCTGTGACCCCTCTTTTTCGGCGTTTATCCGGAAGCGGTGGCGAAATTT 660  
Db 601 AACCCCAAGGCTCTGCTGACTCTCTTCTGCTGCTTTCATCGCTAACCGTGGAGAGTTC 660  
QY 661 GTATCTCGCGGTGTATCGGTGTTGAGACGTGAAGTGGTCTCTCAAGAGCATTTACAACC 720  
Db 661 GTGTCTGCTCGTGTATTCGGATTCGAGACTCGAAGGTGCTGCTCTCAAGGGGTATACCAACC 720





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QY 1201 CTCTCCAGCGGAAAGACCTCAATCGACATTTGCGCCCTTCGCACCAAAACCGCTTTGGT 1260
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Db 1201 CTCTCCAGGTGAGAGACCTCTATCGACATCTCTCCATTCGCACCAAAACCGCTTCGGT 1260

QY 1261 ATTGGCAAAATCCAAAGCAAAACGGTCCGGCAAGTTAA 1296
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Db 1261 ATTGGTAAGTCCAAAGCAAAACTGGTCCGATCCTAA 1296

RESULT 11
AR016604
LOCUS AR016604 1296 bp DNA PAT 05-DEC-1998
DEFINITION Sequence 17 from patent US 5776760.
ACCESSION AR016604
VERSION AR016604.1 GI:3972881
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1296)
AUTHORS Barry,G.Francis and Kishore,G.Murthy.
TITLE Glyphosate tolerant plants.
JOURNAL Patent: US 5776760-A 17 07-JUL-1998;
FEATURES
source Location/Qualifiers
BASE COUNT 267 a 360 c 309 g 360 t
ORIGIN

Query Match 77.7%; Score 1006.4; DB 5; Length 1296;
Best Local Similarity 86.0%; Pred. No. 6.6e-276;
Matches 1115; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

QY 1 ATCGGTGAGAACCAACAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGCTGATGACAT 60
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Db 1 ATGGCTGAGAACCAACAAAGAGTGGTATCGCTCGAGCTGGAATCGTTGCTGATGACAT 60

QY 61 GCTTTGATGCTTCAACGTCGTGGATCAAAAGTCAACCTTGATTGACCCGAACCCCTCTCGG 120
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Db 61 GCTTTGATGCTTCAACGTCGTGGATCAAGTTACCTTGATTGATCCAAACCCACCAAGT 120

QY 121 GAAGGTGCATCGTTTGGGAATCCGGATGCTTCAACGGCTCATCCGTCGCTCATGTCC 180
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Db 121 GAAGGTGCCTCTTTTCGGTAACGCTGTTGCTTCAACGGTTCCTCCGTTGTTCCAATGTCC 180

QY 181 ATCCCGGAAACTTTGACGAGCTGCGGAAGTGGCTCGTTGACCCGATGGGCGCTTGTC 240
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Db 181 ATGCCAGGAAACTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCAAATGGGTCCATTTGTC 240

QY 241 ATCCGGTTTCAGCTATTTCACCAACATCATCCCTGCTGTTGATTGCTTCTGTTAGCGGA 300
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Db 241 ATCCGTTTCGGCTACTTTTCCAAACATCATCGCTTGGTTGATTGCTTCTGTTGCTTGGA 300

QY 301 AGACCAAAACAGGTGAAGGAGCAGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360
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Db 301 AGACCAAAACAGGTGAAGGAGCAAGCTAAGGCACCTCGTAACTCATCAAGTCCACTGTG 360

QY 361 CCTCTCATCAAGTCATTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGTT 420
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Db 361 CCTTTGATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGT 420

QY 421 CAPCTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAAGGACCGCGAGGTTGGGAACCTG 480
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QY 481 CGCGCTCTCAACGGTGTTCGACGAGATCCCTCTCTGCTGATGCTTTGGCTGATTTTCGAT 540
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Db 481 CGTCGCTCAACGGTGTTCGTAATACTCAATCCTCAGCGCTGATGATTCGATTTTCGAT 540

QY 541 CCTAACTTTGTCGATGCTTTTACCAAGGGCAATCTTTATAGAAGAACGGTTCACAGATT 600
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Db 541 CCTAACTTTGTCACGGCTTTTACCAAGGGAATCCTTATCGAAGAGAACGGTTCACACCATC 600
QY 601 AATCCGCAAGGGTCGTGACCCCTCTTGTTCGGGGTTTTTATCGCGAAGCGGTGGCGAATTT 660
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Db 601 AACCACAAGGTCTCGTGAATCTCTTGTTCGGTCTTTCATCGCTAACGGTGGAGAGTTC 660

QY 661 GTATCTCGCGGTGTATCATCGGTTTTGAGACTCAAGGTCGTCTCTCAAGGGGTATCACACC 720
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Db 661 GTGTCTGCTCGTGTATCATCGGATTTCGAGACTGAAGTCTGCTCTCAAGGGGTATCACACC 720

QY 721 ACTAACGGGTGTTCTGGCTGTTGATGAGCTGTTGTCAGCTGTGTCACACTCTAAATCA 780
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Db 721 ACCAACGGTGTCTGCTGTTGATGAGCTGTTGTCAGCTGTGTCACACTCTCAAGTCT 780

QY 781 CTTGCTAAATTCGGTATGAGATGACATCCGCTGATACCGAACGTGATATCATATCATC 840
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Db 781 CTTGCTAACTCCCTTGGTGTGATGACATCCCATTTGATACCGAACGTGATACCATCGTG 840

QY 841 ATCCGGAATCCGGAAGCCGCTCCACGCAATTCGACGACCCGATGCGTCAGGAAATTCATC 900
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Db 841 ATCGCCAACCCAGAAGCTGCTCCACGTAATTCCAACTACCGATGCTTCTGGAAGTTCATC 900

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QY 961 GCTGCTCCTAACTGGAACCGTGGCATGTCTATACGACGCTCGAAAACCTTCTTCCA 1020
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Db 961 GCTGCTCCTAACTGGAAGCGTGTCTACGTTCTCTACACTCGGCTCTGATAGTTGCTTCCA 1020

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Db 1021 GCTCTCGCTCTCTGCGAGTTCTGAAGAACGTTACTCCAAGTGGATGGGTTTTTCGCTCAAGC 1080

QY 1081 ATTCTCGATTTCTTCCAGTGTATGGTGGTGCATCTGTCACCCGACGTAATCTATGCT 1140
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QY 1201 CTCTCCAGCGGAAAAAGACCTCAATCGACATTTTCGCCCTTCGCCACCAAAACCGCTTTGGT 1260
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Db 1201 CTCTCCAGGTGAGAGACCTCTATCGACATCTCTCCATTCGCACCAAAACCGGTTTCGGT 1260

QY 1261 ATTGGCAAAATCCAAAGCAAAACGGTCCGGCAAGTTAA 1296
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Db 1261 ATTGGTAAGTCCAAAGCAAAACTGGTCCGATCCTAA 1296

RESULT 12
I15337
LOCUS I15337 1296 bp DNA PAT 02-APR-1996
DEFINITION Sequence 17 from patent US 5463175.
ACCESSION I15337
VERSION I15337.1 GI:1250245
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1296)
AUTHORS Barry,G.F. and Kishore,G.M.
TITLE Glyphosate tolerant plants.
JOURNAL Patent: US 5463175-A 17 31-OCT-1995;
FEATURES
source Location/Qualifiers
BASE COUNT 267 a 360 c 309 g 360 t
ORIGIN

Query Match 77.7%; Score 1006.4; DB 5; Length 1296;
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Db 634  CGGTAACTCATCAAGTCCACTGTGCTTTTGATCAAGTCTTGGCTGAGAGGCTGATGC 693
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Db 694  TAGCCACCTTATCCGTACCAAGGTCACTACCGTGTACCGTGGAGAACGACACTTCGC 753
QY 456  CAAGGACCCGGAGGTGGAACTGGCGCTCTCAAGCGTGTTCGACCGAGATCTCTTC 515
Db 754  CAAGGACCGTGGAGTGGAACTTCGTCTCTCAAGCGTGTTCGTAATACTCAATCTCTCAG 813
QY 516  TCGTGATGCTTTTCGGTCATTTCCATCCTTAACCTTGTCCGATGCTTTTACCAAGGCACTTC 575
Db 814  CGCTGATGCAATTGCGTGATTTCCATCCTTAACCTTGTCTCAGCGCTTTTACCAAGGAAATCCT 873
QY 576  TATAGAAGAGAAGCGGTACACAGATTAATCGCAAGGCGTGTGACCCCTCTGTTTTCGGCG 635
Db 874  TATCGAAGAGAAGCGGTACACACATCAACCCCAAGGTCTCTGACACTCTGTTCGTCG 933
QY 636  TTTTATCGCGAAGCGGTGGCGAATTTGTATCTGCGCGTGTTCATCGGTTCGAGACTGAAG 695
Db 934  TTTTCATCGCTTAACGGTGGAGATTCTGCTCTCGTCTGTTATCGGATTCGAGACTGAAG 993
QY 696  TCGTGCTCTCAAGGCAATACACCACTTAACCGTGTTCGCTGTTCGCTGTTCGCTGTTCGATG 745
Db 994  TCGTGCTCTCAAGGCAATACACCACTTAACCGTGTTCGCTGTTCGCTGTTCGATGCTTCCTA 1053
QY 746  -----CAGCTGTTGTTGTCAGCTGTTGTCAGCTGTTGTCAGCTGTTGTCAGCTGTTGTCAGCT 790
Db 1054  GTCAATTCAGCTTACTGTCAGTGTTCGACCTGTTGTCAGCTGTTGTCAGCTGTTGTCAGCT 1113
QY 791  CGGTAGCGATGACATCCCGCTCGATACCGAAGTGGATATCATATCATCGTATCCGCAATC 850
Db 1114  CCCTTGTGTATGATACATCCCATCCCATACCAAGCTGATACCACTGATGTCGCAAC 1173
QY 851  CGAAGCGCTCCACGATTCACCAAGCGTCCGTCAGGAAATTCATCGCGACACCTA 910
Db 1174  CAGAAGCTGCTCCACGATTCACCAAGCTCCGTCAGGAAATTCATCGCGTACTCCTA 1233
QY 911  TGGAAATGGGTCCTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 970
Db 1234  TGGAGATGGTCTTCGTGTTGCTGGAACCGTTCAGTTCGCTGCTGCTGCTGCTGCTGCTGCT 1293
QY 971  ACTGGAAGCGTGGCATGCTCTATACGACGCTCCAAACCTTCCTCCAGCCCTCCGCG 1030
Db 1294  ACTGGAAGCGTGGCATGCTCTATACGACGCTCCAAACCTTCCTCCAGCTCTCGCTC 1353
QY 1031  CTCGGAGTCTGAAGAAGCATATTCCAATGATGGGTTTTCGTCCTAGCATTCCTGATTT 1090
Db 1354  CTCGCCAGTTCTGAAGAAGCATATTCCAATGATGGGTTTTCGTCCTAGCATTCCTGATTT 1413
QY 1091  CTCCTCCAGTGATTTGCTGCTGCAACTCGTACACCCGACGCTTAATCTATGCTTTTGGTCACG 1150
Db 1414  CCCTTCAGTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1473
QY 1151  GTCATCTCGGTATGACAGGTGCTTCCAAATGACGCACTCTCGCTCAGAGCTCTCCGACG 1210
Db 1474  GTCATCTCGGTATGACAGGTGCTTCCAAATGACGCACTCTCGCTCAGAGCTCTCCGACG 1533
QY 1211  GCGAAAGACCTCAATTCGACATTTCCGCTTCGACCAACCGCTTTGGTATTTGGCAAT 1270
Db 1534  GTGAGAAGACCTCTATCGACATCTCTCCATTCGCAACCAACCGCTTTGGTATTTGGTAA 1593
QY 1271  CCAAGCAAAACGGTCCGCGAAGTTAA 1296
Db 1594  CCAAGCAAACTGCTCTGCACTCTAA 1619
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RESULT 14  
PSEAKSD 3430 bp DNA BCT 26-APR-1993  
LOCUS Pseudomonas putida alpha-ketoglutarate semialdehyde dehydrogenase  
DEFINITION gene, complete cds.

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M69158
M69158.1 GI:150981
ketoglutarate semialdehyde dehydrogenase.
Pseudomonas putida DNA.
ORGANISM
Pseudomonas putida
bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
Pseudomonas.
REFERENCE
1 (bases 1 to 3430)
AUTHORS
Burlingame,R.P., Maruya,A., Ally,A.H., Ally,D. and Backman,K.C.
TITLE
Nucleotide sequences of hydroxyproline-specific alpha-ketoglutarate
semialdehyde dehydrogenase genes from two strains of Pseudomonas
putida
JOURNAL
Unpublished (1991)
FEATURES
Location/Qualifiers
1..3430
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603..2180
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PLAFSVAGGDTASALAAAGTSPVVKHSAHPGTSELVQQAQVAKIKCGLPAGVFSLLY
GSGREVIAGLVSDPRIKAVGPTGSRSGGIALCQATQARPEPIPVYAEMSNIPVFLFE
AALQARAEALQGFVASTQAGQCFCTNPGLVIAPOGPALQRFIDAAESHVQAAAQT
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EYFGASLVVACASDEQVHAEHLLEGOLATLQDDADIDRALRATLPLERKAGRIL
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BASE COUNT 562 a 1140 c 1157 g 571 t
ORIGIN

Query Match 6.7%; Score 87.4; DB 2; Length 3430;
Best Local Similarity 46.6%; Pred. No. 8.6e-14;
Matches 450; Conservative 0; Mismatches 506; Indels 9; Caps 5;

QY 23 TAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCATCGCTTTTGATGCTTCAACGTCGTG 82
Db 2208 TCGCCGTGGTGGCGCGGGATTTGTCGGCGTTGCCTTGCCCTGCAACTGCCCGCCAGG 2267
QY 83 GATTCAAAAGTCACCTTTGATTGACCCGGAACCTCTCTGCCGAAGGTGCATCGCTTTGGCAATG 142
Db 2268 GCCTCCGGTGTATTGGTCGACCGCAGCACCCGCCCATGGCGCTCTCTATGGCAACG 2327
QY 143 CGGGATGCTTCAACGGCTCATCGTCTGCTATGTCCTATGTCGCGGAGGTGCATCGCTTTGACGAGCG 202
Db 2328 CCGGGACCTTGGCCACCGAGCAGGTGTTCGGATTCGGACCTGTGATCCTCAACGCGCT 2387
QY 203 TGCGGAAGTGGCTCCTTGACCCGATGGGCGCTTGTCAATCCGGTTTCAGCTATTTTCCAA 262
Db 2388 TGCCGGCGCATGCTGCTGGACCCGATGGGCCACTGGCCCTGGACTGGAAGTACTCGCCA 2447
QY 263 CCATCATGCCCTGGTTGATTTCGCTTTCTGTTAGCCGGAAGACCAACAAAGGTGAAGAGC 332
Db 2448 CGGCCATCGCTGTTTACCGCGCTGCTGCTCAACCTGCGCCGCCCGCCCTTCCAGCGCA 2507
QY 323 AGCGAAGACACTCCCGCAATCTCATCAAGTCCACGGTGCCTCTGATCAAGTCAATTTGGCGG 382
Db 2508 GTGTGCCCGCATCCGCAAGCTGAACGAAGGACGCTGGGTGCATGGCAGCGCTCTCTGG 2567
QY 383 AGGAGGCTGATGCGAGCCCATCTGATCCGCCATCAAGTCAATCTGACCGGTATATCTGGGAG 442
Db 2568 GCTCGATCGGCGCACGACCTGTTCCAGGAGGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2626
QY 443 AAGCAGACTTCGCGCAAGGACCGCGGAGGTGGGAAGTGC-GGCGTCTCAACAGCTGTTCGC 501
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[illegible]

Search completed: January 1, 2001, 03:15:47  
Job time: 29231 sec

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 ALEARGEALAGQFVASTQGAQSGTFLGNARQGPALDAF1KAAANLVQRSPAOT  
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 MFGAAS1VQOASDDIRIQTVEHLEQGLTARLLHDADLESARALLPVLKERAGRLIV  
 NWPTQVEVCDAMVHGQFPFATSDARTT5VGTAAILURFLRPVCYQDFPDTLLPAALQH  
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 378 a 766 c 734 g 411 t  
 BASE COUNT  
 ORIGIN

Query Match	5.3%	Score 69.2	DB 2	Length 2289
Best Local Similarity	52.4%	Pred. No. 1.3e-08		
Matches 152	Conservative	0	Mismatches 138	Indels 0
				Gaps 0

Qy	4	GCTGAGAACACAAAAGATTAGGCATCGCTGGAGCTGGAATCGTTGGTGTGATGCACATGCT	63
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Qy	64	TTGATGCTTCAACGTCGTGGATTCAAAGTCACCTTGATTGACCGGAACCCCTCCCTGGCGAA	123
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Qy	124	GGTGATCGTTTGGGAATCCCGGATGCTTCAACGGCTCATCCCTCGTCCCTATGTCCATG	183
Db	1848	GGTGCCCTGTTGGGCAATGCCGGCATCTGGGACCCAGCAGGTGTTTCCCATCGCGGAT	1907
Qy	184	CCGGGAACCTTGACGAGGTGCCGAAGTGGCTCCTTGACCCGATGGGCGCGTGTGTCATC	243
Db	1908	TTGTCGATCTCGAAGCGCTTGCCCTGCCATCGCTATGACCCGATGGGCGCGCTGCGGCTG	1967
Qy	244	CGFTTCAGCTATTTCCAAACCATCATCCCTGGTGTGATTCGCTTTCTGTGTT	293
Db	1968	GACTGGAAGTACATGCGCGCGCCCTCCCGTGGTTTCCCGGCTACATGTT	2017

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 03:42:34 ; Search time 263.11 Seconds  
(without alignments)  
1850.400 Million cell updates/sec

Title: US-08-484-274-7  
Perfect score: 1296  
Sequence: 1 ATGGCTGAGACACAAAAA.....AACGGGTCCGCAAGTTAA 1296

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Capext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

Database : N\_Geneseq\_16.\*

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- 4: /SID56/gcgdata/geneseq/geneseq/NA1983.DAT.\*
- 5: /SID56/gcgdata/geneseq/geneseq/NA1984.DAT.\*
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- 9: /SID56/gcgdata/geneseq/geneseq/NA1988.DAT.\*
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- 12: /SID56/gcgdata/geneseq/geneseq/NA1991.DAT.\*
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- 21: /SID56/gcgdata/geneseq/geneseq/NA2000.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1294.4	99.9	1321	13 Q20834	Modified glyphosat
2	1200	92.6	1321	13 Q20833	Manipulated glypho
3	1193.6	92.1	1692	13 Q22705	Glyphosate oxidore
4	1157.6	89.3	1689	13 Q20832	Glyphosate oxidore
5	1011.2	78.0	1296	13 Q20835	Synthetic glyphosa
6	1011.2	78.0	8418	20 X57309	Sugar beet T-DNA c
7	926.8	71.5	1631	18 T85664	CPTI-GOX gene fusi
8	703	54.2	8798	20 X57308	Sugar beet T-DNA c
9	701.8	54.2	8012	20 X57305	Sugar beet T-DNA c
C 10	37.4	2.9	3292	14 Q46544	Yeast SSRP DNA seq
C 11	37.4	2.9	3292	19 V09625	S. cerevisiae SSRP
C 12	35.8	2.8	6558	21 Z45602	CDNA sequence of a

13	35.6	2.7	5460	17	T16508
C 14	35.4	2.7	501	6	N50025
C 15	35.2	2.7	501	6	N50023
16	35	2.7	38734	20	Z32020
17	34.4	2.7	32207	20	V73805
18	34.4	2.7	137507	19	V19411
C 19	34	2.6	1209	12	Q12569
C 20	34	2.6	1513	12	Q12567
C 21	33.8	2.6	1220	18	V75229
C 22	33.8	2.6	3690	13	Q30849
C 23	33.6	2.6	501	6	N50030
C 24	33.6	2.6	501	6	N50031
C 25	33.6	2.6	501	6	N50032
C 26	33.6	2.6	10266	17	T33007
27	33.4	2.6	2516	15	Q56832
28	33.2	2.6	1694	17	T15232
29	33.2	2.6	1694	18	T94635
30	33.2	2.6	2442	20	X59335
31	33.2	2.6	2442	20	X31981
32	33	2.5	423	18	T80725
C 33	33	2.5	2800	20	X57965
C 34	33	2.5	2800	20	X57966
C 35	33	2.5	2800	20	X29247
C 36	33	2.5	2800	20	X29248
C 37	33	2.5	2800	20	V82065
C 38	33	2.5	2800	20	V82066
C 39	33	2.5	2800	20	V82058
C 40	33	2.5	2800	20	V82059
C 41	33	2.5	5059	20	X84332
C 42	32.8	2.5	543	13	Q23092
C 43	32.8	2.5	922	19	V15073
C 44	32.8	2.5	1526	20	Z42235
C 45	32.8	2.5	2455	21	Z45836

ALIGNMENTS

RESULT 1	
Q20834	
ID Q20834	standard; DNA; 1321 BP.
XX	
AC Q20834;	
XX	
DT 01-MAY-1992	(first entry)
XX	
DE Modified glyphosate oxidoreductase gene.	
XX	
KW Recombinant; GOR; resistance; ss.	
XX	
OS Bacterial isolate LBAA.	
XX	
PH Key	Location/Qualifiers
FT CDS	9..1304
FT	/*tag= a
FT	/note= "encodes wild type glyphosate oxidoreductase"
XX	
PN W09200377-A.	
XX	
PD 09-JAN-1992.	
XX	
PF 24-JUN-1991;	91WO-US04514.
XX	
PR 24-JUN-1991;	91US-0717370.
PR	
25-JUN-1990;	90US-0543236.
XX	
XX (MONS ) MONSANTO CO.	
PA	
PI Kishore GM, Barry GF;	
XX	
XX WPI; 1992-041559/05.	
DR	
DR P-PSDB; R20642.	
XX	







/note= "not present in alternative sequence"

FT XX W09200377-A.  
PN XX  
XX XX  
PD XX  
XX XX  
PF 24-JUN-1991: 91W0-US04514.  
XX XX  
XX 24-JUN-1991: 91US-0717370.  
PR 25-JUN-1990: 90US-0543236.  
XX XX  
XX (MONS ) MONSANTO CO.  
PI Kishore GM, Barry GF;  
XX WPI: 1992-041559/05.  
DR P-PSDB; R22262.  
XX XX  
PT Gene encoding glyphosate oxido-reductase enzyme - used to  
PT transform plants to produce plants tolerant to glyphosate  
PT herbicide  
XX  
PS Claim 1; Fig 2; 142pp; English.  
XX  
CC The sequence is that of a gene encoding a glyphosate oxidoreductase  
CC (GOR) enzyme. It was obtd. from bacterial isolate LBAA. It is used  
CC to transform plants such that they express the enzyme sufficient  
CC to enhance the glyphosate tolerance of the plant. Transformed plants  
CC resistant to glyphosate can be obtd. so that weeds can be selectively  
CC controlled in fields contg. crops. This sequence (fig 2) contains  
CC apparent discrepancies (see feature table) with a supposedly identical  
CC sequence (SEQ ID No.3 in the specification), since it is unclear from  
CC the specification which of these is correct, both sequences have been  
CC indexed. See also Q20833-Q20841 and Q20832 - the alternative sequence  
CC for the GOR gene.  
XX  
XX Sequence 1692 BP; 381 A; 478 C; 471 G; 361 T; 1 other;  
SQ

Query Match 92.1%; Score 1193.6; DB 13; Length 1692;  
Best Local Similarity 95.1%; Pred. No.: 0;  
Matches 1232; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

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QY 61 GCTTTGATGCTTCAACGTCGTGATTCAAAGTCACCTTGATTGACCCGAAACCTCTG 120  
DB 180 ggcgtgatgcttcagcgccgcgggattcaaaagtcaacttgattgaccgcgaagccctctggc 239  
QY 121 GAAGTGGCATCGTTTGGGAATGCCGATGCTTCAACGGGTCTATCCGTCGTCCTATGTC 180  
DB 240 gaagtgcatcgcttgaggatgccgagatgcttcaacgctcatccgctccctatgtcc 299  
QY 181 ATGCCGGGAAACTTACGAGCGTGCAGAAAGTGCTCTTGAACCCGATGGGCGCGTTGTCA 240  
DB 300 atgcgggaaacttgacgagcgctgcgaagtggtccttgaccgcatggggcgttgta 359  
QY 241 ATCCGGTTTTCAGCTATTTTCCACCATCATGCCCCTGTTGATTCGGCTTCTGTTAGCCGGA 300  
DB 360 atccggttcagctattttccaaacatcgccctgggtgattgcgtttctgttagcgga 419  
QY 301 AGACCAAAACAAAGGTGAAGGAGCAGGCGAAAGCACTCCGCAATCTCATCAAGTCACCGGTG 360  
DB 420 agacaaaacaaagtgagggagcagcgaagcaactccgcaactcctcaagtccacggcg 479  
QY 361 CCTCTGATCAAGTCATTTGGCGGAGGAGGTGATGCGAGCCATCTGATCCGCCATGAAGGT 420  
DB 480 cctctgatcaagtcattgycggaggagcgtgatgcgagccatctgatcccatgaagt 539  
QY 421 CATCTGACCGTATATCGTGGAGNAGCAGACTTCGCCCAAGACCGCGGAGGTGGGAACGTG 480

Db 540 catctgaccgtatctatcgtggagaagcagactctgcgaagaccgcgaggtgtgggaactg 599  
QY 481 CGCGCTCTCAACGGTGTTCGCACGCACAGATCCTCTCTCTGATGCTTTTCGCTGATTTTCGAT 540  
Db 600 cggcgtctcaacggtgttcgcacgcagatcctccagccgcatcggttgcggagattcgcgat 659  
QY 541 CCTAACTTGTTCGATGCTTTTACCAAGGGATCTTATAGAAGAGAACGGTTCACACGATTT 600  
Db 660 ccgaacttgctgcgcatcgctttaccgaaggcattcttatagaagagaacggtccacagatt 719  
QY 601 AATCCGCAAGGGTCTGACGACCTCTTCTTTTCGGCGTGTATTCGGCAACGGTGGCGAAATTT 660  
Db 720 aatccgcaagggtcgtgacccctctgttttcg9cgttttatcgcgaacggtg9cgaattc 779  
QY 661 GTATCTCGCGGTCTCATCGGTTTGTAGACATGAAGGTGCTGCTCTCAAGACGATTTACAACC 720  
Db 780 gtatctgcgctgtcatcgcgcttttgagactggaaggttgcgagccggtctaaaggcattcacacc 839  
QY 721 ACTAACGGTGTCTGCGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
Db 840 acgaacggttcttgcgctgtgatgcagcgttgcgagccggtgcgacactcgaaatca 899  
QY 781 CTTCCTAATTCGCTAGCGGATGACATCCCGCTCGATACCCGCTGATATCATATATCGTC 840  
Db 900 ctgtctaattcgttagcgatgacatcccgctcgataccgaacgtggatatcatctgct 959  
QY 841 ATCCGGAATCCGAAGCGCTCCACGCATTCGACGACCGATGCGTCAGGAAATTCATC 900  
Db 960 atcggaatccggaagccgctccacgcatcccgagaccgcatcgctcaggaataattcatg 1019  
QY 901 GCGACACCTATGAAATGGGTCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
Db 1020 gcgacacctatgaaatggggcttcgctgctgcggttacggttgagttcgtgggtcaca 1079  
QY 961 GCTGCTCTTAACCTGGAACGCTGCGCATGCTCTATACGACGCTCGAAACCTCTTCCA 1020  
Db 1080 gccgctctaactggaaacgtgcgcatgtgctctatcgcagcgtcgaaactcttcca 1139  
QY 1021 GCCTCTCGCGCTCGAGTCTGAAGAACGATATTCCAAATGGATGGTGTTCGTCCTPAGC 1080  
Db 1140 gccctcgctcgaggtcttgaaagacgatatctcaaatggtatgggttccggcgagc 1199  
QY 1081 ATTCTCGATTTCTTTCAGTGATTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
Db 1200 atcccggtatcgtcccgctgattggcgggcaaccccgaccccgacgtaattctatgct 1259  
QY 1141 TTTTGGTCCAGGCTCATCTCGGTATGACAGGTGCTTCCAATGACTGCAACTCTCTGCTCAGAG 1200  
Db 1260 ttcggccatggtcatctcgcgatgacaggggcccgcgatgaccgcaacgctcgtctcagag 1319  
QY 1201 CTCTCTCGCAGCGCAAAAGACCTCAATCGACATTTTCGGCCCTTCGCACCAACCCGCTTTGGT 1260  
Db 1320 ctctcgcgaggcgaagaaagacctcaatcgacatttcgccccttcgacccaacccgcttttgg 1379  
QY 1261 ATTGGCAAAATCCAAAGCAACGGGTCCGCGCAAGTTAA 1296  
Db 1380 attggcaaatcccaagcaaacgggtccggcgaagttaa 1415

RESULT 4  
Q20832  
ID Q20832 standard; DNA; 1689 BP.  
XX  
AC Q20832;  
XX  
DT 01-MAY-1992 (first entry)  
XX  
DE Glyphosate oxidoreductase gene.  
XX  
KW Recombinant; GOR; resistance; ss.  
XX  
OS Bacterial isolate LBAA.  
XX



ID Q20835 standard; DNA; 1296 BP.  
AC Q20835;  
XX  
DT 01-MAY-1992 (first entry)  
XX  
DE Synthetic glyphosate oxidoreductase gene.  
XX  
KW Recombinant; GOR; resistance: ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1296  
FT /tag= a  
XX  
XX W09200377-A..  
XX  
XX 09-JAN-1992..  
XX  
XX 24-JUN-1991; 91WO-US04514.  
XX  
XX 24-JUN-1991; 91US-0717370.  
PR 25-JUN-1990; 90US-0543236.  
XX  
XX (MONS ) MONSANTO CO.  
XX  
XX Kishore GM, Barry GF;  
XX  
XX WPI; 1992-041559/05.  
DR P-PSDB; R20642.  
XX  
PT Gene encoding glyphosate oxido-reductase enzyme - used to  
PT transform plants to produce plants tolerant to glyphosate  
PT herbicide  
XX  
PS Claim 1; Page 1032; 142pp; English.

CC The sequence is that of the gene encoding a glyphosate oxidoreductase  
CC (GOR) enzyme, the gene sequence was synthesised so that it could be  
CC redesigned to eliminate as much as possible the following sequences or  
CC sequence features (while avoiding the introduction of unnecessary  
CC restriction sites), stretches of G's and C's of 5 or more; A + T rich  
CC regions (predominantly) that could function as polyadenylation sites  
CC or potential RNA destabilisation regions, and codons not frequently  
CC found in plant genes. The G + C% for the synthetic gene is 51% and  
CC the potential to form short, high energy, hair-pin structures is  
CC reduced. However it still encodes the wild type GOR enzyme. It is  
CC used to transform plants such that they express the enzyme  
CC sufficiently to enhance the glyphosate tolerance of the plant.  
CC Transformed plants resistant to glyphosate can be obt'd. so that  
CC weeds can be selectively controlled in fields contg. crops.  
CC See also Q20832-Q20841 and Q22705.

XX Sequence 1296 BP; 271 A; 359 C; 305 G; 361 T; 0 other;

Query Match 78.0%; Score 1011.2; DB 13; Length 1296;  
Best Local Similarity 86.3%; Pred. No. 0;  
Matches 1118; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

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DB 1 atggctgagaaacacaaaagtgtgtatcgctggagctggaatcgttggtgttgcaact 60  
QY 61 GCATTTCATGCTTCAACGCTCGTGGATTCAAGTCAACCTTGATTGACCGAACCTCTCTGGC 120  
DB 61 gctttgatgctcaacgctggtggttaacaggttaccttgattgatccaacaccacagggt 120  
QY 121 GAAGGTGTCATCGTTTGGGAATGCCGATGCTTCAACGGCTCACTCCGTCGTCCTATGTCC 180  
DB 121 gaaggtgctcttccttgtaacgctggttgcttcaacagggttcctccgtttgttccaatgtcc 180

QY 181 ATGCCGGGAAACTGTGACGAGCGTGCCCAAGTGGCTCTCTTGAACCCGATGGGGCCGCTTGTCA 240  
DB 181 atgccaggaacttgactagcgttccaaagtggcttcttgacccaaatgggtccattgtcc 240  
QY 241 ATCCGGTTTCAGCTATTTCCTCAACCATCATGCCCTGGTGTGATTCGCTTCTGTTAGCCGGA 300  
DB 241 atccggttccagctacttccaaacatcatgcttgggtgattgattgcttcttctgctgctgga 300  
QY 301 AGACCAAAACAAGGTGAAGGAGCAGCGGCAAAAGCACTCCGCAATCTCATCAAGTCACACGGT 360  
DB 301 agaccaaacaagggtgaagagagaagcactaagcactcgttaacatcacaagtcacatgtg 360  
QY 361 CCTCTGATCAAGTCATTGGCGGAGGAGGCTGTGATGCGAGCCATCTGTATCCGCCATGAAGGT 420  
DB 361 cctctgatcaagtccttggctgagaggctgagtgcagaccacttatccgtcacaagaaggt 420  
QY 421 CATCTGACCGTATATCGTGGAGAGCAGACTTCGCCAAGGACCCGCGAGGTTGGGAAGT 480  
DB 421 cactttaccgtgtacogtggagaagcacttcgccaagaccgtggaggttgggaactt 480  
QY 481 CGGCGTCTCAACGGTGTTCGCACGCAGACTCTCTCTGCTGATGCTTTTCGCTGATTTTCGAT 540  
DB 481 cgtcgtctcaacggtgttctgtactcaaatcctcagcgtgatgcattgctgatttcgat 540  
QY 541 CCTAACTTGTGCGATGCTTTTACCAAGGGCATTTCTTATAGAAGAGAACGGTTCACACGATT 600  
DB 541 cctaaactgtctcacgcttttaccaaaggaaatccttatacgaagagaacggttcacaccatc 600  
QY 601 AATCCGCAAGGGCTCGTGACCCCTTGTGTTTCGGGGTATTTATCCGGAACGGTGGCGAATTT 660  
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QY 661 GTATCTGCGGTGTATCATCGGTTTGTGAGACTGAAGTGTGCTCTCAAAAGGCAATTCACAACT 720  
DB 661 gtctctgctgctgtatctcagagactgaaaggctcgtctcctcaagggttatcaccacc 720  
QY 721 ACTAACGGTCTTTCGGCTGTTGATGACAGCTGTGTGTCAGCTGTGTGTCACACTCTTAAATCA 780  
DB 721 accaaagggttctctgtgtgtatgacagctgtgtgtcagctggtgcacactccaagtct 780  
QY 781 CTGTCTAATTTTCGTAGCGGATGACATCCCGTCTCGATACCGACGTTGATATCATATCGTC 840  
DB 781 ctgtctaactcccttgggtgatgacatcccatgtgataccgaaacggtgataccacatcgtg 840  
QY 841 ATCCGGAATCCGGAAGCCGCTCACGCATTCGAGACGACCGTGTGTCAGGAAAATTCATC 900  
DB 841 atcgccaacccagaagcgtgctcaccgttatccaaactaccagatgcttctggaagttcatc 900  
QY 901 GCGACACCTATGGAATTTGGCTCTTTCGTTGCTGTGTTACTGTGAGTTTGTGTTCTCACA 960  
DB 901 gctactcctatggagatgggttcttcgttgctggaaacggttgagttcgtctggtctcact 960  
QY 961 GCTGCTCTTAACCTGGAACCGTGGCGATGTGCTCTATACGCGACGCTCGAAAACACTTCTTCCA 1020  
DB 961 gctgctcctaaactggaaagcgtgctcactcctcactcactcactcactcactcactcactc 1020  
QY 1021 GCCTCTCGCGCTCGAGTCTTCTGAAGAACGATATTTCCAAATGGATGGGTTTTCGTCCTAGC 1080  
DB 1021 gctctgctcctcgccagttctcgaagaacggttactccaagtggatgggttccgttccaagc 1080  
QY 1081 ATTTCTGATTTCTTTCAGTGTGTTGGTGTGCAACTCGTACACCCGACGTAATCTATGCT 1140  
DB 1081 atctccagattcctctccagtgtggttcgtgctaccogtactccagacggttatctacgct 1140  
QY 1141 TTTGGTTCACGCTATCTCGGTATGACAGGTGCTCCCAATGACTGCAACTCTCGTCTCAGAG 1200  
DB 1141 ttctggtcacoggttcacctcgtgtatgactggtgctccaatgaccocaaacctcgtttctcgag 1200  
QY 1201 CTCTCTCGAGCGCAAAAGACCTCAATGCACATTTTCGCCCTTCGCACCAAAACCGGTTTGGT 1260  
DB 1201 ctctctcgagtgagaagacctctatgcacatctctccattctgcacccaacacggttctcgtt 1260  
QY 1261 ATTTGGCAAAATCCAAGCAAAACGGGTTCGGCAAGTTAA 1296















PT New modified human beta interferon polypeptide(s) - prepd. by  
PT plasmid transformed bacteria, with improved antiviral,  
PT anti-proliferative and immune regulating actions  
XX  
XX  
PS Claim 28; Chart 2c, page 34; 71pp; English.  
XX  
CC Compared with interferon beta prepd. by recombinant methods, the  
CC INFs of the invention are more active and have different affinities  
CC for cell surface receptors (allowing selective targeting); they  
CC have higher therapeutic index; improved stability against microbial  
CC breakdown during synthesis; and better in vivo solubility and  
CC stability. They are also easier to recover from incubation mixts.  
XX  
SQ Sequence 501 BP; 112 A; 30 C; 69 G; 85 T; 205 other;

Query Match 2.7%; Score 35.4; DB 6; Length 501;  
Best Local Similarity 28.9%; Pred. No. 0.24;  
Matches 69; Conservative 50; Mismatches 120; Indels 0; Gaps 0;  
Qy 505 CAGATCCCTCTCGTGGTAACTTCGGATCTTAACCTTTCGATGCTTTTACC 564  
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Db 351 CATVARYTTNCCHCKNGTAAATCTCTTCVARYTTTCVARNACNGTIVTVAR 292  
Qy 565 AAGGCATTCTTATAGAGAAGAGCGTACACAGGATTATCCGCAAGGCTCGTGACCCCTC 624  
: : : : || : : || : : || : : || : : || : : || : : || : : || : :  
Db 291 RTGRTTDATYTGRTGTANACRTTNGCVARVARTTYTCNACDATNGTTCCTCCANCC 232  
Qy 625 TTGTTTCGGCGTTTATCCGAACGGTGGCAATTTGTATCTGCGCGTGTATCGGTTTTT 684  
: : : : || : : || : : || : : || : : || : : || : : || : : || : :  
Db 231 NGTNWNWNWRTCTATGHCRAADATNGCRAADATRTTATGVARCATYTCRTADATNGT 172  
Qy 685 GAGACTGAAGTCTGCTCTCAAAGGCATTACAACTTAACGCTGCTGCTGCTGCTGA 743  
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Db 171 VARNGCNGRCYTCYTYTGRAAYTGRTTNCRCRTCAAATCYTCATGNGGDATRTCRA 113

RESULT 15  
N50023/c  
ID N50023 standard; DNA; 501 BP.  
XX  
AC N50023;  
XX  
DT 04-SEP-1991 (first entry)  
XX  
DE Sequence encoding new modified human beta interferon polypeptides  
DE IFN 416.  
XX  
KW Antiviral; cell growth regulator; Immune system regulator;  
KW antiproliferative; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..501  
FT /\*tag= a  
XX  
PN EP163993-A.  
XX  
PD 11-DEC-1985.  
XX  
PF 17-MAY-1985; 85EP-0105750.  
XX  
PR 17-MAY-1984; 84GB-0012564.  
XX  
PA (SEAR ) SEARLE G D & CO.  
XX  
PI Bell LD, Boseley PG, Porter AG;  
XX  
DR WPI; 1985-311944/50.  
DR P-PSDB; P50022.  
XX  
PT New modified human beta interferon polypeptide(s) - prepd. by

PT plasmid transformed bacteria, with improved antiviral,  
PT anti-proliferative and immune regulating actions  
XX  
XX  
PS Claim 28; Chart 2a, page 32; 71pp; English.  
XX  
CC Compared with interferon beta prepd. by recombinant methods, the  
CC INFs of the invention are more active and have different affinities  
CC for cell surface receptors (allowing selective targeting); they  
CC have higher therapeutic index; improved stability against microbial  
CC breakdown during synthesis; and better in vivo solubility and  
CC stability. They are also easier to recover from incubation mixts.  
XX  
SQ Sequence 501 BP; 107 A; 31 C; 69 G; 80 T; 214 other;

Query Match 2.7%; Score 35.2; DB 6; Length 501;  
Best Local Similarity 29.0%; Pred. No. 0.28;  
Matches 63; Conservative 47; Mismatches 107; Indels 0; Gaps 0;  
Qy 505 CAGATCCCTCTCGTGGTAACTTCGGATCTTAACCTTTCGATGCTTTTACC 564  
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Db 351 CATVARYTTNCCHCKNGTAAATCTCTTCVARYTTTCVARNACNGTIVTVAR 292  
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Db 291 RTGRTTDATYTGRTGTANACRTTNGCVARVARTTYTCNACDATNGTTCCTCCANCC 232  
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Db 231 NGTNWNWNWRTCTATGHCRAADATNGCRAADATRTTYTGVARCATYTCRTADATNGT 172  
Qy 685 GAGACTGAAGTCTGCTCTCAAAGGCATTACAACTTAACGCTGCTGCTGCTGCTGA 721  
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Db 171 VARNGCNGRCYTCYTYTGRAAYTGRTTNCRCRTCR 135

Search completed: January 1, 2001, 03:43:13  
Job time: 20201 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 03:17:58 ; Search time 157.96 Seconds  
(without alignments)  
1240.873 Million cell updates/sec

Title: US-08-484-274-7  
Perfect score: 1296  
Sequence: 1 ATGGCTGAGAACACAGAAAA.....AAACGGGTCCGCCAGTTAA 1296

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 262060 seqs, 75620496 residues

Total number of hits satisfying chosen parameters: 524120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
- 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
- 3: /cgn2\_6/ptodata/2/ina/5C\_COMB.seq:\*
- 4: /cgn2\_6/ptodata/2/ina/5D\_COMB.seq:\*
- 5: /cgn2\_6/ptodata/2/ina/6\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*
- 7: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1296	100.0	1296	1	US-08-391-339-7
2	1296	100.0	1296	2	US-08-484-274A-7
3	1201.6	92.7	1296	1	US-08-391-339-6
4	1201.6	92.7	1296	2	US-08-484-274A-6
5	1196.8	92.3	1692	2	US-08-484-274A-3
6	1160.8	89.6	1293	1	US-08-391-339-4
7	1160.8	89.6	1293	2	US-08-484-274A-4
8	1160.8	89.6	1689	1	US-08-391-339-3
9	1011.2	78.0	1296	1	US-08-391-339-8
10	1011.2	78.0	1296	2	US-08-484-274A-8
11	1006.4	77.7	1296	1	US-08-391-339-17
12	1006.4	77.7	1296	2	US-08-484-274A-17
13	69	5.3	69	1	US-08-391-339-30
14	69	5.3	69	1	US-08-391-339-33
15	69	5.3	69	2	US-08-484-274A-30
16	69	5.3	69	2	US-08-484-274A-33
17	68	5.2	68	1	US-08-391-339-32
18	68	5.2	68	2	US-08-484-274A-32
19	63.4	4.9	65	1	US-08-391-339-28
20	63.4	4.9	65	2	US-08-484-274A-28
21	62	4.8	62	1	US-08-391-339-27
22	62	4.8	62	2	US-08-484-274A-27
23	61	4.7	61	1	US-08-391-339-31
24	61	4.7	61	2	US-08-484-274A-31
25	41	3.2	41	1	US-08-391-339-29
26	41	3.2	41	2	US-08-484-274A-29

C 27	37.4	2.9	3292	1	US-07-814-964-12	Sequence 12, Appl
C 28	37.4	2.9	3292	1	US-08-238-442-12	Sequence 12, Appl
C 29	37.4	2.9	3292	2	US-08-328-809-7	Sequence 7, Appl
C 30	37.4	2.9	3292	6	PCT-US92-11107-12	Sequence 12, Appl
C 31	36.4	2.8	7218	1	US-08-232-463-14	Sequence 14, Appl
C 32	34.4	2.7	3489	4	US-08-728-323A-1	Sequence 1, Appl
C 33	34.4	2.7	32207	3	US-08-770-379-20	Sequence 20, Appl
C 34	33.2	2.6	1694	2	US-08-698-351-9	Sequence 9, Appl
C 35	33.2	2.6	1694	3	US-08-602-228-9	Sequence 9, Appl
C 36	33.2	2.6	1694	3	US-08-494-440B-9	Sequence 9, Appl
C 37	33.2	2.6	1694	3	US-08-533-901B-9	Sequence 9, Appl
C 38	33.2	2.6	1694	3	US-08-839-032A-9	Sequence 9, Appl
C 39	33.2	2.6	1694	4	US-08-839-031A-9	Sequence 9, Appl
C 40	33.2	2.6	1694	6	PCT-US93-12724-9	Sequence 9, Appl
C 41	33	2.5	423	1	US-08-470-179-144	Sequence 144, App
C 42	33	2.5	2800	3	US-08-874-138-1	Sequence 1, Appl
C 43	33	2.5	2800	3	US-08-874-138-5	Sequence 5, Appl
C 44	32.8	2.5	543	7	5273901-6	Patent No. 5273901
C 45	32.6	2.5	3181	2	US-08-655-086-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1  
US-08-391-339-7  
; Sequence 7, Application US/08391339  
; Patent No. 5463175  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dennis R. Hoerner, Jr.,  
; ADDRESSEE: Monsanto CO. BB4F,  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391,339  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/156,968  
; FILING DATE:  
; APPLICATION NUMBER: US/07/717,370  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner, Dennis R., Jr.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10533)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1296 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (recombinant)  
US-08-391-339-7

Query Match 100.0%; Score 1296; DB 1; Length 1296;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGCGTGAAGAACACAAAAAGTAGCATCGCTGGAGCTGGAAATCGTTGGTGTATGCACT	60
Db	1	ATGSGCTGAGAACACAAAAAGCTAGCATCGCTGGAGCTGGAAATCGTTGGTGTATGCACT	60
Qy	61	GCATTGATGCTTCAACGTCGTGGATGTCAAAGTCACCTTGATTGACCCCAACCCCTCGTGGC	120
Db	61	GCATTGATGCTTCAACGTCGTGGATGTCAAAGTCACCTTGATTGACCCCAACCCCTCGTGGC	120
Qy	121	GAAGTGCATCGTTTGGGAATCCGGAGTCTTCAACGGCTCATCCGTCGTCCTCATGTGCC	180
Db	121	GAAGTGCATCGTTTGGGAATCCGGAGTCTTCAACGGCTCATCCGTCGTCCTCATGTGCC	180
Qy	181	ATGCCGGGAACCTTGACGAGCTGCCGAAGTGGCTCTTGTACCCGATGGGCGCGTTGTCA	240
Db	181	ATGCCGGGAACCTTGACGAGCTGCCGAAGTGGCTCTTGTACCCGATGGGCGCGTTGTCA	240
Qy	241	ATCCGGTTCAGCTATTTTCCAAACCATCATCGCCCTCGTTTGAITTCGGCTTTCGTATAGCCGGA	300
Db	241	ATCCGGTTCAGCTATTTTCCAAACCATCATCGCCCTCGTTTGAITTCGGCTTTCGTATAGCCGGA	300
Qy	301	AGACCAAAACGTTGAAGGACGAGCGGAAGCACATCCGGAATCTCATCAAGTCCACCGGT	360
Db	301	AGACCAAAACGTTGAAGGACGAGCGGAAGCACATCCGGAATCTCATCAAGTCCACCGGT	360
Qy	361	CCTCTGATCAAGTCATTGTGGCGAGGAGGCTGATCGAGGCCATCTGATCCGCCCATGAAGGT	420
Db	361	CCTCTGATCAAGTCATTGTGGCGAGGAGGCTGATCGAGGCCATCTGATCCGCCCATGAAGGT	420
Qy	421	CATCTGACCGCTATATCGTGGAGAAGCAGACTTCGCCCAAGCACCCGGAGTGGGAAC	480
Db	421	CATCTGACCGCTATATCGTGGAGAAGCAGACTTCGCCCAAGCACCCGGAGTGGGAAC	480
Qy	481	CGCGCTCAACCGTCTCGCAGCAGATCCCTCTGCTGATGCTTTGCGTGTATTTCGAT	540
Db	481	CGCGCTCTCAACCGTGTTCGCAGCAGATCCCTCTGCTGATGCTTTGCGTGTATTTCGAT	540
Qy	541	CCTAACTTGTGCGATCGTTTATACCAAGGCGCATCTTATAGAAGAGAACGGTCCACACGATT	600
Db	541	CCTAACTTGTGCGATCGTTTATACCAAGGCGCATCTTATAGAAGAGAACGGTCCACACGATT	600
Qy	601	AATCCGCAAGGGCTCGTGACCCCTCTGTTTCGGCGTTTATTCGCGAACGGTGGCGAATTT	660
Db	601	AATCCGCAAGGGCTCGTGACCCCTCTGTTTCGGCGTTTATTCGCGAACGGTGGCGAATTT	660
Qy	661	GTATCTCGCGGTGTCATCSGTTTGGAGACTGAAGTCTGCTCTCAAGGCGATTACAACC	720
Db	661	GTATCTCGCGGTGTCATCSGTTTGGAGACTGAAGTCTGCTCTCAAGGCGATTACAACC	720
Qy	721	ACTAACGGTGTTCGTGCTGTTGATGACGTGTGTTCGAGCTGGTGGACACTCTAAATCA	780
Db	721	ACTAACGGTGTTCGTGCTGTTGATGACGTGTGTTCGAGCTGGTGGACACTCTAAATCA	780
Qy	781	CTTGCTAAITTCGCTAGCGCATACATCCCGTTCGATCCGAACCGTGGATATCATATCGTC	840
Db	781	CTTGCTAAITTCGCTAGCGCATACATCCCGTTCGATCCGAACCGTGGATATCATATCGTC	840
Qy	841	ATCCGGAATCCGGAAGCCGCTCCACGCAATCCGAGCACCGATGGCTCAGGAAAAATTCATC	900
Db	841	ATCCGGAATCCGGAAGCCGCTCCACGCAATCCGAGCACCGATGGCTCAGGAAAAATTCATC	900
Qy	901	GCACACCTATGGAATGGGTCTTCGTGTTGCTGGTACTGTTGAGTTTGTGGTCTCACA	960
Db	901	GCACACCTATGGAATGGGTCTTCGTGTTGCTGGTACTGTTGAGTTTGTGGTCTCACA	960
Qy	961	GCTGCTCCTAACTTGAACCTCGCGATGTGCTCTATACGCACGCTCGAAAACTTCCTTCCA	1020
Db	961	GCTGCTCCTAACTTGAACCTCGCGATGTGCTCTATACGCACGCTCGAAAACTTCCTTCCA	1020
Qy	1021	GCCTTCGCGCTCGGAGTTCTTGAAGAACGATATTCCAAATGGATGGGTTTTCGCTCTAGC	1080
Db	1021	GCCTTCGCGCTCGGAGTTCTTGAAGAACGATATTCCAAATGGATGGGTTTTCGCTCTAGC	1080

Qy	1081	ATTGCTGATTCTCTTCCAGTGATGGTCTGGAACTCGTCACACCGACGTAATCTATGCT	1140
Db	1081	ATTCTGATTCTCTTCCAGTGATGGTCTGGAACTCGTCACACCGACGTAATCTATGCT	1140
Qy	1141	TTTTGGTCACGGTCATCTCGGTATGACAGGTGCTTCCAATGACITGCAACCTCTCGTCTCAGAG	1200
Db	1141	TTTTGGTCACGGTCATCTCGGTATGACAGGTGCTTCCAATGACITGCAACCTCTCGTCTCAGAG	1200
Qy	1201	CTCCTCGCAGCGCAAAAGACCTCAATCGACATTTTCGCCCTTTTCGCACCAAAACCGCTTTTGGT	1260
Db	1201	CTCCTCGCAGCGCAAAAGACCTCAATCGACATTTTCGCCCTTTTCGCACCAAAACCGCTTTTGGT	1260
Qy	1261	ATTGGCAAAATCCCAAGCAAAACGGGTCGGGCAAGTTAA	1296
Db	1261	ATTGGCAAAATCCCAAGCAAAACGGGTCGGGCAAGTTAA	1296

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RESULT      2
US-08-484-274A-7
; Sequence 7, Application US/08484274A
; Patent No. 5776760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,274A
; FILING DATE: 07 June 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)789-2679
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (recombinant)
US-08-484-274A-7

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Query Match 100.0%; Score 1296; DB 2; Length 1296;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGCTGAGAACCAAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCACCT	60
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Db	61	GCATTGATGCTTCAACGCTCGTGGATTCAAAAGTCACCTTGATTGACCCGAACCCCTCTGGC	120
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Db 121 GAAGTGCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC 180  
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Qy 361 CCTCTGATCAAGTCAATGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT 420  
Db 361 CCTCTGATCAAGTCAATGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT 420  
Qy 421 CATCTGACCGTATATCGTGAGAGAGCAGACTTCCCAAGGACCGCGGAGGTTGGGAAGT 480  
Db 421 CATCTGACCGTATATCGTGAGAGAGCAGACTTCCCAAGGACCGCGGAGGTTGGGAAGT 480  
Qy 481 CGGCGTCTCAACGGTGTTCGACGCGAGATCCTCTCTGCTGATGCTTTCGCTGATTTTCGAT 540  
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Qy 541 CTTAACTGTGCGATGCTTTTACCAAGGCAATCTTATAGAAGAGAACGGTTCACAGATT 600  
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Db 1261 ATTGGCAAAATCCAAAGCAACGGGTCCGCAAGTTAA 1296  
RESULT 3  
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; Sequence 6, Application US/08391339  
; Patent No. 5463175  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dennis R. Hoerner, Jr.,  
; ADDRESSEE: Monsanto Co. BBAF  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391,339  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/156,968  
; FILING DATE:  
; APPLICATION NUMBER: US/07/717,370  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner, Dennis R., Jr.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10533)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1296 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (recombinant)  
; US-08-391-339-6

Query Match 92.7%; Score 1201.6; DB 1; Length 1296;  
Best Local Similarity 95.4%; Pred. No. 0;  
Matches 1237; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

Qy 1 ATGCGTGAAGAACCAAAAAAGTAGGCATCGCTGAGCTGGAATCGTTGGTGTATGCACT 60  
Db 1 ATGCGTGAAGAACCAAAAAAGTAGGCATCGCTGAGCGCGGAATCGTCGGCGCTATGCAAG 60  
Qy 61 GCTTTGATGCTTCAACGTCGTCGGATTCACAAAGTCACCTTGATTGACCGCAACCCCTCCTGGC 120  
Db 61 GCGCTGATGCTTCAAGGTCACCTTGATTGACCGCAACCCCTCCTGGC 120  
Qy 121 GAAGGTGCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGTCCTATGTC 180  
Db 121 GAAGGTGCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGTCCTATGTC 180  
Qy 181 ATGCCGGGAAACTTGACGAGCGTCCGGAAGTGGCTCCTTGACCCGATGGGCGCGTTGTCA 240  
Db 181 ATGCCGGGAAACTTGACGAGCGTCCGGAAGTGGCTCCTTGACCCGATGGGCGCGTTGTCA 240





Qy 421 CATCTGACCGTATATCGTGGAGAACGACACTTCGCCAAGGACCGCGGAGGTTGGAACTG 480  
Db 421 CATCTGACCGTATATCGTGGAGAACGACACTTCGCCAAGGACCGCGGAGGTTGGAACTG 480  
Qy 481 CGGGCTCTCAACGGTGTTCGACGCGAGATCCTCTCTGCTGATGCTTTTCGCTGATTTTCGAT 540  
Db 481 CGGGCTCTCAACGGTGTTCGACGCGAGATCCTCTCTGCTGATGCTTTTCGCTGATTTTCGAT 540  
Qy 541 CCTAACTTGTGCGATGCTTTTACCAAGGGCATTTCTTATAGAGAGAACGGTTCACACGATT 600  
Db 541 CCGAACTTGTGCGATGCTTTTACCAAGGGCATTTCTTATAGAGAGAACGGTTCACACGATT 600  
Qy 601 AATCCGAAGGGCTCGTACACCTCTTTTTCGCGGTTTTATCGCGAAGCGTGGCGAATTT 660  
Db 601 AATCCGAAGGGCTCGTACACCTCTTTTTCGCGGTTTTATCGCGAAGCGTGGCGAATTT 660  
Qy 661 GTATCTGCGCGTGCATCGGTTTTGAGACTGAAGTCTGCTCTCAAGGCATTACAACC 720  
Db 661 GTATCTGCGCGTGCATCGGTTTTGAGACTGAAGTCTGCTCTCAAGGCATTACAACC 720  
Qy 721 ACTAACGGTGTTCGGCTGTTGATGACAGTGTGTTGACAGTGGTGGACACTCTAAATCA 780  
Db 721 ACTAACGGTGTTCGGCTGTTGATGACAGTGTGTTGACAGTGGTGGACACTCTAAATCA 780  
Qy 781 CTTCGTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAAGTGGATATCATATCGTC 840  
Db 781 CTTCGTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAAGTGGATATCATATCGTC 840  
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Db 841 ATCGGGAATCCGGAAGCGCGCTCCAGCATTCGAGACCGATGCTCAGGAAAATTCATC 900  
Qy 901 GCGACACCTATGGAATGGGCTTCGCTGTTGCTGGTACTGTTGAGTTTGGTCTCACA 960  
Db 901 GCGACACCTATGGAATGGGCTTCGCTGTTGCTGGTACTGTTGAGTTTGGTCTCACA 960  
Qy 961 GCTGCTCTAACTGGAACGTCGGCATGTGCTCTATACGACAGCTCGGAAACTCTTCCA 1020  
Db 961 GCGGCTCTAACTGGAACGTCGGCATGTGCTCTATACGACAGCTCGGAAACTCTTCCA 1020  
Qy 1021 GCCCTCGCGCTGCGAGTTCCTGAAGAACGATATCCAAATGATGGGTTTTGCTCTAGC 1080  
Db 1021 GCCCTCGCGCTGCGAGTTCCTGAAGAACGATATCCAAATGATGGGTTTTGCTCTAGC 1080  
Qy 1081 ATTCTGATCTCTTCCAGTATGGTTCGTCGAACCTCGTACACCGACGTAATCTATGCT 1140  
Db 1081 ATCCGGGATTCGCTCCCGCTGATTGGCCGCGCAACCCGACACCGACGTAATCTATGCT 1140  
Qy 1141 TTTGGTCAAGGTCAATCTCGGTATGACAGTGTCTCAATGACTGCAACTCTCTCTCAGAG 1200  
Db 1141 TTTGGTCAAGGTCAATCTCGGTATGACAGTGTCTCAATGACTGCAACTCTCTCTCAGAG 1200  
Qy 1201 CTCCTCGGAGGGAAGAACCTCAATCAGATTTTCGCCCTTCGCAACCAACCGCTTTCGT 1260  
Db 1201 CTCCTCGGAGGGAAGAACCTCAATCAGATTTTCGCCCTTCGCAACCAACCGCTTTCGT 1260  
Qy 1261 ATTGGCAATCCAAAGCAACGGGTCGGCAAGTTAA 1296  
Db 1261 ATTGGCAATCCAAAGCAACGGGTCGGCAAGTTAA 1296

RESULT 5

us-08-484-274A-3  
: Sequence 3, Application US/08484274A  
: Patent No. 5776760  
: GENERAL INFORMATION:  
: APPLICANT: Kishore, Ganesh M.  
: APPLICANT: Barry, Gerard F.  
: TITLE OF INVENTION: Glyphosate Tolerant Plants  
: NUMBER OF SEQUENCES: 33  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Arnold, White & Durkee  
: STREET: P.O. Box 4433

: CITY: Houston  
: STATE: Texas  
: COUNTRY: USA  
: ZIP: 77210-4433  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/484,274A  
: FILING DATE: 07 June 1996  
: CLASSIFICATION: 435  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Patterson, Melinda L.  
: REGISTRATION NUMBER: 33,062  
: REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (713)789-2679  
: INFORMATION FOR SEQ ID NO: 3:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 1692 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: double  
: TOPOLOGY: linear  
: MOLECULE TYPE: DNA (genomic)  
: us-08-484-274A-3

Query Match 92.3%; Score 1196.8; DB 2; Length 1692;  
Best Local Similarity 95.2%; Pred. No. 0;  
Matches 1234; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 1 ATGGCTGAGAACCAAAAAAGTAGGCATCGCTGGAGTGGAACTCGTTGGTGTATGCACT 60  
Db 120 ATGCTGAGAACCAAAAAAGTAGGCATCGCTGGAGCGGAACTCGTGGCGTATGCAAG 179  
Qy 61 GCTTTGATGCTTCAACGTCGTGGATTCAAAGTCACTTTGATTGACCCGGAACCTCTGTC 120  
Db 180 GCGCTGATGCTTCAGCGCGCGGATTCAAAGTCACTTTGATTGACCCGGAACCTCTGTC 239  
Qy 121 GAAGGTGATCGTTTGGGAATCCCGGATGCTTCAACGGCTCATCGTCTGCTATGTC 180  
Db 240 GAAGGTGATCGTTTGGGAATCCCGGATGCTTCAACGGCTCATCGTCTGCTATGTC 299  
Qy 181 ATCCGGGAAACTTCACGAGCGTCCGGAAGTGGCTCTTGACCCGATGGGCGGTTGTCA 240  
Db 300 ATCCGGGAAACTTCACGAGCGTCCGGAAGTGGCTCTTGACCCGATGGGCGGTTGTCA 359  
Qy 241 ATCCGGTTCAGCTATTTTCCAACCATCATGCCCTGGTTGATTTCGCTTTCTGTAGCCGA 300  
Db 360 ATCCGGTTCAGCTATTTTCCAACCATCATGCCCTGGTTGATTTCGCTTTCTGTAGCCGA 419  
Qy 301 AGACCAACAGGTGAAGGAGGAGCGGAAAGCACTTCGCAATCTCATCAAGTCCACGGTG 360  
Db 420 AGACCAACAGGTGAAGGAGGAGCGGAAAGCACTTCGCAATCTCATCAAGTCCACGGTG 479  
Qy 361 CCTCTGATCAAGTCAATTCGCGGAGGAGCTGATGGAGCCATCTCATCGCCCATGAAGT 420  
Db 480 CCTCTGATCAAGTCAATTCGCGGAGGAGCTGATGGAGCCATCTCATCGCCCATGAAGT 539  
Qy 421 CATCTGACCGTATATCGTGGAGAACGACACTTCGCCAAGGACCGCGGAGGTTGGAACTG 480  
Db 540 CATCTGACCGTATATCGTGGAGAACGACACTTCGCCAAGGACCGCGGAGGTTGGAACTG 599  
Qy 481 CGCGCTCTCAACGGTGTTCGACGCGAGATCCTCTCTGCTGATGCTTTTCGCTGATTTTCGAT 540  
Db 600 CGCGCTCTCAACGGTGTTCGACGCGAGATCCTCTCTGCTGATGCTTTTCGCTGATTTTCGAT 659  
Qy 541 CCTAACTTGTGCGATGCTTTTACCAAGGGCATTTCTTATAGAGAGAACGGTTCACACGATT 600  
Db 560 CCGAACTTGTGCGATGCTTTTACCAAGGGCATTTCTTATAGAGAGAACGGTTCACACGATT 719

Qy	601	AATCCGCAAGGGCTCGTGACCCCTCTTTGTTTCGGCGT	TTTTATCGCGAACGGTGGCGAAATTT	660
Db	720	AATCCGCAAGGGCTCGTGACCCCTCTTTGTTTCGGCGT	TTTTATCGCGAACGGTGGCGAAATTC	779
Qy	661	GTATCTCGCGGTGTCAATCGGTTTTGAGACTGAAGGT	TCGTCTCAAAGGATTAACAACC	720
Db	780	GTATCTCGCGGTGTCAATCGGTTTTGAGACTGAAGGT	TAGGGCGCTTAAAGGCAATTAACAACC	839
Qy	721	ACTAACGGTGTCTTGGCTGTGTGATCGACGTGTGT	TTCAGCTTGGTGCACACTCTAAATCA	780
Db	840	ACGAACGGCGTTCTTGGCGGTTGATGACGGCGTGT	TCGACCGGGCGCACACTCGAAATCA	899
Qy	781	CTTGCTAAATTCGCTAGCGGATGACATCCCGCTCG	ATACCGGACGTTGATATCATATCGTC	840
Db	900	CTTGCTAAATTCGCTAGCGGATGACATCCCGCTCG	ATACCGGACGTTGATATCATATCGTC	959
Qy	841	ATCCGGAATCCGGAACCGCTCCACGATTCGAGCAC	CCGATGCGTCAAGAAAATTCATC	900
Db	960	ATCCGGAATCCGGAACCGCTCCACGATTCGAGCAC	CCGATGCGTCAAGAAAATTCATC	1019
Qy	901	CGGACACTATGAAATGGGTCTTCGTGTTCGTGTA	CTACTGTTGAGTTTTCGTGCTCACA	960
Db	1020	CGGACACTATGAAATGGGTCTTCGTGTTCGTGTA	CTACTGTTGAGTTTTCGTGCTCACA	1079
Qy	961	GCTGCTCCTTAATCGGAACGTGCGATGTCCTAT	ATGCGCACGCTCGAAAACTTCTTCCA	1020
Db	1080	GCGCTCTTAATCGGAACGTGCGATGTCCTAT	ATGCGCACGCTCGAAAACTTCTTCCA	1139
Qy	1021	GCCCTCGCGGCTCGGAGTTCTGAAGAACGATAT	TCCAAATGGATGGGTTTTCGTCTAGC	1080
Db	1140	GCCCTCGCGGCTCGGAGTTCTGAAGAACGATAT	TCCAAATGGATGGGTTTTCGTCTAGC	1199
Qy	1081	ATTCTCTGATTTCTTCCAGTGATGGTTCGTGCACT	TCGTACACCGGACGTAATCTATGCT	1140
Db	1200	ATTCTCTGATTTCTTCCAGTGATGGTTCGTGCACT	TCGTACACCGGACGTAATCTATGCT	1259
Qy	1141	TTTGGTCAACGGTCATCTCGGTAATGACAGGTGCT	CTCAATGACTGCAACTTCTCGTCTCAGAG	1200
Db	1260	TTTGGTCAACGGTCATCTCGGTAATGACAGGTGCT	CTCAATGACTGCAACTTCTCGTCTCAGAG	1319
Qy	1201	CTCCTTCGACGGCCAAAAGACCTCAATTCGACAT	TTTCGCCCTTCGCAACCAACCGCTTTGGT	1260
Db	1320	CTCCTTCGACGGCCAAAAGACCTCAATTCGACAT	TTTCGCCCTTCGCAACCAACCGCTTTGGT	1379
Qy	1261	ATTGGCAAAATCCAAGCAAAACGGGTCCGGCAAG	TATTA	1296
Db	1380	ATTGGCAAAATCCAAGCAAAACGGGTCCGGCAAG	TATTA	1415

## RESULT 6

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US-08-391-339-4
;
; Sequence 4, Application US/08391339
; Patent No. 5463175
;
; GENERAL INFORMATION:
;
; APPLICANT: Kishore, Ganesh M.
;
; APPLICANT: Barry, Gerard F.
;
; TITLE OF INVENTION: Glyphosate Tolerant Plants
;
; NUMBER OF SEQUENCES: 33
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Dennis R. Hoerner, Jr.,
;
; ADDRESSEE: Monsanto Co. BB4F
;
; STREET: 700 Chesterfield Village Parkway
;
; CITY: St. Louis
;
; STATE: Missouri
;
; COUNTRY: USA
;
; ZIP: 63198
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/391,339
;

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Qy 661 GTATCTGCGCGTGTCTATCGGTTTTCAGACTGAAGTCTGTCTCTCAAAAGCATTTACAACC 720  
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Qy 721 ACTAAGCGTGTCTGCGTGTTCATCCAGCTGTTCGTCAGCTGGTGGCACACTCTAAATCA 780  
Db 718 ACGAACGCGTGTTCGCGTGTTCATCCAGCTGTTCGTCAGCTGGTGGCACACTCTAAATCA 777  
Qy 781 CTTCGTAATTCGCTAGGCGATGACATCCGCTCGATACCGAAGTGGATATCATATCTGTC 840  
Db 778 CTTCGTAATTCGCTAGGCGATGACATCCGCTCGATACCGAAGTGGATATCATATCTGTC 837  
Qy 841 ATCGCGAATTCGGAAGCGCTCCAGCAATTCGACGACCGATGCGTCAGGAAATTCATC 900  
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Qy 901 CGGACACCTATGGAATGGTCTTCGCTGTCTGCTGCTACTGTTCAGTTTTCGCTCTACA 960  
Db 898 CGGACACCTATGGAATGGGCTTCGCGTGGCGGTACGGTTGAGTTTCGCTGGGCTACA 957  
Qy 961 GCTGCTCTAACTGGAACGTCGCGATGTCTATAGCACGCTCGGAAACTTCTTCCA 1020  
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Qy 1081 ATTCCTGATCTCTTCCAGTGTTCGCTGCTGCAACTCTGACCCGACGCTATCTATGCT 1140  
Db 1078 ATTCGCGATTCGCTCCCGTGTTCGCGGCAACCGGACCGACCGATCTATCTATGCT 1137  
Qy 1141 TTTGCTACGCTCATCTCGGTATGACAGTGTCTCAATGACTGCAACTCTCTGCTCTCAGAG 1200  
Db 1138 TTTGCGCATGCTCATCTCGGCATGACAGGCGCGCATGACCGCAACCGTCTCTCAGAG 1197  
Qy 1201 CTCTCGCAGGGAAGACCTCAATGACATTTTCGCCCTTCGCGACCAACCGCTTTGGT 1260  
Db 1198 CTCTCGCAGGGAAGACCTCAATGACATTTTCGCCCTTCGCGACCAACCGCTTTGGT 1257  
Qy 1261 ATTCGCAATCCAAGCAACGGTCCGCAAGTTAA 1296  
Db 1258 ATTCGCAATCCAAGCAACGGTCCGCAAGTTAA 1293

RESULT 7  
US-08-484-274A-4  
; Sequence 4, Application US/08484274A  
; Patent No. 5776760  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,274A  
; FILING DATE: 07 June 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Patterson, Melinda L.

; REGISTRATION NUMBER: 33,062  
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (713)789-2679  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1293 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1293  
US-08-484-274A-4

Query Match 89.6%; Score 1160.8; DB 2; Length 1293;  
Best Local Similarity 95.0%; Pred. No. 0;  
Matches 1231; Conservative 0; Mismatches 62; Indels 3; Gaps 3;  
Qy 1 ATGGCTGAGAACACCAAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCACT 60  
Db 1 ATGCTGAGAACACCAAAAAAGTAGGCATCGCTGGAGCGGGAATCGTCGGCGTATGCAAG 60  
Qy 61 GCTTTGATGCTTCAACGTCGTGGATTCAAAGTCACTTTGATTGACCCGGAACCCCTCCTGCG 120  
Db 61 GCGCTGATGCTTCAGCGCGCGGATTCAAAGTCACTTTGATTGACCCGGAACCCCTCCTGCG 120  
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Db 181 ATGCCGGGAAACTTCACGAGGTGCCGAAGTGGCTCTTGACCCGATGGGCGGTTGTCA 239  
Qy 241 ATCCGGTTTCAAGTATTTTCCAACCATCATGCTGCTGTTGATTGCTGTTTCTGTAGCCGA 300  
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Qy 301 AGACCAACAAAGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360  
Db 298 AGACCAACAAAGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 357  
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Db 358 CCTCTGATCAAGTCAATTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 417  
Qy 421 CATCTGACCGTATATCGTGGAGAACAGACACTTCGCCAAGGACCGCGGAGGTTGGGAACG 480  
Db 418 CATCTGACCGTATATCGTGGAGAACAGACACTTCGCCAAGGACCGCGGAGGTTGGGAACG 477  
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Qy 541 CCTAACTTGTGCGATGCTTTTACCAAGGCGATCTTATAGAGAACAGACGCTCACACGATT 600  
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Qy 661 GTATCTGCGCGTGTCTATCGGTTTTCAGACTGAAGTCTGTCTCTCAAAAGCATTTACAACC 720  
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Qy 721 ACTAAGCGTGTCTGCGTGTTCATCGACTGTTGTTGACGCTGGTGGCACACTCTAAATCA 780  
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Db 838 ATCGCGAATCCGGAAGCGCTCCACGCAATCCGACGACCGATCGTCAGGAAATTCATC 897
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QY 961 GCTGCTCTAATCGGAACGTCGCGATGCTCTATACGACGCTCGAATCTCTTCCA 1020
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QY 1021 GCGCTCGCGCTCGGAGTCTCGGAAGACGATATTCGGAATGGATGGTTCGTCCTAGC 1080
Db 1018 GCGCTCGCGCTCGGAGTCTCGGAAGACGATATTCGGAATGGATGGTTCGCGCGAGC 1077
QY 1081 ATTCTCGATTCTCTTCAGTGATTGGTCTGCAACTCGTACACCGGACGTAATCTATGCT 1140
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Db 1138 TTTGGTCACGGTCATCTCGGCATGACAGGGCGCGGATGACCGCAACGCTCTCAGAG 1197
QY 1201 CTCTCGCAGCGCAAGACCTCAATGACATTTCCGCCCTTCGCACCAACCGCTTTGGT 1260
Db 1198 CTCTCGCAGCGCAAGACCTCAATGACATTTCCGCCCTTCGCACCAACCGCTTTGGT 1257
QY 1261 ATTGGCAATCCAAAGCAAGCGGTCCGGCAAGTTAA 1296
Db 1258 ATTGGCAATCCAAAGCAAGCGGTCCGGCAAGTTAA 1293
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RESULT 8

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US-08-391-339-3
; Sequence 3, Application US/08391339
; Patent No. 5463175
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr.,
; ADDRESSEE: Monsanto Co. BB4F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,339
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/156,968
; FILING DATE:
; APPLICATION NUMBER: US/07/717,370
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
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; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-391-339-3

Query Match      89.8%; Score 1160.8; DB 1: Length 1689;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 1231; Conservative 0; Mismatches 62; Indels 3; Gaps 3;

QY 1 ATGCTCAGAACACAAAAAGTAGGCATCGCTGAGCTTGAATCGTTGGTGTATGCAC 60
Db 120 ATGCTCAGAACACAAAAAGTAGGCATCGCTGAGCCGGAATCGTCGGCGTATGCACG 179
QY 61 GCTTTGATGCTTCAACGCTCGTGATTTCAAAAGTCACCTTTGATTGACCCGAAACCTCTCTGGC 120
Db 180 GCCTGATGCTTCAGCGCCGCGGATTTCAAAGTCACCTTTGATTGACCCGAAACCTCTCTGGC 239
QY 121 GAAGGTGCATCGTTTGGGAATGCGGATGCTTCAACGGCTCATCGCTGCTCCCTATATGCC 180
Db 240 GAAGGTGCATCGTTTGGGAATGCGGATGCTTCAACGGCTCATCGCTGCTCCCTATATGCC 299
QY 181 ATCCCGGAAACTTGACGAGCGTCCGCAAGTGGCTTCCTTACCCGATGGGCGCTTGTCA 240
Db 300 ATCCCGGAAACTTGACGAGCGTCCGCAAGTGGCTTCCTTACCCGATGGGCGCTTGTCA 358
QY 241 ATCCGGTTTACGCTATTTTCCAAACCATCATGCCCTGGTTGATTGCTTCTTGTAGCCGGA 300
Db 359 ATCCGGTTTACGCTA-TTTTCCAAACCATCATG-CCTGGTTGATTGCTTCTTGTAGCCGGA 416
QY 301 AGACCAAAACAAAGGTGAAGGAGCAGGCGGAAAGACACTCCGCAATCTCATCAAGTCCACGGTG 360
Db 417 AGACCAAAACAAAGGTGAAGGAGCAGGCGGAAAGACACTCCGCAATCTCATCAAGTCCACGGTG 476
QY 361 CCTCTGATCAAGTCATTTGGCGGAGGAGGCTGATCCGAGCCATCTGATCCGCCATGAAGGT 420
Db 477 CCTCTGATCAAGTCATTTGGCGGAGGAGGCTGATCCGAGCCATCTGATCCGCCATGAAGGT 536
QY 421 CATCTGACCGTATATCGTGAGAGCAGACTTCGCCAAGGACCGCGGAGGTGGGAACTG 480
Db 537 CATCTGACCGTATATCGTGAGAGCAGACTTCGCCAAGGACCGCGGAGGTGGGAACTG 596
QY 481 CGCGCTCTCAACGGTGTTCGCACGACAGATCCTCTCTGCTGATGCTTTGCGTGTATTCGAT 540
Db 597 CGCGCTCTCAACGGTGTTCGCACGACAGATCCTCTGAGCTGAGGCTGCTCTCAAGGCAATTCACAC 656
QY 541 CCTAACTTGTGCGATGCTTTTACCAAGGCGATTTCTTATAGAAGAACGCTCACACGATT 600
Db 657 CCGAATTTGTCGATGCGTTTACCAAGGCGATTTCTTATAGAAGAACGCTCACACGATT 716
QY 601 AATCCGCAAGGGCTCGTGACCCCTCTTTTTCGGCGTTTATCGCAACGCTGGCGAATTT 660
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QY 661 GTATCTCGCGGTGTCTCGGTTTGGAGACTGAAGGTGCTGCTCTCAAGGCAATTCACAC 720
Db 777 GTATCTCGCGGTGTCTCGGTTTGGAGACTGAAGGTGCTGCTTAAAGGCAATTCACAC 836
QY 721 ACTAAGCGTGTCTTGGCTGTTGATGAGCTGTTTGTGAGCTGCTGACACTCTTAATCA 780
Db 837 ACGAACGGCGTCTTGGCGGTTGATGACGCGGTTGTCGACCGCGGCGACACTCGAATCA 896
QY 781 CTTGCTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGTGGATATCATATCGTC 840
Db 897 CTTGCTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGTGGATATCATATCGTC 956
QY 841 ATCCGCAATCCGGAAGCGGCTCCACGATTTCCGACGACCGATGCTGTCAGGAAATTCATC 900
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Db 957 ATCGGAAATCGGAAGCGCTCCACGCAATCCGAGCAGCGATGCGTCAGGAAATTCATC 1016  
Qy 901 CCGACACCTATGGAATGGCTTTCGTGTGCTGCTACTGTGTAGTGTGCTGCTCACA 960  
Db 1017 CGGACACCTATGGAATGGGCTTCGCGCTGGCGGTACGGTTGAGTTGCTCGCTGCCTCACA 1076  
Qy 961 GCTGCTCTTAAGTGAAGAGCGGCGATGCTCTATAGCAGCGCTCGAAATCTTCTCCA 1020  
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Qy 1021 GCGCTCGGCGCTCGCAGTCTTGAAGACGATATCCAAATGAGTGGGTTCGTCCTAGC 1080  
Db 1137 GCGCTCGGCGCTCGCAGTCTTGAAGACGATATCCAAATGAGTGGGTTCGCGCGAGC 1196  
Qy 1081 ATTCCTGATCTCTTCCAGTGAATGGTCTGCACTCTACACCGAGCTTAATCTATGCT 1140  
Db 1197 ATCCCGGATTCGCTCCCGCTGATGGCGGGCAACCGGACACCGCTAATCTATGCT 1256  
Qy 1141 TTGCTCAGGTCATCTCGGTATGACAGGTGCTCAATGACTGCACTCTGCTCTCAGAG 1200  
Db 1257 TTGCGCCATGCTCATCTCGGATGACAGGGCGCGGATGACCGCAACGCTGCTCTCAGAG 1316  
Qy 1201 CTCTTCGCGAGCGAAACAGCTCAATCGACATTTTCGCCCTTCGCAACCAACGCTTTTGGT 1260  
Db 1317 CTCTTCGCGAGGAAAGACCTCAATCGACATTTTCGCCCTTCGCAACCAACGCTTTTGGT 1376  
Qy 1261 ATTGCAAAATCCAAAGCAACGGGTCGCGCAAGTTAA 1296  
Db 1377 ATTGCAAAATCCAAAGCAACGGGTCGCGCAAGTTAA 1412

RESULT 9

US-08-391-339-8  
; Sequence 8, Application US/08391339  
; Patent No. 5463175  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dennis R. Hoerner, Jr.,  
; ADDRESSEE: Monsanto Co. B4F  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391.339  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/156.968  
; FILING DATE:  
; APPLICATION NUMBER: US/07/717.370  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner, Dennis R., Jr.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10533)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1296 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double

; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (synthetic)  
US-08-391-339-8  
  
Query Match 78.0%; Score 1011.2; DB 1; Length 1296;  
Best Local Similarity 86.3%; Pred. No. 0;  
Matches 1118; Conservative 0; Mismatches 178; Indels 0; Gaps 0;  
  
Qy 1 ATGGCTGAGAACCAAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCACT 60  
Db 1 ATGGCTGAGAACCAACAAGAGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTATGCACT 60  
Qy 61 GCTTTGATGCTTCAACGCTGCTGGATTCAAAGTTCACCTTTGATTGACCCGAAACCCCTCTGGC 120  
Db 61 GCTTTGATGCTTCAACGCTGCTGGATTCAAAGTTCACCTTTGATTGATCCAAACCCACAGT 120  
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Qy 181 ATGCCGCGAAACTTTCACGAGCGTCCGAAAGTGGCTTTCGACCCGATGGGCGCTGTGCA 240  
Db 181 ATGCCAGAAACTTTCAGCTAGGCTTCCAAAGTGGCTTTCGACCCAAATGGTCCATGTCC 240  
Qy 241 ATCCGCTTTCAGCTATTTTCCAAACCATCATGCCCTGGTGTGATTGCTTCTTGTAGCCGA 300  
Db 241 ATCCGCTTTCAGCTATTTTCCAAACCATCATGCCCTGGTGTGATTGCTTCTTGTCTGGA 300  
Qy 301 AGACCAACAGGTGAGGAGGAGCGGAGGAGCAAGCTAAGGCACTCCGCTCAAGCTCCACTGTG 360  
Db 301 AGACCAACAGGTGAGGAGGAGCAAGCTAAGGCACTCCGCTCAAGCTCCACTGTG 360  
Qy 361 CCTCTGATCAAGTTCATTCGCGAGGAGGCTGATGGAGCCATCTCATCGGCATCAAGGT 420  
Db 361 CTTTGTATCAAGTCTTGGCTGAGGAGGCTGATGCTAGCCACTTATCCGTCACGAAGT 420  
Qy 421 CATCTGACCGTATATCGTGGAGAGCAGACTTCGCCAAGGACCGCGAGGTGGGAACGTG 480  
Db 421 CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAAGGACCGGTGGAGTGGGAACTT 480  
Qy 481 CGGCTCTCAAGGCTGTTGCGACGAGATCCTCTCTGCTGATGCTTTCGCTGATTTCCAT 540  
Db 481 CGTCTCTCAAGGCTGTTGCTACTCAAAATCCTCAGCGCTGATGCAATTCGCTGATTTCCAT 540  
Qy 541 CTTAACTTGTGCGATGCTTTTACCAAGGCACTTCTATAGAAAGAGACGGTACACAGATT 600  
Db 541 CTTAACTTGTCTCAGCGCTTTTACCAAGGCACTTCTATCGAAGAGACGGTACACCATC 600  
Qy 601 AATCGGAAGGCTGCTGACCGCTCTTGTTCGGCGTTCGCGAAGCGGTGGCAATTT 660  
Db 601 AACCCAAAGGCTGCTGCTGCTCTTGTTCGCTGCTTTCATCGCTAACCGTGGAGAGTTC 660  
Qy 661 GTATCTGCGGTGCTCATCGGTTTTCAGACTGAGGCTGCTCTCAAGGCAATTCACACC 720  
Db 661 GTGCTGCTGCTGTTATCGGATTCGAGACTGAAAGTCTGCTCTCAAGGCTATCACCACC 720  
Qy 721 ACTAACGCTGTTTCGCTGTTGATCAGCTGTTTTCAGCTGGTGGCACTCTAAATCA 780  
Db 721 ACCAACGCTGTTTCGCTGTTGATCAGCTGTTTTCAGCTGGTGGCACTCTCAAGTCT 780  
Qy 781 CTTGTAATTCGCTAGGCGATGACATCCGCTCGATACCGACGCTGGATATCATATGCTC 840  
Db 781 CTTGTAATTCGCTAGGCGCTCCACGCTATCCCAATCCGACGCTGGATACCCACATCGTG 840  
Qy 841 ATCGGAATCCGAAGCGCTCCACGCTATTCGAGACGCTGCTCAGGAAATTCATC 900  
Db 841 ATCGCAACCCAGAAAGCTGCCAGCTATTCCAACTACCGATGCTTCTGGAAAGTTCATC 900  
Qy 901 GCGACACCTATGGAATGGTCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
Db 901 GCTACTCTATGGAGATGGGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960

QY 961 GCTGCTCCTTAACGTGGAACCGTGGCCATGTGCTCTATACGCACGCTCGAAAACATTCTTTCCA 1020  
Db 961 GCTGCTCCTTAACGTGGAACCGTGGCCATGTGCTCTATACGCACGCTCGAAAACATTCTTTCCA 1020  
QY 1021 GCCTCCGCGCTCGAGCTCTGAAGACGATATCCAAATGGATGGGTTTTCGTCCTAGC 1080  
Db 1021 GCTCTCGCTCTCGCACTCTGAAGAACGTTACTCCAAAGTGGATGGGTTTTCGTCCTAGC 1080  
QY 1081 ATTCTCTGATTCTCTTCCAGTGATTGGTGCCTGCAACTCGTACACCCGACGTAATCTATGCT 1140  
Db 1081 ATCCAGATTCCCTTCAGTAGTGGTGGTCTACCGTACTCCAGACGTTATCTAGCT 1140  
QY 1141 TTTGGTCAACGCTCATCTCGGTATGACAGGTGCTCCAAATGACTGCAACTCTCGTCTCAGAG 1200  
Db 1141 TTCGGTCAACGCTCATCTCGGTATGACAGGTGCTCCAAATGACTGCAACTCTCGTCTCAGAG 1200  
QY 1201 CTCTCCGAGCGGAAAGACCTCAATCGACATTTTCGGCTTCGCACCAACCGCTTTGGT 1260  
Db 1201 CTCTCCGAGGTGAGAAGACCTCTATCGACATCTCTCCATTCGCACCAACCGCTTTGGT 1260  
QY 1261 ATTGGCAATCCAAAGCAACCGGTCCGGCAAGTTAA 1296  
Db 1261 ATTGGTAAGTCCAAAGCAACCGGTCTCTGCATCCTAA 1296

RESULT 10

US-08-484-274A-8  
: Sequence 8, Application US/08484274A  
: Patent No. 5776760  
: GENERAL INFORMATION:  
: APPLICANT: Kishore, Ganesh M.  
: APPLICANT: Barry, Gerard F.  
: TITLE OF INVENTION: Glyphosate Tolerant Plants  
: NUMBER OF SEQUENCES: 33  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Arnold, White & Durkee  
: STREET: P.O. Box 4433  
: CITY: Houston  
: STATE: Texas  
: COUNTRY: USA  
: ZIP: 77210-4433  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patent In Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/484,274A  
: FILING DATE: 07 June 1996  
: CLASSIFICATION: 435  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Patterson, Melinda L.  
: REGISTRATION NUMBER: 33,062  
: REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (713)789-2679  
: INFORMATION FOR SEQ ID NO: 8:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 1296 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: double  
: TOPOLOGY: linear  
: MOLECULE TYPE: DNA (synthetic)  
US-08-484-274A-8

Query Match 78.0%; Score 1011.2; DB 2; Length 1296;  
Best Local Similarity 86.3%; Pred. No. 0;  
Matches 1118; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

QY 1 ATGGCTGAGAACCAAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATCGACT 60  
Db 1 ATGGCTGAGAACCAAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATCGACT 60

QY 61 GCTTTGATGCTTCAACGTCGTGGATTCAAGTCACCTTGATTGACCCGAAACCCCTCCCTGGC 120  
Db 61 GCTTTGATGCTTCAACGTCGTGGATTCAAGTCACCTTGATTGATCCAAACCCACAGGT 120  
QY 121 GAAGGTGCATCGTTTGGGAATGCGGATGTTCACCGCTCATCCGCTCGTCCCTATGTCC 180  
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QY 181 ATGCCGGAAACCTTGACGAGCGTCCGAAGTGCTCTTGACCCGATGGGCGCTGTGTCA 240  
Db 181 ATGCCAGAAACCTTGACGAGCGTTCCTCAAGTGCTCTTGACCCAAATGGGTTCCTATGTCC 240  
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Db 301 AGACCAAAACAGGTGAAGGAGCAGGCTAAGGCACTCCGTAACCTTCATCAAGTCCACCTGTG 360  
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Db 361 CCTTTGATCAAGTTCCTTTGGCTGAGGAGGCTGATGCTTAGCCACCTTATCCGTCACGAAGGT 420  
QY 421 CATCTGACCGTATATCTGTGAGAGCAGACTTCGCCAAGGACCGCGGAGGTTCGGAACTG 480  
Db 421 CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAAGGACCGCTGGAGGTTCGGAACTT 480  
QY 481 CGGCGTCTCAACGGTGTTCGACGCGAGATCCTCTCTGCTGATGCTTTTTCGCTGATTTTCGAT 540  
Db 481 CGTCTGCTCAACGGTGTTCGTAACCTCTCAAGGCACTTCGTAACCTTCGTAACCTTCGAT 540  
QY 541 CCTAACTTGTGCGATGCTTTTACCAAGGCACTTCCTTATAGAAAGACGCTGCACACGATT 600  
Db 541 CCTAACTTGTGCTACCGCTTTTACCAAGGCACTTCCTTATAGAAAGACGCTGCACACGATT 600  
QY 601 AATCCGCAAGGCTCGTGACCCCTCTTCTTTCGGCGTTTATCCGGAACCGTGGCGAATTT 660  
Db 601 AACCCACAAGTCTCGTGACTCTCTGTTTCGCTGCTTTCATCGCTACCGTGGAGAGTTC 660  
QY 661 GTATCTCGCGCTGCTATCGGTTTTCGAGACTGAAGGTGCTGCTCTCAAGGCACTTACAAAC 720  
Db 661 GTCTCTCTCTCTGCTGTTGATGAGCTGCTGCTGAGACTGAAGGTGCTGCTCTCAAGGCTATCACCACC 720  
QY 721 ACTAAGGCTGCTCTGCTGTTGATGAGCTGCTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
Db 721 ACCAAGGCTGCTCTGCTGTTGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
QY 781 CTTTCTTAATTCGCTAGCGGATGACATCCCGCTCGATACCCGAGCTGGATATCATATCGTCT 840  
Db 781 CTTTCTTAATTCGCTAGCGGATGACATCCCGCTGGATACCCGAGCTGGATACCCGAGCTGCTG 840  
QY 841 ATCCGGAATCCGGAAGCGCTCCACGATTTCCGACGACCGATCGCTGAGGAAATTCATC 900  
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QY 901 GCGACACCTATGAAATGGGCTCTTCGTTGCTGGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
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QY 961 GCTGCTCTTAACCTGGAACCGTGGCGATGCTGCTATACGACGCTCGGAAACCTTCTTCTCA 1020  
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Db 1081 ATCCAGATTCCTCTCCAGTTCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140

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Db 1201 CTCCTCGCAGGTGAGAGACCTCTATCAGACATCTCTCCATTCGACCAAAACCGCTTTGGT 1260  
Qy 1261 ATTGGCAATCCAAAGCAACCGGTCGGCCAAAGTTAA 1296  
Db 1261 ATTGGTAAGTCCAAAGCAACCTGGTCTGCATCCTAA 1296

RESULT 11

US-08-391-339-17  
; Sequence 17, Application US/08391339  
; Patent No. 5463175  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dennis R. Hoerner, Jr.,  
; ADDRESSEE: Monsanto Co. B&F  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391,339  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/156,968  
; FILING DATE:  
; APPLICATION NUMBER: US/07/717,370  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner, Dennis R., Jr.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10533)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1296 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (recombinant)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1296  
US-08-391-339-17

Query Match 77.7%; Score 1006.4; DB 1; Length 1296;  
Best Local Similarity 86.08; Pred. No. 4.8e-300;  
Matches 1115; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

Qy 1 ATGGCTGAGAACCAACAAAAAGTAGGACATCGCTGGAGCTGGAATCGTTGGTGTATGCACT 60  
Db 1 ATGGCTGAGAACCAACAAAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTATGCACT 60  
Qy 61 GCTTTGATGCTTCAACGTCGGTGATTCNAAGTCACCTTGATTTGACCCCAACCCCTCGTGGC 120  
Db 1141 TTTGGTCACGGTCATCTCGGTATGACAGGTGCTCCCATGACTGCAACTCTCGTCTCAGAG 1200

Db 61 GCTTTGATGCTTCAACGTCGGTGATTCNAAGGTTCACCTTTGATTTGATTCNAACCCCAACAGGT 120  
Qy 121 GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCGCTCGTCCCTCATGTGCC 180  
Db 121 GAAGGTGCCTCTTTCGGTAACGCTGGTTGCTTCAACGGTTCCTCGTTGTTCCTCAATGTGCC 180  
Qy 181 ATGCCGGGAAACTTTGACGAGCGTCCGGAAGTGGTCTCTTGACCCGATGGGCGGTGTGTCA 240  
Db 181 ATGCCAGGAAACTTTGACATVAGGCTTCCAAAGTGGCTTCTTGACCCCAATGGGTCCATGTGCC 240  
Qy 241 ATCCGGTTCAGCTATTTTCCAAACCATCATGCTGGTTGATTCGGCTTCTGTACGCCGA 300  
Db 241 ATCCGTTTCGGCTACTTTCCAAACCATCATGCTGGTTGATTCGGTTCCTGTCTCGA 300  
Qy 301 AGACCAAAAGGTGAAGGAGCAGCGAAAGCACTCCCAATCTCATCAAGTCCACCGTGTG 360  
Db 301 AGACCAAAAGGTGAAGGAGCAAGCTAAGGCACTCCGTAACCTCATCAAGTCCACCTGTG 360  
Qy 361 CCTGTGATCAAGTCATTTGGCGGAGGAGGCTGATGGGAGCCATCTGTATCCGCGATGAAGGT 420  
Db 361 CCTTTGATCAAGTCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAGGT 420  
Qy 421 CATCTGACCGTATATCGTGGAGAGCAGACTTCGCCAAGGACCGCGGAGGTGGGAACTG 480  
Db 421 CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAGGAGCCGTTGGAGGTTGGGAACTT 480  
Qy 481 CGGGTCTCAACGGTGTTCGCACGCGAGATCCTCTCTGCTGATGCTTTCGGCTGATTTCCGAT 540  
Db 481 CGTGTCTCAACGGTGTTCGTAACCTCAATCCTCAGCGCTGATGCAATCGGTCGATTTCCGAT 540  
Qy 541 CCTAACTTGTCTCAGCGCTTTTACCAAGGGCAATCTTATAGAAGAGAACGGTTCACACGAT 600  
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Qy 601 AATCGCAAGGCTCGTCACCGCTCTTGTTCGGCGCTTTTATCGCGAAACGGTGGCGAAATTT 660  
Db 601 AATCGCAAGGCTCGTCACCGCTCTTGTTCGGCGCTTTTATCGCGAAACGGTGGCGAAATTT 660  
Qy 661 GTATCTGCGCGTGTCTCATCGGTTTGTAGACTGAAGTTCGCTCTCTCAAAAGGCAATACAACC 720  
Db 661 GTGTCTGCTGCTGTATTCGGATTCGAGACTGAAGTTCGCTCTCAAAAGGATTCACACACC 720  
Qy 721 ACTAAGGCTTCTGGCTGTTGTGATGACGCTGTGTGTGAGCTGGTGGTGCACACTTAAATCA 780  
Db 721 ACTAAGGCTTCTGGCTGTTGTGATGACGCTGTGTGTGAGCTGGTGGTGCACACTTAAATCA 780  
Qy 781 CTGTCTAATTCGCTAGCGGATCAGATCCGCTCGATACCGAACCTGGATATCATATCATCTGC 840  
Db 781 CTGTCTAATTCGCTAGCGGATCAGATCCGCTCGATACCGAACCTGGATATCATATCATCTGC 840  
Qy 841 ATCCGGAATCCGGAAGCGCTCCACGCAATCCGACGACCGATGCGTCAGGAAATTCATC 900  
Db 841 ATCCGGAATCCGGAAGCGCTCCACGCAATCCGACGACCGATGCGTCAGGAAATTCATC 900  
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Db 901 GCTACTCTATGGAGATGGGTCTTCGTGTGCTGGTAAACCGTTGAGTTCGCTGGTCTCACT 960  
Qy 961 GCTGCTCCTAACTGGAAACGTCGCGCATGTGCTATACGCGACGCTCGGAAACCTTCTTCCA 1020  
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Db 1021 GCTCTCGCTCCTGCCAGTTCAGAACGATATTCCTCAAGTGGATGGTTCGCTCCAAGC 1080  
Qy 1081 ATTCTGTATCTCTTCCAGTGGTGTGCTGCAACTCTGTACACCCGACGATATCTATGCT 1140  
Db 1081 ATCCCGGATTCCTTCCAGTGGTGTGCTGCTACCCGCTACTCCAGACGCTATCTACGCT 1140  
Qy 1141 TTTGGTCACGGTCATCTCGGTATGACAGGTGCTTCAATAGTGCACACTCTCGTCTCAGAG 1200  
Db 1141 TTTGGTCACGGTCACCTCGGTATGACTGCTCCCAATGACCGCAACCCCTCGTCTGAG 1200

QY 1201 CTCTCCAGGCGGAAAGACCTCAATCGACATTTCCGCCCTTCCACACAAACCGCTTTGGT 1260  
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QY 1261 ATTGGCAAAATCCAAAGCAAAACGGGTCCGGCAAGTTAA 1296  
Db 1261 ATTGGTAAGTCCAAGCAAACTGGTCTGCATCCTAA 1296

RESULT 12

US-08-484-274A-17  
; Sequence 17, Application US/08484274A  
; Patent No. 5776760  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,274A  
; FILING DATE: 07 June 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Patterson, Melinda L.  
; REGISTRATION NUMBER: 33,062  
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (713)789-2679  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1296 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (recombinant)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1296  
US-08-484-274A-17

Query Match 77.7%; Score 1006.4; DB 2; Length 1296;  
Best Local Similarity 86.0%; Pred. No. 4.8e-300;  
Matches 1115; Conservative 0; Mismatches 181; Indels 0; Gaps 0;  
QY 1 ATGGCTGAGAACCAACCAAAAGTAGGCTGCTGGAGCTGGAATCGTTGGTGATGCACT 60  
Db 1 ATGGCTGAGAACCAACCAAGAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTGATGCACT 60  
QY 61 GCTTTGATGCTTCAAGCTCGTGGATTCAAAAGTCACCTTGATTGACCCGAAACCCCTCTGGC 120  
Db 61 GCTTTGATGCTTCAAGCTCGTGGATTCAAGGTTACCTTGATTGATCCAAACCCACCAAGGT 120  
QY 121 GAAGGTGCATCGTTTGGGAATCCGGATGCTTCAACGGCTCATCCGTCGCTATGTCC 180  
Db 121 GAAGGTGCCTCTTTCGGTAACCGTGGTTGCTTCAACGGTTCCTCCGTTGTTCCAATGTCC 180  
QY 181 ATCCGGGGAACCTTGACGAGCTGCGGAAGTGGCTCCTTGACCCGATGGGCGGTTGTCA 240  
Db 181 ATCCAGGAAACCTTGACTACCGTTTCCAAAGTGGCTTCTTGACCCCAATGGTTCATTTGTCC 240

QY 241 ATCCGGTTACAGCTATTTTCCAACCATCATGCCCTGGTGTGATTCGCTTTCTGTTAGCCGA 300  
Db 241 ATCCGGTTTCGGCTACTTTTCCAACCATCATGCCCTGGTGTGATTCGCTTTCTGTTAGCCGA 300  
QY 301 AGACCAAAACAAAGGTGAAGAGCAGCGGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360  
Db 301 AGACCAAAACAAAGGTGAAGAGCAGCGTAAAGCACTCCGTAACCTCATCAAGTCCACGTGTG 360  
QY 361 CCTCTGATCAAGTCATTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT 420  
Db 361 CCTTTGATCAAGTCTCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGT 420  
QY 421 CATCTGACCGTATATCGTGAGAGCAGACTTCCCAAGGAGCCGCGGAGGTGGGAACTG 480  
Db 421 CACCTTACCGTGTACCGTGAGAGCAGACTTCCGCAAGGAGCCGCTGGAGGTGGGAACTT 480  
QY 481 CGCGCTCTCAACGGTGTTCGACGCGAGATCCTCTCTGCTGATGCTTTGCGTGTGATTTGAT 540  
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QY 541 CCTAACTTGTGCGATGCTTTTACCAAGGCGATCTTTATAGAAGAGACGCTCACACGATT 600  
Db 541 CCTAACTTGTCTCAGCGCTTTTACCAAGGGAATCTTTATCAAGAGAACGCTCACACCATC 600  
QY 601 AATCCGCAAGGCTCGTGACCCCTCTTCTTTCGGCGTTCCTATCGCAACGCTGGCGAAATTT 660  
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QY 661 GTATCTGCGCGTGTATCGTGGTGTGAGACTGAAGGCTGCTCTCAAGAGCATTTACAAAC 720  
Db 661 GTCTCTGCTGCTGTATATCGGATTCGAGACTGAAGGCTGCTCTCAAGGCTATCACCAAC 720  
QY 721 ACTAAGGCTGCTGCTGCTGTTGATGAGCTGTTGTCAGCTGCTGCACACTCTAAATCA 780  
Db 721 ACCAAGGCTGCTGCTGCTGTTGATGAGCTGTTGTCAGCTGCTGCACACTCTCAAAGTCT 780  
QY 781 CTTCCTAATTCGCTAGCGGATGACATCCCGCTCGATACCGCAAGCTGGATATCATATGCTC 840  
Db 781 CTTCCTAATTCGCTAGCGGATGACATCCCGCTCGATACCGCAAGCTGGATATCATATGCTC 840  
QY 841 ATCGCAATCCGGAAGCGGCTCCAGCATTTCCGACGACCGATGCGTCAGGAAATTCATC 900  
Db 841 ATCGCAATCCGGAAGCGGCTCCAGCATTTCCAGCATTTCCAGCATTTCCAGGAAATTCATC 900  
QY 901 GCGACACCTATGAAATGGGTCTTCGTTGGTGGTACTGTTGAGTTTGGTGTCTCACA 960  
Db 901 GCTACTCTATGAGATGGGTCTTCGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 960  
QY 961 GCTGCTCCTAATTCGGAACGCTGCGCATGCTCTATACCGACCGCTCGAAACCTTTCTTCCA 1020  
Db 961 GCTGCTCCTAATTCGGAACGCTGCGCATGCTCTATACCGACCGCTCGTAAGTTGCTTCCA 1020  
QY 1021 GCCTCGCGCTCGAGTTCTGAAGAACGATATTCAAATGGATGGGTTTCGCTCTCTAGC 1080  
Db 1021 GCCTCGCTCTCGCCAGTTCTGAAGAACGTTACTTCAAGTGGATGGGTTTCGCTCTCAAGC 1080  
QY 1081 ATTCCTGATTCTCTCCAGTGATTGGTGGTCAACTCGTACACCGCAGCTGAATCTATGCT 1140  
Db 1081 ATCCCGGATTCCTCTCCAGTGATTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1140  
QY 1141 TTTGGTTCAGGTCATCTCGGTATGACAGGTTGCTTCAATGACTGCAACTCTCGTCTCAGAG 1200  
Db 1141 TTTGGTTCAGGTCATCTCGGTATGACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1200  
QY 1201 CTCTCGCAGGCGAAAGACCTCAATCGACATTTTCGCGCTTCGACCAAAACCGCTTTGGT 1260  
Db 1201 CTCTCGCAGGCGAAGACCTCTATCGACATCTCTCCATTCGACACCAACCGCTTTGGT 1260  
QY 1261 ATTGGCAAAATCCAAAGCAAAACGGGTCCGGCAAGTTAA 1296  
Db 1261 ATTGGTAAGTCCAAGCAAACTGGTCTGCATCCTAA 1296



RESULT 13  
US-08-391-339-30  
; Sequence 30, Application US/08391339  
; Patent No. 5463175  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dennis R. Hoerner, Jr.,  
; ADDRESSEE: Monsanto Co. BB4F  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391,339  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/156,968  
; FILING DATE:  
; APPLICATION NUMBER: US/07/17,370  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner, Dennis R., Jr.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10533)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 69 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (synthetic)  
US-08-391-339-30

Query Match 5.3%; Score 69; DB 1; Length 69;  
Best Local Similarity 100.0%; Pred. No. 2.5e-12;  
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 714 TACAACTAAGCGTGTCTGGCTGTGATGCAGCTGTGTGCGAGCTGTGCGACACTC 773  
Db 1 TACAACTAAGCGTGTCTGGCTGTGATGCAGCTGTGTGCGAGCTGTGCGACACTC 60  
Qy 774 TAAATCACT 782  
Db 61 TAAATCACT 69

RESULT 14  
US-08-391-339-33  
; Sequence 33, Application US/08391339  
; Patent No. 5463175  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dennis R. Hoerner, Jr.,  
; ADDRESSEE: Monsanto Co. BB4F

; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391,339  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/156,968  
; FILING DATE:  
; APPLICATION NUMBER: US/07/17,370  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner, Dennis R., Jr.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10533)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 69 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (synthetic)  
US-08-391-339-33

Query Match 5.3%; Score 69; DB 1; Length 69;  
Best Local Similarity 100.0%; Pred. No. 2.5e-12;  
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1128 CGTAATCTATGCTTTTGGTCACGGTCATCTCGGTATGACAGTGTCTCCAATGACTGCAAC 1187  
Db 1 CGTAATCTATGCTTTTGGTCACGGTCATCTCGGTATGACAGTGTCTCCAATGACTGCAAC 60  
Qy 1188 TCTCGTCTC 1196  
Db 61 TCTCGTCTC 69

RESULT 15  
US-08-484-274A-30  
; Sequence 30, Application US/08484274A  
; Patent No. 5776760  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,274A  
; FILING DATE: 07 June 1996  
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Patterson, Melinda L.  
REGISTRATION NUMBER: 33,062  
REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (713)789-2679  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 69 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (synthetic)  
US-08-484-274A-30

Query Match 5.3%; Score 69; DB 2; Length 69;  
Best Local Similarity 100.0%; Pred.No. 2.5e-12;  
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 714 TACAACCACTAAGCGTGTCTGATGCGAGCTGTTGTCAGCTGGTGCACACTC 773  
|||||  
Db 1 TACAACCACTAAGCGTGTCTGATGCGAGCTGTTGTCAGCTGGTGCACACTC 60  
QY 774 TAAATCACT 782  
|||||  
Db 61 TAAATCACT 69

Search completed: January 1, 2001, 03:18:19  
Job time: 29323 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 01:12:46 ; Search time 3327.86 Seconds  
(without alignments)  
2407.829 Million cell updates/sec

Title: US-08-484-274-7  
Perfect score: 1296  
Sequence: 1 ATGGCTGAGAACCAAAAA.....AAACGGGTCCGCCAAGTTAA 1296

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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7: gb\_est7:\*  
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10: gb\_est10:\*  
11: gb\_est11:\*  
12: gb\_est12:\*  
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15: gb\_est15:\*  
16: gb\_est16:\*  
17: gb\_est17:\*  
18: gb\_est18:\*  
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116: gb\_gss17:\*







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FEATURES
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  /organism="Homo sapiens"
  /db_xref="taxon:9606"
  /clone="IMAGE:2277213"
  /clone_lib="NCI_CGAP_Utd"
  /tissue_type="serous papillary carcinoma, high grade, 2
  pooled tumors"
  /lab_host="DH10B"
  /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
  Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
  Average insert size 1.48 kb. Life Technologies catalog #:
  11542-016"
BASE COUNT      124 a 128 c 135 g 90 t
ORIGIN

Query Match      2.9%; Score 38; DB 12; Length 477;
Best Local Similarity 51.1%; Pred. No. 1.3;
Matches 89; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy 447 AGACTTCGCCAAGGACCGGAGGTGGGAAGTGGCGGCTCTCAACGGTGTTCGCACGCA 506
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Db 315 AGCCCTGGCAGGGGTGGGTACCAGAGATGCTGCTTCCCCCAAGCGTGCCTCT 256
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 507 GATCCTCTCTGCTGATGCTTTGGCGATTTCGATGCTTAACCTGTGCGCATGCTTTTACCAA 566
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Db 255 GCCTCATTTCTGAGGCTCTTCGGGGTCTGTGCTCATTTGGCGGCTGTGTTCAACAA 196
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 567 GGGCATTCCTATACAGAGACGGTCACAGATTAAATCCGCAAGGGCTCGTCAC 620
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 195 GGGGTTCTCCAGAAAGTGGAGGCGCTTTTCCTTCATCCCTTGGGGCACGGGGC 142
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
LOCUS      AA754683      576 bp      mRNA      EST      21-JAN-1998
DEFINITION      vu20e10.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone
      IMAGE:1181226 5' similar to gb:M16362 Mouse opa repeat mRNA, 3' end
      (MOUSE);, mRNA sequence.
ACCESSION      AA754683
VERSION
KEYWORDS
SOURCE
  ORGANISM
    Mus musculus
    house mouse.
REFERENCE
  AUTHORS
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
    1 (bases 1 to 576)
  TITLE
    Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
    Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
    Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
    Theising,B., Wyllie,T., Lennon,G., Soares,B., Willson,R. and
    Waterston,R.
  JOURNAL
    The WashU-HMHI Mouse EST Project
  COMMENT
    Unpublished (1996)
    Contact: Marra M/Mouse EST Project
    WashU-HMHI Mouse EST Project
    Washington University School of MedicineP
    4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
    Tel: 314 286 1800
    Fax: 314 286 1810
    Email: mouseest@watson.wustl.edu
    This clone is available royalty-free through LLNL; contact the
    IMAGE Consortium (info@image.llnl.gov) for further information.
    MGI:639074
    Seq primer: -28ml3 rev2 ET from Amersham
    High quality sequence stop: 466.
    Location/Qualifiers
1..576
  /organism="Mus musculus"
  /strain="C3H"
  /db_xref="taxon:10090"
  /clone="IMAGE:1181226"

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/clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer 15'
TGTTACCAATCTGAAGTGGAGGGCGCCCTTTTTTTTTTTTTTTTTTTTTT
3'; double-stranded cDNA was ligated to Eco RI adaptors
[AAATTCGATCCTTG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pT7T3 vector.
Library constructed by Bob Barstead. The C2C12 cell line
(available from ATCC, catalog # CRL-1772) differentiates
rapidly, forming contractile myotubes and producing
characteristic muscle proteins."
BASE COUNT      169 a 184 c 137 g 86 t
ORIGIN

Query Match      2.9%; Score 37.4; DB 6; Length 576;
Best Local Similarity 57.1%; Pred. No. 2.1;
Matches 68; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy 649 GGTGGCGAATTTGATCTGCGGTCATCGGTTTGTGAGACTGAAGTCTGCTCTCAA 708
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 194 GCTGTGCGTGTGTTGCTGCTGTTCCCGTAGCATCTGCTGCTGCTGTTGCTCTCGA 135
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 709 GGCATTACAACACTAACGGTGTCTGGCTGTGATGCAGCTGTTGTTCAGCTGGTGC 767
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 134 TATGCTACTGCTGTGTTGCTGCTGCTGCTGCTGCTGTTGTTGTTGCTGCTGCTGC 76
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
LOCUS      AT069309/c      946 bp      mRNA      EST      09-DEC-1999
DEFINITION      mgae0006c09f Magnaporthe grisea Appressorium Stage cDNA Library
      Pyricularia grisea cDNA clone mgae0006c09f 5', mRNA sequence.
ACCESSION      AT069309
VERSION
KEYWORDS
SOURCE
  ORGANISM
    Pyricularia grisea.
    Eukaryota; Fungi; Ascomycota; Ascomycota Incertae sedis;
    Magnaportheaceae; anamorphic Magnaportheaceae; Pyricularia.
    1 (bases 1 to 946)
  REFERENCE
    Choi,W., Fang,E., Sasinowski,M., Wing,R. and Dean,R.A.
    Expressed sequence characterization during appressorium formation
    in rice blast fungus, Magnaporthe grisea
    Unpublished (1998)
  JOURNAL
    Contact: Dean,R.A.
    Clemson University Genomics Institute
    100 Jordan Hall, Clemson University, Clemson, SC 29634, USA
    Tel: 864 656 5737
    Fax: 864 656 4293
    Email: rdean@clemson.edu
    Seq primer: T3 primer (AATTAAACCTCACTAAAGGG)
    High quality sequence stop: 403.
    Location/Qualifiers
1..946
  /organism="Pyricularia grisea"
  /strain="70-15"
  /db_xref="taxon:89476"
  /clone="mgae0006c09f"
  /clone_lib="Magnaporthe grisea Appressorium Stage cDNA
  Library"
  /dev_stage="Germinated conidia on appressorium-Inductive
  surface"
  /note="Vector: pBluescriptII SK(+) Vector; Site_1: EcoRI;
  Site_2: XhoI; The appressorium formation-specific cDNA
  library was constructed from conidia germinated for 5-8
  hr on an inductive surface. The library has an average
  insert size of 1.5 kbp."
BASE COUNT      304 a 270 c 246 g 123 t 3 others

```





Df 232 TGTCGGGCGCTGTATGCCTCCTGCTGCTGCTGCCACCA 186

RESULT 11  
BE253678/c  
LOCUS BE253678 mRNA EST 13-JUL-2000  
DEFINITION G01110742F1 NIH\_MGC\_16 Homo sapiens cDNA clone IMAGE:3351490 5',  
mRNA sequence.  
ACCESSION BE253678  
VERSION BE253678.1 GI:9124097  
KEYWORDS EST.  
SOURCE human,  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE NIF-MGC http://www.ncbi.nlm.nih.gov/MGC/.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Tel.: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: Image.llnl.gov  
Plate: LHCN149 row: C column: 11  
High quality sequence stop: 719.

FEATURES Location/Qualifiers  

	1..816
/organism=	"Homo sapiens"
/db_xref=taxon:	"9606"
/clone=IMAGE:	"3351490"
/library="NIH_MGC_L16"	
/tissue_type="retinoblastoma"	
/lab_host="DH10B (phage-resistant)"	
/notes=Organ:	eye; Vector: pOTB7; Site_1: XhoI; Site_2: EcORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAG(C). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note:	this is a NIH_MGC library."

BASE COUNT 214 A 203 C 206 G 193 T  
ORIGIN

Query Match                2.8%; Score 36.8; DB 34; Length 816;  
Best Local Similarity     54.4%; Pred. No. 3.6;  
Matches 74; Conservative 0; Mismatches 62; Indels 0; Gaps

Qy 640 ATCCGAACGGTGCGGAATTGTATCATCGGTGTATCGTTTCAGACTGAAGGTCTG 699  
||||| |||| | || | ||||| |||| | |||||  
Db 286 AGCGCGACTGCGTCGGCACGGGCTGAGCGGTGTAGGCGCTGATCGGCCCCATGCTG 227  
||||| |||| | || | ||||| |||| | |||||  
Qy 700 GCCTCAAAGGCATTACAACCATAACGGGTGTTCTGGCTGTTGATGCGAGCTGTTGTC 759  
||||| |||| | || | ||||| |||| | |||||  
Db 226 GTCAAGCTGCCCTCCGGCGCGCTGGCCCCTGTCGGGCTGTTGATGCTGCTGCTGCTG 167  
||||| |||| | || | ||||| |||| | |||||  
Qy 760 CTGGTGCGACACTTA 775  
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Db 166 GCTGCTGCTCCACCA 151

RESULT 12  
CNOS15Y8/c  
LOCUS CNOS15Y8 922 bp DNA GSS 26-JUL-1999  
DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC  
BACNT15P08 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.)

ACCESSION	AL106058
VERSION	AL106058.1 GI:5619823
KEYWORDS	GSS.
SOURCE	fruit fly.
ORGANISM	Drosophila melanogaster
REFERENCE	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
AUTHORS	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
JOURNAL	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
TITLE	1 (bases 1 to 922)
COMMENT	Genoscope. Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <a href="http://www.edgp.ebi.ac.uk">http://www.edgp.ebi.ac.uk</a> . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelOBAC11.
FEATURES	Location/Qualifiers
source	1..922
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	/plasmid="pBelOBAC11"
	/db_xref="taxon:7227"
	/clone_lib="proBAC"
	/clone="BACN15P08"
	/note="end : SP6"
BASE COUNT	359 a 147 c 154 g 24 t 238 others
ORIGIN	
Query Match	2.8%; Score 36.8; DB 121; Length 922;
Best Local Similarity	32.2%; Pred. No.3.7;
Matches	59; Conservative 45; Mismatches 79; Indels 0; Caps 0;
Qy	113 CTCCTGCGGAAGTGCATCGTTTCGGAAATGCCGATGCTTCAACGGCTCATCCGTCGTCC 172
Db	:   :          : ::  :  :   :   :   :   :   :   :   :
Qy	173 CTATGTCATCCCGGGAACATTGACGCGCTGCCGAAGTGCTCCTTTGACCCGATGGGCG 232
Db	::  ::   :   :   :   :   :   :   :   :   :   :
Qy	667 CTYTGWMNTGMCMGMMTHTMGHGACBTGMGHMGMTGMTMTMGMGMGMC GCGGG 608
Qy	233 CGTTGTCANTCCGTTTCAGCTATTTTCCAACCATCATGCCCCGTGATTCGCTTTCTGT 292
Db	:   :   :   :   :   :   :   :   :   :   :   :   :   :
Qy	293 TAG 295
Db	
Qy	547 TTG 545
RESULT	13
LOCUS	AI350691/c
DEFINITION	AI350691 377 bp mRNA EST 13-FEB-1999
ACCESION	q040408.x1 Soares_Nhhmpu_S1 Homo sapiens cDNA clone IMAGE:1931510
VERSION	3' similar to contains element MER22 repetitive element ;, MRNA
KEYWORDS	sequence.
SOURCE	EST.
ORGANISM	human.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	1 (bases 1 to 377)
JOURNAL	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)





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OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 03:15:47 ; Search time 7299.04 Seconds  
(without alignments)  
775.497 Million cell updates/sec

Title: US-08-484-274-8  
Perfect score: 1296  
Sequence: 1 ATGGCTGAGAACCAAGAA.....AAACTGGTCTCGATCCTAA 1296

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues

Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*

- 1: gb\_bal:\*
- 2: gb\_bal:\*
- 3: gb\_om:\*
- 4: gb\_ov:\*
- 5: gb\_pat:\*
- 6: gb\_ph:\*
- 7: gb\_pl1:\*
- 8: gb\_pl2:\*
- 9: gb\_pr1:\*
- 10: gb\_pr2:\*
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- 26: em\_vi:\*
- 27: gb\_htg1:\*
- 28: gb\_htg2:\*
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- 30: gb\_in2:\*
- 31: em\_bal:\*
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- 35: gb\_pr4:\*
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- 39: gb\_htg6:\*
- 40: gb\_htg7:\*
- 41: em\_htg1:\*
- 42: em\_htg2:\*
- 43: em\_htg3:\*

- 44: em\_hum5:\*
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- 47: gb\_htg8:\*
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- 49: gb\_htg10:\*
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- 67: em\_htg9:\*
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- 83: gb\_pr7:\*
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- 85: gb\_htg21:\*
- 86: gb\_htg22:\*
- 87: gb\_htg23:\*
- 88: gb\_ro:\*
- 89: gb\_sts1:\*
- 90: gb\_sts2:\*
- 91: gb\_sy:\*
- 92: gb\_un:\*
- 93: gb\_vil:\*
- 94: gb\_v12:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1296	100.0	1296	5	AR016595	AR016595 Sequence
2	1296	100.0	1296	5	I15328	I15328 Sequence 8
3	1288	99.4	1296	5	AR016604	AR016604 Sequence
4	1288	99.4	1296	5	I15337	I15337 Sequence 17
5	1205.2	93.0	1631	5	A59869	A59869 Sequence 1
6	1011.2	78.0	1296	5	AR016594	AR016594 Sequence 7
7	1011.2	78.0	1296	5	I15327	I15327 Sequence 7
8	961.6	74.2	1296	5	AR016593	AR016593 Sequence 6
9	961.6	74.2	1296	5	I15326	I15326 Sequence 6
10	960	74.1	1692	5	AR016591	AR016591 Sequence
11	928.8	71.7	1293	5	AR016592	AR016592 Sequence
12	928.8	71.7	1293	5	I15325	I15325 Sequence 4

13	928.8	71.7	1689	5	I15324	I15324 Sequence 3
14	66.2	5.1	3430	2	PSEAKSD	M69158 Pseudomonas
15	58.8	4.5	62	5	AR016613	AR016613 Sequence
16	58.4	4.5	62	5	I15346	I15346 Sequence 27
17	58.4	4.5	69	5	AR016616	AR016616 Sequence
18	58.4	4.5	69	5	I15349	I15349 Sequence 30
19	56.2	4.3	69	5	AR016619	AR016619 Sequence
20	56.2	4.3	69	5	I15352	I15352 Sequence 33
21	53.6	4.1	68	5	AR016618	AR016618 Sequence
22	53.6	4.1	68	5	I15351	I15351 Sequence 32
23	53	4.1	61	5	AR016617	AR016617 Sequence
24	53	4.1	61	5	I15350	I15350 Sequence 31
25	52.8	4.1	65	5	AR016614	AR016614 Sequence
26	52.8	4.1	65	5	I15347	I15347 Sequence 28
C 27	50.2	3.9	3334	11	AF0356191	AF0356191 Homo sapi
C 28	50	3.9	767	54	EINMAX	M30933 E.tenella a
C 29	50	3.9	2289	2	PSEKSDA	M69159 Pseudomonas
30	49.8	3.8	7218	5	I66494	I66494 Sequence 14
31	49.4	3.8	45438	39	AC017841	AC017841 Drosophill
C 32	49.4	3.8	232361	29	AE003724	AE003724 Drosophill
C 33	46.4	3.6	178553	49	AC024233	AC024233 Homo sapi
C 34	46.4	3.6	209973	57	AC037375	AC037375 Mus muscu
C 35	46	3.5	1586	88	MMU70653	U70653 Mus musculu
C 36	46	3.5	1598	88	MMU70654	U70654 Mus musculu
C 37	45.6	3.5	223469	56	AC069019	AC069019 Mus muscu
C 38	45.2	3.5	186935	48	AC022332	AC022332 Homo sapi
C 39	44.8	3.5	31202	37	AC013022	AC013022 Drosophill
C 40	44.8	3.5	302357	29	AE003443	AE003443 Drosophill
C 41	43.2	3.3	1540	2	EHU17017	U17017 Ectothiorho
C 42	43.2	3.3	186935	48	AC022332	AC022332 Homo sapi
C 43	42.8	3.3	3941	88	RNLAR2	X83546 R.norvegicu
C 44	42.6	3.3	4420	88	U67916	U67916 Mus muscu
C 45	42.6	3.3	5719	88	MMCATS1	AF051726 Mus muscu

## ALIGNMENTS

RESULT	1
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LOCUS	AR016595 1296 bp DNA
DEFINITION	Sequence 8 from patent US 5776760.
ACCESSION	AR016595
VERSION	AR016595.1 GI:3972872
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 1296)
AUTHORS	Barry,G.Francis and Kishore,G.Murthy.
TITLE	Glyphosate tolerant plants
JOURNAL	Patent: US 5776760-A 8 07-JUL-1998;
FEATURES	Location/Qualifiers
source	1..1296
BASE COUNT	271 a 359 c 305 g 361 t
ORIGIN	/organism="unknown"
Query Match	100.0%; Score 1296; DB 5; Length 1296;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1296; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	1 ATCGCTGAGAACCCACAAGAAGTTGGTATCGCTGGAGCTGGAATCGGTGTTGCAC T 60
Db	1 ATGGCTGAGAACCCACAAGAAGTTGGTATCGCTGGAGCTGGAATCGGTGTTGCAC T 60
QY	61 GC TTTCATGCTTCACGFCGTTGGATTCAAGGTTACCTTGATTGATCCAACCACCAGGT 120
Db	61 GC TTTCATGCTTCACGFCGTTGGATTCAAGGTTACCTTGATTGATCCAACCACCAGGT 120
QY	121 GAAGTGCTCTCTTCGCGTAACGCTGGTTGCTTCAACGGTTCCTCCCGTGTGTTCCAATGTCC 180

Qy 1261 ATTGGTAAAGTCCAAAGCAAACTGGTCCGTCATCCCTAA 1296  
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Db 1261 ATTGGTAAAGTCCAAAGCAAACTGGTCCGTCATCCCTAA 1296  
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RESULT 2  
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LOCUS I15328 1296 bp DNA PAT 02-APR-1996  
DEFINITION Sequence 8 from patent US 5463175.  
ACCESSION I15328  
VERSION I15328.1 GI:1250236  
KEYWORDS  
SOURCE unknown.  
ORGANISM unknown.  
REFERENCE 1 (bases 1 to 1296)  
AUTHORS Barry,G.F. and Kishore,G.M.  
TITLE Glyphosate tolerant plants  
JOURNAL Patent: US 5463175-A 8 31-OCT-1995;  
FEATURES Location/Qualifiers  
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          /organism="unknown"  
BASE COUNT 271 a 359 c 305 g 361 t  
ORIGIN

Query Match 100.0%; Score 1296; DB 5; Length 1296;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCTGAGAACCAAGAGTTGGTATCGTCGGAGCTGGAATCGTTGGTTGCACT 60  
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Qy 61 GCTTTGATGCTTCAACGTCGCGGATTCAGGTTACCTGATTGATCCAAACCCACCAAGGT 120  
Db 61 GCTTTGATGCTTCAACGTCGCGGATTCAGGTTACCTGATTGATCCAAACCCACCAAGGT 120  
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Qy 121 GAAGGTGCTTCTTCGGTAACGCTGGTTGCTTCAACGGTTCCCTCCGTTGTTCCAAATGCC 180  
Db 121 GAAGGTGCTTCTTCGGTAACGCTGGTTGCTTCAACGGTTCCCTCCGTTGTTCCAAATGCC 180  
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Qy 181 ATGCCAGAACTTGACTAGGCTTCCAAAGTGGCTTCTTGACCAAGAGGGTCCATGTGCC 240  
Db 181 ATGCCAGAACTTGACTAGGCTTCCAAAGTGGCTTCTTGACCAAGAGGGTCCATGTGCC 240  
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Qy 241 ATCCGTTTCAGCTACTTTCACCAACCATCATGCTTGGTTGATTGCTTCTTCGTTGCTGGA 300  
Db 241 ATCCGTTTCAGCTACTTTCACCAACCATCATGCTTGGTTGATTGCTTCTTCGTTGCTGGA 300  
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Qy 301 AGACCAACAAAGGTGAAGGAGCAAGCTAAGGCATCCGTAACCTCATCAAGTCCACATGTG 360  
Db 301 AGACCAACAAAGGTGAAGGAGCAAGCTAAGGCATCCGTAACCTCATCAAGTCCACATGTG 360  
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Qy 421 CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAAGGACCGTGGAGGTTGGAACTT 480  
Db 421 CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAAGGACCGTGGAGGTTGGAACTT 480  
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Qy 481 CGTCTCTCAACGGTGTTCGTTACTCAAACTCCTCAGCGCTGATGCTTCCGTTGATTTCGAT 540  
Db 481 CGTCTCTCAACGGTGTTCGTTACTCAAACTCCTCAGCGCTGATGCTTCCGTTGATTTCGAT 540  
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Qy 541 CCTAACTGTCTCAGCGCTTTTACCAAGGGAATCCTTATCGAAGAGACGGTCCACACCATC 600  
Db 541 CCTAACTGTCTCAGCGCTTTTACCAAGGGAATCCTTATCGAAGAGACGGTCCACACCATC 600  
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Qy 601 AACCACAAAGTCTCGTGACTCTCTTGTTCGTTTCATCGCTTAACGGTGGAGAGTTC 660  
|||||

Db 601 AACCACAAAGTCTCGTGACTCTCTTGTTCGTCGTTTCATCGCTAAGGTTGAGAGTTC 660  
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Db 661 GTGTCTGCTCGTTATATCGGATTCGAGACTGAAGTCTCCTCTCAAGGGTATCACCACC 720  
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Db 721 ACCAAGCGTGTCTTGTGTTGATGCGAGCTGTTGTTGAGCTGGTGACACCTCAAGTCT 780  
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Qy 781 CTGTCTAACTCCCTTGGTGTGATGACATCCCATTTGGATACCGAAGCTGGATACCATCGTG 840  
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Qy 841 ATGCCAACCCAGAGCTGCTCCACGTTATCCAACTACCGATGCTTCTGGAAGTTTCATC 900  
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Db 841 ATGCCAACCCAGAGCTGCTCCACGTTATCCAACTACCGATGCTTCTGGAAGTTTCATC 900  
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Qy 901 GCTACTCCTATGGAGATGGGTCCTTCTGCTGGAACCGTTGAGTTCGGTGGTCTCACT 960  
Db 901 GCTACTCCTATGGAGATGGGTCCTTCTGCTGGAACCGTTGAGTTCGGTGGTCTCACT 960  
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Qy 961 GCTGCTCTAACTGGAAGCGTCTCAGCTTCTCTACACTCAGCTCGTAAAGTTCCTCCA 1020  
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Qy 1021 GCTCTCGCTCCTGCCAGTTCTGAAGAACGTTTACTCCAAAGTGGATGGGTTCCGTCCTCAAGC 1080  
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Db 1021 GCTCTCGCTCCTGCCAGTTCTGAAGAACGTTTACTCCAAAGTGGATGGGTTCCGTCCTCAAGC 1080  
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Qy 1261 ATTGGTAAAGTCCAAAGCAAACTGGTCCGTCATCCCTAA 1296  
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RESULT 3

AR016604  
LOCUS AR016604 1296 bp DNA PAT 05-DEC-1998  
DEFINITION Sequence 17 from patent US 5776760.  
ACCESSION AR016604  
VERSION AR016604.1 GI:3972881  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1296)  
AUTHORS Barry,G.Francis and Kishore,G. Murthy.  
TITLE Glyphosate tolerant plants  
JOURNAL Patent: US 5776760-A 17 07-JUL-1998;  
FEATURES Location/Qualifiers  
          1..1296  
          /organism="unknown"  
BASE COUNT 267 a 360 c 309 g 360 t  
ORIGIN

Query Match 99.4%; Score 1288; DB 5; Length 1296;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1291; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 301 AGACCAAAACAGGTGAAGGAGCAAGCTTAAGGCACCTCCGTAACCTCATCAAGTCCACTGTG 360  
QY 361 CCTTTGATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTACAGGAAGT 420  
Db 361 CCTTTGATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTACAGGAAGT 420  
QY 421 CACCTTACCGTGTACCGTGGAGAACGACACTTCGCCAAGGACCGTGGAGTTGGGAACTT 480  
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Db 781 CTTGCTTAAGTCCCTTGGTGATGACATCCCATTTGGATACCGAAGCGTGGATACCAATCGTG 840  
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Db 841 ATGCCCAACCCAGAAAGCTGCTCACAGTATTCACAACTACCGATGCTTCTGGAAAGTTTCATC 900  
QY 901 GCTACTCTTATGGAGATGGGTCTTCGTTGCTGGAACCGTTGAGTTCCGTTGCTCTCACT 960  
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QY 961 GGTGCTCTTAAGTGAAGGCTGCTACGTTCTCTACACTCACGCTCGTAAGTTGCTTCCA 1020  
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Db 1141 TTCCGGTCACGGTCACCTCGGTATGACTGGTGTCTCCAAATGACCGCAACCCCTCTTCTGAG 1200  
QY 1201 CTCTCCGAGGTGAGAGACCTCTATCGACATCTCTCTCATTCGCACCAAAACCGTTTCGGT 1260  
Db 1201 CTCTCCGAGGTGAGAGACCTCTATCGACATCTCTCTCATTCGCACCAAAACCGTTTCGGT 1260  
QY 1261 ATTGGTAAAGTCCAAAGCAAACTGGTCTCGATCTCTAA 1296  
Db 1261 ATTGGTAAAGTCCAAAGCAAACTGGTCTCGATCTCTAA 1296  
RESULT 4  
LOCUS I15337 1296 bp DNA PAT 02-APR-1996  
DEFINITION Sequence 17 from patent US 5463175.  
ACCESSION I15337  
VERSION I15337.1 GI:1250245  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1296)  
AUTHORS Barry, G.F. and Kishore, G.M.  
TITLE Glyphosate tolerant plants  
JOURNAL Patent: US 5463175-A 17 31-OCT-1995;  
FEATURES Location/Qualifiers  
source  
BASE COUNT 267 a 360 c 309 g 360 t  
ORIGIN  
Query Match 99.4%; Score 1288; DB 5; Length 1296;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1291; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 ATGGCTGAGAACACAGAAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTTCGACT 60  
Db 1 ATGGCTGAGAACACAGAAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTTCGACT 60  
QY 61 GCATTGATGCTTCACAGTCGTGATTCACAGGTTACCTTGATTCATCCAAACCCACCAAGGT 120  
Db 61 GCATTGATGCTTCACAGTCGTGATTCACAGGTTACCTTGATTCATCCAAACCCACCAAGGT 120  
QY 121 GAAGGTGCTTCTTTCGGTAACCGTGGTTCGTTCAACGGTTCCCTCCGTTGTTCCTCAATGTCC 180  
Db 121 GAAGGTGCTTCTTTCGGTAACCGTGGTTCGTTCAACGGTTCCCTCCGTTGTTCCTCAATGTCC 180  
QY 181 ATGCCAGGAACCTTGACTAGCGTTCCAAAGTGGCTTCCTTGACCCCAATGGGTCCATTGTCC 240  
Db 181 ATGCCAGGAACCTTGACTAGCGTTCCAAAGTGGCTTCCTTGACCCCAATGGGTCCATTGTCC 240  
QY 241 ATCCGTTTACAGTACTTTCACACCATCATGCTTGGTTGATTCTGTTCTTCTTGGTGTGGA 300  
Db 241 ATCCGTTTTCGGCTACTTTCACACCATCATGCTTGGTTGATTCTGTTCTTCTTGGTGTGGA 300  
QY 301 AGACCAAAACAGGTGAAGGAGCAAGCTTAAGGCACCTCCGTAACCTCATCAAGTCCACTGTG 360  
Db 301 AGACCAAAACAGGTGAAGGAGCAAGCTTAAGGCACCTCCGTAACCTCATCAAGTCCACTGTG 360  
QY 361 CCTTTGATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTACAGGAAGT 420  
Db 361 CCTTTGATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTACAGGAAGT 420  
QY 421 CACCTTACCGTGTACCGTGGAGAACGACACTTCGCCAAGGACCGTGGAGTTGGGAACTT 480  
Db 421 CACCTTACCGTGTACCGTGGAGAACGACACTTCGCCAAGGACCGTGGAGTTGGGAACTT 480  
QY 481 CGTCTGCTCAACCGTGTTCGTACTCAAAATCCTCAGCGCTGATGCAATGGCTGATTTTCGAT 540





Db 1174 CAGAAAGTGTCTCCACGATATTTCCAACTACCGATGCTTCTGGAAAGTTTCATCGCTACTCCTA 1233  
QY 911 TGGAGATGGGTCTTGGTGTGGTGGAAACCGTTGAGTTCGGCTGGTCTCAGTCTGCTCCTA 970  
Db 1234 TGGAGATGGGTCTTGGTGTGGTGGAAACCGTTGAGTTCGGCTGGTCTCAGTCTGCTCCTA 1293  
QY 971 ACTGGAAGCGTGTCTACAGTCTCTACACTCAGCTCGTAAGTTGCTTCCAGCTCTCGCTC 1030  
Db 1294 ACTGGAAGCGTGTCTACAGTCTCTACACTCGTCTCGTAAGTTGCTTCCAGCTCTCGCTC 1353  
QY 1031 CTGCCAGTCTGAAGAAGCTTACTCCAAGTGGATGGGTTTCCGTCCAAGCATCCAGATT 1090  
Db 1354 CTGCCAGTCTGAAGAAGCTTACTCCAAGTGGATGGGTTTCCGTCCAAGCATCCAGATT 1413  
QY 1091 CCCTTCCAGTGATTTGGTGTGGTGTACCGGTACTCCAGAGCTTATCTACGCTTTCCGGTCAGG 1150  
Db 1414 CCCTTCCAGTGATTTGGTGTGGTGTACCGGTACTCCAGAGCTTATCTACGCTTTCCGGTCAGG 1473  
QY 1151 GTCACCTCGGTATGACTGTGGTGTCTCAATGACCGCAACCCCTCGTTTCTGAGCTCCTCGCAG 1210  
Db 1474 GTCACCTCGGTATGACTGTGGTGTCTCAATGACCGCAACCCCTCGTTTCTGAGCTCCTCGCAG 1533  
QY 1211 GTGAGAAGACCTCTATCGACATCTCTCCATTTCGCACCAACCCGTTTTCGGTATTTGGTAAGT 1270  
Db 1534 GTGAGAAGACCTCTATCGACATCTCTCCATTTCGCACCAACCCGTTTTCGGTATTTGGTAAGT 1593  
QY 1271 CCAAGCAAACTGGTCTGCAATCCTAA 1296  
Db 1594 CCAAGCAAACTGGTCTGCAATCCTAA 1619

RESULT 6

LOCUS AR016594 1296 bp DNA PAT 05-DEC-1998  
DEFINITION Sequence 7 from patent US 5776760.  
ACCESSION AR016594  
VERSION AR016594.1 GI:3972871  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1296)  
AUTHORS Barry,G.Francis and Kishore,G.Murthy.  
TITLE Glyphosate tolerant plants  
JOURNAL Patent: US 5776760-A 7 07-JUL-1998;  
FEATURES  
Location/Qualifiers  
Source 1..1296  
BASE COUNT 287 a 344 c 332 g 333 t  
ORIGIN

Query Match 78.0%; Score 1011.2; DB 5; Length 1296;  
Best Local Similarity 86.3%; Pred. No. 1.5e-274;  
Matches 1118; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

QY 1 ATGGCTGAGAACCAAGAAGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTTCGACT 60  
Db 1 ATGGCTGAGAACCAAAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCACT 60  
QY 61 GCPTTTCATGCTTCAACGTCGTGGATTCAAGGTTACCTTGATGATCCAAACCCACCAGGT 120  
Db 61 GCPTTTCATGCTTCAACGTCGTGGATTCAAAAGTCACCTTGATTGACCCGAACCCCTCGGC 120  
QY 121 GAAGTTCCTTCTTTCGGTAAACCGTGTCTTCAACGGTTCCTCCGTTGTTCCAATGTCC 180  
Db 121 GAAGTTCCTTCTTTCGGTAAACCGTGTCTTCAACGGTTCCTCCGTTGTTCCAATGTCC 180  
QY 181 ATGCCAGGAAACTTGACTAGCGTTCCAAAGTGGCTTCTTGACCAATGGTTCATTGTCC 240  
Db 181 ATGCCAGGAAACTTGACTAGCGTTCCAAAGTGGCTTCTTGACCAATGGTTCATTGTCC 240

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RESULT 7
115327 LOCUS 115327 1296 bp DNA PAT 02-APR-1996
DEFINITION Sequence 7 from patent US 54631175.
ACCESSION I15327
VERSION I15327.1 GI:1250235
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1296)
AUTHORS Barry,G.F. and Kishore,G.M.
TITLE Glyphosate tolerant plants
JOURNAL Patent: US 54631175-A 7 31-OCT-1995;
FEATURES Location/Qualifiers
source 1..1296
BASE COUNT 287 a 344 c 332 g 333 t
ORIGIN

Query Match 78.0%; Score 1011.2; DB 5; Length 1296;
Best Local Similarity 86.3%; Pred. No. 1.5e-274;
Matches 1118; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

Qy 1 ATGGCTGAGAACACAGAAGGTGGATATCGCTGGAGCTGGAATCGTTGGTGTATGCACT 60
Db 1 ATGGCTGAGAACACAAAAAGTAGGCAATCGCTGGAGCTGGAATCGTTGGTGTATGCACT 60

Qy 61 GCTTTGATGCTTCAACGTCGTGGATTCAAGGTACCTTTGATTGATCCAAACCCACCAAGT 120
Db 61 GCTTTGATGCTTCAACGTCGTGGATTCAAGGTACCTTTGATTGATCCAAACCCCTCTGGC 120

Qy 121 GAAGGTGCTTCTTTGGTAACGCTGGTTGCTTCAACGGTTTCTCGTTGTTTCCAAATGTCC 180
Db 121 GAAGGTGATCGTTTGGGAATGCCGATGCTTCAAGGCTCATCGTCTCCCTATGTCC 180

Qy 181 ATGCCAGAAATTTGACTAGGCTTCCAAAGTGGCTTCTTTGACCAATGGGTCCATTTGCC 240
Db 181 ATGCCGGGAAATTTGACGAGGCTGCCGAAGTGGCTTCTTGACCCGATGGGCGCGTTGTCA 240

Qy 241 ATCGTTTCACTACTTTTCAACCATCATCGCTTGGTTGATTCTGCTTCTGCTGCGA 300
Db 241 ATCGGTTTCACTATTTTCAACCATCATCGCTTGGTTGATTCTGCTTCTGTTAGCCGGA 300

Qy 301 AGACAAACAAGGTGAAGGAGCAAGCTAAGGCACCTCCGTAACCTCATCAAGTCCACTGTG 360
Db 301 AGACAAACAAGGTGAAGGAGCAGGCAAGCACTCCCGCAATCTCATCAAGTCCACGGTG 360

Qy 361 CCTTTGATCAAGTCTTGGCTGAGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGT 420
Db 361 CCTTGTATCAAGTCTTGGCTGAGAGGCTGATGCGGAGCCATCTGATCCGCCATGAAGGT 420

Qy 421 CACCTTACCGTTACCGTGAGAGACACATTCGCCAAGGACCGTGGAGGTTGGCAACTT 480
Db 421 CATCTGACCGTATATCTGTGGAGAGACACATTCGCCAAGGACCGCGGAGTTGGGAATG 480

Qy 481 CTCTGCTCAACGGTGTTCGTACTCAAAATCCTCAGCGCTGATGCAATTCGCTATTTCGAT 540
Db 481 CGGGCTCTCAACGGGTTCGCGACGACAGATCTCTCTGCTGATGCTTTTCGCTGATTTCGAT 540

Qy 541 CTTAACTTGTCTACGCCCTTTTACCAGGGAATCTTATTCGAAGAGACGGTCAACACATC 600
Db 541 CTTAACTTGTCTGCGATGCTTTTACCAGGCGATTTCTTATAGAAGAGACGGTCAACAGAT 600

Qy 601 AACCCACAAGGTCTGCTGACCTCTCTGTTTCTGCTTTTCTGCTTATCATCGTTAACCCTGAGAGTTC 660
Db 601 ATCCGAAAGGGCTGCTGACCCCTCTGTTTCTGCGGCTTTTATCGCAAGCGGTGGGGAATTT 660

Qy 661 GTGCTGCTGCTGTTATCGGATTCGAGACTGAAGGTCTGCTCTCAAGGGGTATCACACC 720
Db 661 GTATCTGGCGCTGTCATCGGTTTGTAGACTGNAAGTCTGCTCTCAAGGGCATTCACACC 720
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Qy 721 ACCAACGGTGTCTTCTGCTGTGATGCGAGCTGTTGTTGCGAGCTGGTGTGCACACTTCCAAGTCT 780
Db 721 ACTAACGGTGTCTTCTGCTGTGATGCGAGCTGTTGTTGCGAGCTGGTGTGCACACTTCTAAATCA 780

Qy 781 CTTGCTAACTCCCTTGGTGATGAGATCCCAATTGGATACCGAAGCTGGATACCAATCCGTCG 840
Db 781 CTTGCTAAATTCGCTAGGCGATGACATCCGCTCGATACCGAAGCTGGATATCATATCCTC 840

Qy 841 ATGCCCAACCCAGAGCTGCTCCAGCTATTCCAACTACCGATGCTTCTGGAAAGTTTCATC 900
Db 841 ATCGCGAATCCGAAGCGCTCCACGCATTCGACGACCGATGCGTCAAGAAAATTCATC 900

Qy 901 GCTACTCTATGGAGATGGGTCTTTCGTTGCTGGAACCGTTGAGTTCGCTGGTCTCACT 960
Db 901 CCGACACCTATGGAATGGGTCTTTCGTTGCTGCTACTGTTGAGTTCGCTGGTCTCACA 960

Qy 961 GCTGCTCCTAACTGAAGCGTCTCACGTTCTCTACACTCACGCTCCGTTAAGTTCGTTCTCA 1020
Db 961 GCTGCTCCTAACTGGAAACGTGCGCATGTCTATACGCACGCTCGAANAACCTCTTCTCCA 1020

Qy 1021 GCTCTCGCTTCCGACGTTCTGAAGAACGTTTACTCCAAAGTGGATGGGTTTCCGTCCAAAGC 1080
Db 1021 GCCCTCGCGCTCGGAGTTCTGAAGAACGATATTCCAAATGGATGGGTTTTCGTCTTAGC 1080

Qy 1081 ATCCAGATTCCTTCCAGTATTGGTCTGCTACCCGCTACTCCAGAGCTTATCTACGCT 1140
Db 1081 ATTCTGATTTCTTCTTCCAGTATTGGTCTGCTGCAACTCTGACCCGAGCTAATCTATGCT 1140

Qy 1141 TTGCTGACGCTACCTCGGTATGACTGCTGCTCCAAATGACGCAACCTCGTTTCTGAG 1200
Db 1141 TTGCTGACGCTACCTCGGTATGACAGGTGCTCCAAATGACTGCAACTCTCGTCTCAGAG 1200

Qy 1201 CTCTTCGAGGTGAGAACACCTCTATCGACATCTCTCCATTCGCAACCAACCGTTTTCGCT 1260
Db 1201 CTCTTCGAGCGGAAAGACCTCAATCGACATTTGCGCCTTCGCAACCAACCGCTTTCGT 1260

Qy 1261 ATTTGATAGTCCAGCAAACTGGTCTCGATCCTTAA 1296
Db 1261 ATTTGCAATCCAAAGCAACGGGTCCGGCAAGTTAA 1296

RESULT 8
AR016593 LOCUS AR016593 1296 bp DNA PAT 05-DEC-1998
DEFINITION Sequence 6 from patent US 5776760.
ACCESSION AR016593
VERSION AR016593.1 GI:3972870
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1296)
AUTHORS Barry,G.Francis and Kishore,G.Murthy.
TITLE Glyphosate tolerant plants
JOURNAL Patent: US 5776760-A 6 07-JUL-1998;
FEATURES Location/Qualifiers
source 1..1296
BASE COUNT 286 a 368 c 361 g 281 t
ORIGIN

Query Match 74.2%; Score 961.6; DB 5; Length 1296;
Best Local Similarity 83.9%; Pred. No. 1.5e-260;
Matches 1087; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

Qy 1 ATGGCTGAGAACACAGAAGTTGGTATCGCTGGAGCTGGAAATCGTTGGTGTGTTGCACT 60
Db 1 ATGGCTGAGAACACAAAAAGTAGGCAATCGCTGGAGCGGAATCGTGGCGGTATGTCACG 60

Qy 61 GCTTTGATGCTTCAACGTCGTGGATTCAAGGTACCTTTGATTGATCCAAACCCACCAAGT 120
Db 61 GCGCTGATGCTTCAAGCGCGGGATTCAAGGTCACCTTGTGATTGATGACCCGAAACCTCTCTGC 120
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QY 121 GAAGGTCCTTTTCGGTAACGGTGGTGTCAACGGTTCCTCCGTTGGTTCCAAATGTCC 180  
DB 121 GAAGGTCATCCTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC 180  
QY 181 ATGCCAGGAACCTTGACTAGCGTTCGAAGTGGCTTCTTGACCCAATGGGTCCATTGTCC 240  
DB 181 ATGCCGGGAACCTTGACGAGCGTTCGAAGTGGCTCCTTGACCCGATGGGGCCGTTGTCA 240  
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DB 241 ATCCGGTTCAGCTATTTCCNACCATCATGCCCTGGTGTGATTCGCTTCTGTAGCCGGA 300  
QY 301 AGACCAACAAAGGTGAAGGAGCAAGCTAAGGCATCTCCGTAACTCATCAAGTCCACTGTG 360  
DB 301 AGACCAACAAAGGTGAAGGAGCAGGCGGAAAGCACTCCGCCAATCTCA/CAAGTCCACGGTG 360  
QY 361 CCTTGTATCAAGTCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCAGGAAGGT 420  
DB 361 CCTGTATCAAGTCTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT 420  
QY 421 CACCTTACCGTCTACCGTGGAGAGCAGACTTCCCAAGGACCGTGGAGGTGGGAATTT 480  
DB 421 CATCTGACCGTATATCTGGAGAGCAGACTTCCCAAGGACCGCGGAGGTGGGAATCTG 480  
QY 481 CGTCGTCTCAACGGTGTTCGTACTCAAACTCCTCAGCGCTGATGCATTCGCTGATTCGAT 540  
DB 481 CGCGCTCTCAACGGTGTTCGCACGCAGATCTCAGCGCCGATGCTTTCGCGGATTCGAT 540  
QY 541 CCTAATCTGTCTACGCGCTTTACCAAGGGAATCCTTATCGAAGAGACGGTCACACATC 600  
DB 541 CCGAATCTGTGCGATGCTTTTACCAAGGGAATCTTATAGAAGAGACGGTCACACATTT 600  
QY 601 AACCCAAAGTCTCGTACTCTCTCTTCTTCTGCTTCTATCGTAACTGAGAGTTC 660  
DB 601 AATCCGAAGGCTCTGTGACCCCTTCTTCTGCGGTTTATCCGGAACGGTGGGAATTT 660  
QY 661 GTGTCTCTGTGTATTCGGAATTCGAGACTGAAGGTCTGTCTCTCAAGGTTATCACACC 720  
DB 661 GTATCTCGCGTGTCTACGCGCTTGTGACACTGAAGGTAGGCGCTTAAAGGCATTTACAACC 720  
QY 721 ACCNACGGTGTCTGTCTGTGATGAGCTGTGTTGTCAGCTGGTGCACACTCCAAGTCT 780  
DB 721 ACNAGCGGCTGTGCGCGTGTGATGAGCGGTGTGTCAGCGCGGCGCACACTCGAATCA 780  
QY 781 CTGTCTAACTCCCTTGGTGTGATGACATCCCATTTGGATACCGAACTGGATACCATCGTG 840  
DB 781 CTGTCTAACTCTAGCGATGACATCCCGCTCGATACCGAAGCTGGATATCATATGCTC 840  
QY 841 ATGCCCAACCCAGAGTGTCTCCACGTAATTTCCAACTACCGATGCTTCTGGAAGTTTCATC 900  
DB 841 ATCCGAATCCGGAAGCGCTCCACGCAATTTCCGACGACCGCATGCTCAGGAAATTCATC 900  
QY 901 GCTACTCTATGAGATGGGCTTCTCGTGTGCTGGAAACCGTTCGATTCGCTGGTCTCACT 960  
DB 901 GCGACACTATGAAATGGGCTTCTCGGTTGGCGGTACGGTTTGTGTTCTGGGCTCACA 960  
QY 961 GCTGCTCTAACTGGAAGCTGTCTACGTTCTCTACACTCACGCTCGTAAGTTGCTTCCA 1020  
DB 961 GCGGCTCTAACTGGAACGCTGCGCATGTCTATACGCACTCGAAGCTTCATTTCCA 1020  
QY 1021 GCTCTGCTCTCCGAGTTCTGAAGAACGTTACTTCCAAAGTGGATGGTTCGCTCCAAAGC 1080  
DB 1021 GCGCTCGCGCTCGAGTTCTGAAGAACGATATTTCCAAATGGATGGGTTTCGCGCCGAGC 1080  
QY 1081 ATCCAGATTCCTTCCAGTATTGTGCTGCTACCGTACTCCAGACGTTATCTAGGCT 1140  
DB 1081 ATCCCGGTTTCGCTCCCGTGTATGGCCGGGCAACCGGACACCCGACGTAATCTATGCT 1140  
QY 1141 TTCGGTCACGGTTCACCTTCGGTATGACTGGTGTCTCAATGACCGCAACCCCTGTTCTGAG 1200  
DB 1141 TTCGGCACGGTTCATCTCGCATGACAGGGGCGCGGATGACCGCAACGGCTCTCAGAG 1200

QY 1201 CTCCTCAGAGTGAGAAGACCTCTATCGACATCTCTCAATTCGACCAAAACCGTTTCGGT 1260  
DB 1201 CTCCTCAGCGGAAAAGACCTCAATCGACATTTTCGCCCTTCGCAACAAACCGCTTTGGT 1260  
QY 1261 ATTGGTAAGTCCCAAGCAAACTGGTCTCTGCATCTCTAA 1296  
DB 1261 ATTGGCAATTCCAAGCAAAACGGGTCGCGCAAGTTAA 1296  
RESULT 9  
LOCUS I15326 1296 bp DNA PAT 02-APR-1996  
DEFINITION Sequence 6 from patent US 5463175.  
ACCESSION I15326  
VERSION I15326.1 GI:1250234  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1296)  
AUTHORS Barry,G.F. and Kishore,G.M.  
TITLE Glyphosate tolerant plants  
JOURNAL Patent: US 5463175-A 6 31-OCT-1995;  
FEATURES Location/Qualifiers  
source I..1296  
BASE COUNT 286 a 368 c 361 g 281 t  
ORIGIN  
  
Query Match 74.2%; Score 961.6; DB 5; Length 1296;  
Best Local Similarity 83.9%; Pred.No.1.5e-260;  
Matches 1087; Conservative 0; Mismatches 209; Indels 0; Gaps 0;  
  
QY 1 ATGGCTCAGAACCAACAAGAAGTTGGTATCGCTGAGCTCGAATCGTTGGTGTGGACT 60  
DB 1 ATGGCTCAGAACCAACAAGAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGTATGACG 60  
QY 61 GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTTGATTGATCCAAACCCACCAAGT 120  
DB 61 GCGCTGATGCTTCAGCCCGCGGATTCAAAAGTCACTTTGATTGACCCGAACCCCTTCCTGGC 120  
QY 121 GAAGGTCTTCTTTCGGTAACGCTGGTGTGCTTCAACGGTTCCTCCGTTGTGTCCAAATGTC 180  
DB 121 GAAGGTGCATCGTTTGGGAATGCGGATGCTTCAACGGCTCATCCGTCGTCCTTATGTCC 180  
QY 181 ATGCCAGGAACCTTGACTAGCGTTCGAAGTGGCTTCTTGACCCAATGGGTCCATTGTCC 240  
DB 181 ATGCCGGGAACCTTGACGAGCGTGCAGAGTGGCTCCTTGACCGGATGGGGCCGTTGTCA 240  
QY 241 ATCCGTTTACGTACTTTCACCAACCATCATGCTTGGTGTGATTCGTTTCTGCTTGTCTGGA 300  
DB 241 ATCCGGTTCAGCTATTTTCCNACCATCATGCCCTGGTGTGATTCGCTTCTGTAGCCGGA 300  
QY 301 AGACCAACAAAGGTGAAGGAGCAAGCTAAGGCATCTCCGTAACTCATCAAGTCCACTGTG 360  
DB 301 AGACCAACAAAGGTGAAGGAGCAGGCGGAAAGCACTCCGCCAATCTCA/CAAGTCCACGGTG 360  
QY 361 CCTTGTATCAAGTCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCAGGAAGGT 420  
DB 361 CCTGTATCAAGTCTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT 420  
QY 421 CACCTTACCGTCTACCGTGGAGAGCAGACTTCCCAAGGACCGTGGAGGTGGGAATTT 480  
DB 421 CATCTGACCGTATATCTGGAGAGCAGACTTCCCAAGGACCGCGGAGGTGGGAATCTG 480  
QY 481 CGTCGTCTCAACGGTGTTCGTACTCAAACTCCTCAGCGCTGATGCATTCGCTGATTCGAT 540  
DB 481 CGCGCTCTCAACGGTGTTCGCACGCAGATCTCAGCGCCGATGCTTTCGCGGATTCGAT 540  
QY 541 CTTAACTTGTCTCACGCGCTTTACCAAGGGAATCCTTATCGAAGAGACGGTCACACATC 600  
DB 541 CCGAATCTGTGCGATGCTTTTACCAAGGGAATCTTATAGAAGAGACGGTCACACATTT 600



QY	1081	ATCCAGATTCCCTTCCAGTGATTGGTGGCTACCGGTACTCCAGACGTTATCTACGCT	1140
Db	1200	ATCCCGGATTTCGCTCCCGGATTGGCGGCAACCGGACACCGGATTAATCTATGCT	1259
QY	1141	TTCCGGTCAAGGTACCTCGGTATGACTGGTGTCTCAATGACCGAACCCCTCGTTCTGAG	1200
Db	1260	TTCCGGCATGGTCTATCTCCGATGACAGGGGCGCGATGACCGCAACGCTCGTCTCAGAG	1319
QY	1201	CTCCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTCCGACCAACCCGTTTCGGT	1260
Db	1320	CTCCTCGCAGGCGAAGACCTCAATCGACATTTCCGCTTCGCAACCAACCCGCTTGGT	1379
QY	1261	ATTGGTAAGTCCAAAGCAAACTGCTCTCATCTCTAA	1296
Db	1380	ATTGGCAAAATCCAAGCAACCGGTCCGCAAGTTAA	1415
RESULT 11			
AR016592			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
Source			
BASE COUNT			
ORIGIN			
Query Match			
Best Local Similarity			
Matches 1086; Conservative			
0; Mismatches 207; Indels 3; Gaps 3;			
QY	1	ATGGGTGAGAACACAAAGAGTGTGTATCGCTGGAGCTGGAATCGTTGGTGTTCACCT	60
Db	1	ATGCTCTGAGAACACCAAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGTATGCACG	60
QY	61	GCTTTGATGCTTCAAGCTCGTGATTCAGGTTACCTTGTATGATCCAAACCCACCAAGGT	120
Db	61	GGCTGATGCTTCAGCGCGCGGATTCAAAGTCACCTTGATTGACCGCAACCCCTCTGGC	120
QY	121	GAAGGTGCTTCTTTCGGTAACCGTGGTTGCTTCAACGGTTCTTCCCTGTTGTTCCAATGTCC	180
Db	121	GAAGGTGCTATCGTTGGGAATCCGGATGCTTCAACGGTCTATCCGCTCGCTATGTCC	180
QY	181	ATGCCAGAACTTGACTAGCGCTTCAAAAGTGGCTTCTTGACCAATGGGTCCATTGTCC	240
Db	181	ATGCCGGGAACTTGACGAGCGGTGCCGAAGTGGCTCTCTTGACCCGATGGG-CCGTTGTCA	239
QY	241	ATCCGTTTCAGCTACTTTTCCAAACCATCATCGCTTGGTTGATTCGTTTCTGCTGGA	300
Db	240	ATCCGTTTCAGCTA-TTTCCAACCATCATGCC-TGGTTGATTGCTGTTTCTGTTAGCCGA	297
QY	301	AGACCAAAACAAAGGTGAAGGCAAGCTTAAGCACTCCGTAACCTCATCAAGTCCACTGTG	360
Db	298	AGACCAAAACAAAGGTGAAGGCAAGCGCAAGCACTCCGCAATCTCATCAAGTCCACGGTG	357
QY	361	CCTTTGATCAAGTCTTGGCTGAGGAGGCTGATGTAGCCACCTTATCCGTTCACGAAGT	420
Db	358	CCTCTCATCAAGTCAATTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGT	417
QY	421	CACCTTACCGTGTACCGTGGAGNAGACACTTCGCCAAGGAGCGGTGGGAACTT	480

Db	418	CATCTGACCCTATATATCGTGGAGAAGCAGACTTCGCCAAGGACCGCGAGGTTGGAACTG	477
QY	481	CGTCGCTCAACGGTGTTCGTACTCAAAATCCTCAGCGCTCATGCATTCGCTGATTTCCGAT	540
Db	478	CGCGCTCAACGGTGTTCGCACGAGATCCTCAGCGCCGATCGTTCCGGGATTTCCGAT	537
QY	541	CCTAACTTGTCTCACGCCCTTTACCAAGGAATCCTTTATCGAAGAGAACGGTTCACACCATC	600
Db	538	CCGAACCTTGTGCGATCGCTTTACCAAGGGCATCTTATACAGAGAACGGTTCACACGATT	597
QY	601	AACCCACAAGGTCTCGTACTCTCTTGTTCGTGCTTTCAITCGCTAACGGTGGAGAGTTTC	660
Db	598	AATCCCAAGGGTCTGTGACCTCTTTGTTTCGGCTTTTATCGCAACGGTGGCGAATTC	657
QY	661	GTCTCTGCTGCTGTATATCGGATTCGAGACTGAAGGTGCTGCTCTCAAGGGTATCACCAAC	720
Db	658	GTATCTGCGCGTCTATCGGCTTTGAGACHTGAAGGTAGGGCGCTTAAAGGCATTTACAAAC	717
QY	721	ACCAACGGTGTCTGCTGTGATGCAGCTGTGTTGTCAGCTGGTGCACACTCCAAAGTCT	780
Db	718	ACGAACGGCGTTCGTGCGCTTGATGCAGCGTGTGTCGACCGCGCACACTCGAAATCA	777
QY	781	CTTGTCTAACTCCCTTGGTATGACATCCCAATTCGGATACCGAAGCTGGATACCACTCGTG	840
Db	778	CTTGTCTAAATTCGTAGCGGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC	837
QY	841	ATGCCCAACCCAGAAGCTGCTCCACGTAATTCCAACTACCGATGCTTCTGGAAAGTTTCATC	900
Db	838	ATCGCAATTCGGAAGCGCTCCACGATTCGCAAGACCGATGCGTCAGGAAATTCATC	897
QY	901	GCTACTCTTATGGAGATGGTCTTCTGTTGCTGGAAACCGTTGAGTTCGCTGGTCTCACT	960
Db	898	GGCACACCTTATGCAAAATGGGCTTCGCTGGCGGGTAGGGTTCAGTTTCGCTGGGCTCACA	957
QY	961	GCTGCTCTTAACTTGAAGCGTGTCTCAGCTTCTACACTCACCTCGTAAGTGTCTTCCA	1020
Db	958	GGCGCTCTTAACTGGAACGTCGCGCATGTCTATACGCAACGCTCGAATACTTCTTCCA	1017
QY	1021	GCCTCTGCTCTGCCAGTTCTGAAGAACGTTACTTCAAGTGGATGGTTCCTGTCGAAGC	1080
Db	1018	GCCTCTGCGCTCGGAGTTCTGAAGAACGATATTCAAATGGATGGGTTCCGCGCGAGC	1077
QY	1081	ATCCAGATTCCCTTCCAGTGATTGGTGTGCTACCGCTACTCCAGACGTTATCTACGCT	1140
Db	1078	ATCCCGGATTTCGCTCCCGTGATTGGCGGGCAACCGGACACCCGACGTAATCTATGCT	1137
QY	1141	TTCCGGTCAAGGTCACTCGTATGACTGGTCTCGAATGACCGCAACCCCTCGTTTCTGAG	1200
Db	1138	TTCCGGCATGGTCTATCGGCGATGACAGGGGCGCGGATGACCGCAACGCTCTCAGAG	1197
QY	1201	CTCCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTCGCAACCAACCCGTTTCGGT	1260
Db	1198	CTCCTCGCAGGCGAAGACCTCAATCGACATTTTCGCCCTTCGCAACCAACCCGTTTGGT	1257
QY	1261	ATTGGTAAGTCCAAAGCAAACTGCTCTGCTGATCTCTAA	1296
Db	1258	ATTGGCAAAATCCAAGCAACCGGTCCGCAAGTTAA	1293

RESULT 12			
LOCUS	I15325	Sequence 4 from patent US 5463175.	PAT 02-APR-1996
DEFINITION	I15325		
ACCESSION	I15325		
VERSION	I15325.1	GI:1250233	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1293)		
AUTHORS	Barry,G.F. and Kishore,G.M.		
TITLE	Glyphosate tolerant plants		
JOURNAL	Patent: US 5463175-A 4 31-OCT-1995;		

FEATURES		Location/Qualifiers			
source		1. .1293	/organism="unknown"		
BASE COUNT	286 a	367 c	359 g	281 t	
ORIGIN					
Query Match		71.7%;	Score 928.8;	DB 5;	Length 1293;
Best Local Similarity		83.8%;	Pred. No. 2.8e-251;		
Matches 1086;	Conservative	0;	Mismatches 207;	Indels	3;
Gaps					
Qy	1	ATGCGCTGAGAACCCACAGAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTTCGCACT	60		
Db	1	ATGCTCTGAGAACCCACAAAAGATAGGCATCGCTGGAGCGGAATCGTGGCGGTATGCAGG	60		
Qy	61	GCCTTGTATGCTTCAACGCTCGTGGATTCAAGGTTTACCTTGATTGATCCAAACCCACCAAGT	120		
Db	61	GCGCTGATGCTTCAGCGCCGCGGATTCANAAGTCACCTGATTGACCCGAAACCTCCTGGC	120		
Qy	121	GAAGGTGCTTCTTTCGGTAACGCTGGTTGCTTCAACGGTTCTCTCGTTTCCAAATGTC	180		
Db	121	GAAGGTGCATCGTTTGGGAATCCGGGATGCTTTCAACGGCTCATCCGTCGCTCATGTCC	180		
Qy	181	ATGCCAGGAAACTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCAATGGGTCCATTGTCC	240		
Db	181	ATGCCGGGAACCTTGACGAGCGTGGCCGAAGTGGCTCCTTGACCCGATGGG-CCGTTGTCA	239		
Qy	241	ATCCGTTTTCAGCTACTTTTCCAAACCATCATCCCTTGGTTGATTGCTTCTTGTCTTGTGGA	300		
Db	240	ATCCGGTTCAGCTA-TTTCCAACCATCATGCC-TGGTTGATTGCTTCTGTTAGCCGA	297		
Qy	301	AGACCAACAAGGTGAAGGAGCAAGCTAAGGCACTCCGTAACCTCATCAAGTCCACTGTG	360		
Db	298	AGACCAACAAGGTGAAGGAGCAGGCGGAAGCACTCCGCAATCTCATCAAGTCCACGGTG	357		
Qy	361	CTTTTGATCAAGTCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCCACGAGGT	420		
Db	358	CCTCTGATCAAGTCATTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT	417		
Qy	421	CACCTTTACCGTGTACCGTGGAGAACGACACTTCGCCAAGGACCGTGGAGCTTGGGAACCT	480		
Db	418	CATCTGACCGTATATCGTGGAGANGCAGACTTCGCCAAGGACCGCGGAGTTGGGNACTG	477		
Qy	481	CGTGTCTCAACGGGTGTCGTACTCAAAATCTCAGCGCTGATGCAATGCGTGATTTTCGAT	540		
Db	478	CGGCGTCTCAACGGTGTTCGCCACGAGATCTCAGCGCGCGATGCGTTGCGGGATTTTCGAT	537		
Qy	541	CCTAACTGTCTCAGCGCTTTACCAAGGGAATCCTTATCGAAGAGAACGGTTCACACCATC	600		
Db	538	CCGAACCTTGTGCGATGCGTTTACCAAGGGCATTTCTTATAGAAGAGAACGGTTCACACGATT	597		
Qy	601	AACCCACAAGTCTCTGTGACTCTCTTTTTCGTGTTTTCATCGCTAACGGTTCGAGAGTTTC	660		
Db	598	AATCCGCAAGGGCTCGTGACCCCTCTTGTTCGGCGTTTTATCCGGAACGGTGGCGNAATTC	657		
Qy	661	GTGCTGCTGCTGTTATCGGATTCGAGACTGAAGTTCGTGCTCTCAAGGGTATCACACAC	720		
Db	658	GTATCTGCGCGTCTCATCGGCTTTGAGACTTGAAGTGAAGGTAGGCGGCTTAAAGGCCATTACAACC	717		
Qy	721	ACCAACGGGTGTTCTTGGTGTGATGCGAGCTGTTGTTGCGAGCTGGTGCACACTCCCAAGTCT	780		
Db	718	ACGAACGGGCTTCTGGCGGTTGATGACGCGGTTGTGCGACGCGCGCGCACACTCGAAATCA	777		
Qy	781	CTTTGCTTAACCTCCCTTGGTGATGACATCCCATTTGGATACCGAAGCTGGATACCACTCGTG	840		
Db	778	CTTGTCTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTGC	837		
Qy	841	ATGCCCAACCCAGAAAGCTGCTCCACGATATTCCAACTACCGATGCTTCTTGGAAAGTTTCATC	900		
Db	838	ATCGCGAAATCCGGAACCCGCTCCACGATTTCCGACGACCGATGCGTCAAGAAATTCATC	897		
Qy	901	GCTACTCCTATGAGATGGGTCTTCGTGTTGCTGGAAACCGTTGAGTTTCGCTGGCTCACT	960		

Db	898	GGACACCTATGGAAATGGGGCTTCGCGTGGGGGTACGGTTGAGTTTCGCTGGGCTCACA	957	
QY	961	GCTGCTCTTAACCTGGAAGCGTCTCACGTTCCTCTACACTCACGCTCGCTAAAGTTGCTTTCCA	1020	
Db	958	CGCGCTCTTAACCTGGAACGTCGGCATCTGCTCTATACGCAGCTCCGAAACCTCTTTCCA	1017	
QY	1021	GCTCTGCTCTCGCAGTTCTGAAGAAGCTTACTTCAAGTGGATGGGTTCCGTCGCAAGC	1080	
Db	1018	GCCCTCGCGCTTGGAGTTCTGAAGAAGCATATTTCCAAATGGATGGGTTCCGGCCGAGC	1077	
QY	1081	ATCCAGATTCCCTTTCCAGTGAATGGTCTGTTGCTACCCGCTACTCCAGACGTTATCTACGCT	1140	
Db	1078	ATCCCGGATTCCGCTCCCGTGATTGGCGGGCAACCCGGACACCCGACGTAATCTATGCT	1137	
QY	1141	TTCCGTCACGCTACCTCGGTATGACTTGGTCTCCAAATGACCGCAACCCCTCGTTTCTGAG	1200	
Db	1138	TTCCGCCATGTCATCTCGGCATGACAGGGCGCGCATGACCGCAACGCTCGTCTCAGAG	1197	
QY	1201	CTCCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTCGCGACCAACCGTTTCGGT	1260	
Db	1198	CTCCTCGCAGGCGAAAGACCTCAATCGACATTTTCGCCCTTCGCACCAACCCGCTTTGGT	1257	
QY	1261	ATTGGTAACTCCAAGCAAACTGGTCTCTGCATCTTAA	1296	
Db	1258	ATTGGCAAAATCCAAGCAAAAGGTCGCGCAAGTTAA	1293	
RESULT 13				
LOCUS	I15324	1689 bp	DNA	PAT
DEFINITION	Sequence 3 from patent US 5463175.			
ACCESSION	I15324			
VERSION	I15324.1 GI:1250232			
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 1689)			
AUTHORS	Barry,G.F. and Kishore,G.M.			
TITLE	Glyphosate tolerant plants			
JOURNAL	Patent: US 5463175-A 3 31-OCT-1995;			
FEATURES	Location/Qualifiers			
source	1. .1689			
BASE COUNT	381 a	479 c	468 g	360 t
ORIGIN	/organism="unknown"			
Query Match				
Best Local Similarity 71.7%; Score 928.8; DB 5; Length 1689;				
Matches 1086; Conservative 0; Mismatches 207; Indels 3; Gaps 3;				
QY	1	ATGCGTGAAGACCAAGAGTTGGTATCGCTGGAGCTGGAATCGTTGGTGGTTCGACT	60	
Db	120	ATGCTGAGAACCACAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGTATGCAGC	179	
QY	61	GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTTGATTGATCCAAACCCACCAAGT	120	
Db	180	CGCGTGATGCTTACGCCCGCGGATTCAAGTCACCTTGATGACCCGACCCCTCCTGGC	239	
QY	121	GAAGGTGCTCTTTCGGTAAGCGTGGTTGCTTCAACGGTTCCTCCGTTGTTCCAATGTCC	180	
Db	240	GAAGGTGCATCGTTTGGGAATGCGCGATGCTTCAACGGCTCATCCGTCCTCCCTATGTCC	299	
QY	181	ATGCCAGGAACTTGACTAGGTTCCAAAGTGGCTTCTTGACCCAATGGGTCCATTGTCC	240	
Db	300	ATGCCGGGAACTTGACGAGGTCGCGAAGTGGCTCTTGACCCGATGGG-CCGTTGTCA	358	
QY	241	ATCCCTTTCAGCTACTTTCCAAACCATCATGCTTGGTTGATTTCGTTCTTCGCTTCGCGA	300	
Db	359	ATCCGGTTCAGCTA-TTTCCAACCATCATAGCC-TGGTTGATTTCGCTTCTGTGTAGCCGA	416	
QY	301	AGACCAACAAGGTGAAGGAGCAAGCTAAGGCACCTCCGTTAACCTCATCAAGTCCACTGTG	360	



Db	417		AGACCAAAAGTGAAGGACGAGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG	476
QY	361	CTTTTGATCAAGTCCCTTGGCTGAGGAGGCTGATCTAGCCACCTTATCCGCTCAGCAAGGT	420	
Db	477	CTCTGATCAAGTCATTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCCCATGAAGGT	536	
QY	421	CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAAGGACCGTGGAGGACTT	480	
Db	537	CATCTGACCGCTATATCGTGCAGAGCAGACTTCGCCAAGGACCGGAGGTTGGGAACGTG	596	
QY	481	CGTCGCTCAACCGTGTCTGATCTCAATCCTCAGCGCTGATGCATTCGCTGATTCGAT	540	
Db	597	CGCGCTCTCAACCGTGTCTGCACGCGAGATCCTCAGCGCGCATCGTTGCGGGATTCGAT	656	
QY	541	CTTAACCTTGTCTCACCGCTTTACCAAGGGAATCTTATCGAAGAGAACGCTCACACATC	600	
Db	657	CGAATCTTGTGCGTGGCTTTACCAAGGCAATCTTATAGAAGAGAACGCTCACAGATT	716	
QY	601	AACCCACAAAGGCTCGTGACTCTCTTGTTCGTGCTTTCATCGTCAACGGTGGAGATTC	660	
Db	717	AATCCGCAAGGGCTCGTGACCCCTCTTGTTCGGCGTTTATCGCAACGCTGGCGAATTC	776	
QY	661	GTGCTGCTCGTGTATTCGGATTCGAGACTGAAGTGTGCTCTCAAGGGTATCACCAAC	720	
Db	777	GTATCTGCGGCTGTCTACGCGCTTGAAGTGAAGGCTGAAGGCTTAAAGGCATTTACAAC	836	
QY	721	ACCAACGGTGTCTGCTGTGATGAGCTGTGTTGTCAGCTGCTGCACACTCCAAGTCT	780	
Db	837	ACGAACGGGCTTGTGCGGTTGATGACGCGTGTGTCGACGCGGCGCACTCGAATCA	896	
QY	781	CTTGCTAACTCCCTTGGTGATGACATCCCATTTGGATACCGAAGCTGGATACCATCGTG	840	
Db	897	CTTGTCTAACTTTCGCTAGCGGATGATCCTCCGCTCGATACCGCAACGCTGGATCATATCGTC	956	
QY	841	ATCGCCAAACCCCAAGCTGCTCACGATATTCCAACTACCGATGCTTCTGGAAGTTCATC	900	
Db	957	ATCGCGAATCCCGAAGCGGCTCCACGATTTCCGACGACCGCATGCTCAGGAAAATTCATC	1016	
QY	901	GCTACTCTATGAGATGGGCTTCTGCTGTTGCTGGAACCGTTTGAGTTCGGTGGCTCACT	960	
Db	1017	GCACACCTATGGAATGGGCTTCGCTGGCGGGTACGGTTGAGTTCGCTGGGCTCACA	1076	
QY	961	GCTGCTCCTAACTGGAAGCGTGTACGTTCTCTACACTCACGCTCGTAAGTGTCTTCCA	1020	
Db	1077	GCGGCTCCTAACTGGAACGTCGGCATGTCTCTATACGCAACGCTCGAAAACTTCTTCCA	1136	
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QY	1081	ATCCAGATTTCCCTTCCAGTGATTGGTGTGCTACCGGTACTCCAGACGTTATCTACGCT	1140	
Db	1197	ATCCCGATTCGCTCCCGTGATTGGCGGGCAACCCGGACACCCGACGTAATCTATGCT	1256	
QY	1141	TTCCGGTCAGGTCACCTCGGTATGACTGTGCTTCCAATACCGCAACCCCTGTTCTTGAG	1200	
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QY	1201	CTCCTCGCAGGTGAGAGACCTCTATGACATCTCTCCATTCGCAACCAACCGTTTCGGT	1260	
Db	1317	CTCCTCGCAGGCAAGACCTCAATCGACATTTTCGCCCTTTCGCACCAACCCGCTTGGT	1376	
QY	1261	ATTGGTAAGTCCAAGAACTGCTCTCATCTCTAA	1296	
Db	1377	ATTGGCAATCCAAGCAAGGGTCCGGCAAGTTAA	1412	

RESULT 14  
PSEAKSD PSEAKSD 3430 bp DNA BCT 26-APR-1993  
LOCUS Pseudomonas putida alpha-ketoglutarate semialdehyde dehydrogenase  
DEFINITION gene, complete cds.

ACCESSION	M69158	
VERSION	M69158.1	GI:150981
KEYWORDS	ketoglutarate semialdehyde dehydrogenase.	
SOURCE	Pseudomonas putida DNA.	
ORGANISM	Pseudomonas putida	
	Bacteria; Proteobacteria; gamma subdvlslon; Pseudomonas group;	
	Pseudomonas.	
REFERENCE	1 (bases 1 to 3430)	
AUTHORS	Burlingame, R.P., Maruya, A., Ally, A.H., Ally, D. and Backman, K.C.	
TITLE	Nucleotide sequences of hydroxyproline-specific alpha-ketoglutarate semialdehyde dehydrogenase genes from two strains of pseudomonas putida	
JOURNAL	Unpublished (1991)	
FEATURES	Location/Qualifiers	
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	RRTCTQLRTTFARVVRAGGELVVDNAQPERQPLRADLRQVAGLGPVAVGASNF	
	PIAFSVAGDGTASALAGCPVVVKAHSHPGSELVQVAQVAKLGGPAGVFSLLY	
	GGREVGIALVSDPRIKAVFTGSRGSGALCOATQARPEPIFYAEMSEINPVFLFE	
	AALQARAEALAQFVASLTQGGQFCTNPGLVIAPQGPALQREIYDAASEIVRAAAQT	
	MLTPTGISAYQAGVGGLAGNANAAGAGGQGNQCOALPVTQOAEAPLADPALQA	
	EYFGAASLVVACASDSQVHVAHPLEGLTATLQLDADIDRALLLPTLRKAGRIL	
	VNGWPTGVEVCDAMVHGPPATSDARTTSVGTAAILRLRPLRVCYQDFNPALLPQALQ	
	HGNPLQLRLRLDGLKREG"	
BASE COUNT	562 a	1140 c 1157 g 571 t
ORIGIN		

Query Match	5.1%;	Score	66.2;	DB 2;	Length	3430;			
Best Local Similarity	47.7%;	Pred. No.	1.2e-07;						
Matches	194;	Conservative	0;	Mismatches	213;	Indels	0;	Gaps	0;
QY	29	TCGCTGAGCTGGAATCGTTGGTGTGTTTGCACCTGCTTTGATGCTTCAACGCTCGTGGATTCA	88						
Db	2214	TGGTGGCGCGGGATGTGCGGCTTCCTGTGCCCTGCAACTGCCCGCGCAGGCGCTCC	2273						
QY	89	AGGTTACCTTGATGTGCAAAACCCACAGGTGAAGGTGCTTTCGTTGAACGCTGGTT	148						
Db	2274	GGGTGCTATTTGGTCGACCGCAGCACCGGCCATGCGGGGTCTCTATGCGCAACCGCGGC	2333						
QY	149	GCYTCAACGGTTCCTCGCTGTTTCCCAATGTCCATGCCAGGAAACTTCACTAGCGTTCCAA	208						
Db	2334	ACCTGGCCACGAGAGGTGTTCCTCGATTGCCGACCTGTGCGATCCTCAAGCGCTTGC	2393						
QY	209	AGTGGCTTCTTGACCCAAATGGGTCCATTTGTCCTCCCTTTTCAGTACTTTTCCAAACCATCA	268						
Db	2394	GCATGCTGCTGGACCGCATGGGCCCACTGCGCCTGGACTGGAAGTACCTGCCACAGGCCA	2453						
QY	269	TGCGTTGGTTGATTCGTTTCTTGTGCTGGAAGACCAACAAAGGTGAAGAGCAAGCTA	328						
Db	2454	TGCGCTGCTTACCGCGCTGCTGCTCAACCTGCGCGCGCGCGCTTCCAGCGCAGTGTGG	2513						
QY	329	AGGCACCTCCGTAACCTCATCAAGTCCACTGTGCTTTTGATCAAGTCTCTGGCTGAGGAGG	388						
Db	2514	CCGGCATCCGACGCTGAACGAAGGAGCGCTGGGTGATGGCAGCGCTGCTGGGCTCGA	2573						
QY	389	CTGATGCTAGCCACCTTTATCCGTCACGAAGGTCACTTACCGGTGTAC	435						
Db	2574	TCGGGCGCAGCGACCTGTTTCCAGGAGGATGTTGTTGCTGGTGTTC	2620						



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RESULT 15
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LOCUS Sequence 27 from patent US 5776760.
DEFINITION AR016613
ACCESSION AR016613
VERSION AR016613.1 GI:3972890
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 62)
AUTHORS Barry.G.Francis and Kishore,G.Murthy.
TITLE Glyphosate tolerant plants
JOURNAL Patent: US 5776760-A 27 07-JUL-1998;
FEATURES
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BASE COUNT 12 a 12 c 19 g 19 t
ORIGIN

Query Match 4.5% Score 58.8; DB 5; Length 62;
Best Local Similarity 96.8%; Pred. No. 1.4e-05;
Matches 60; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 30 CGCTGGAGCTGGAATCGTTGGTGTGCTGACCTGCTTTGATGCTTCAACGCTCGTGGATTCAA 89
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Db 1 CCCTGGAGCTGGAATCGTTGGTGTGATGACCTGCTTTGATGCTTCAACGCTCGTGGATTCAA 60
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Qy 90 GG 91
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Db 61 AG 62
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

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Searched: 480022 seqs, 187831343 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match	Length DB ID	Description	
1	1296	100.0	1296 13	Q20835	Synthetic glyphosa
2	1296	100.0	8418 20	X57309	Sugar beet T-DNA c
3	1205.2	93.0	1631 18	T85664	CPT1-GOX gene fusi
4	1009.6	77.9	1321 13	Q20834	Modified glyphosat
5	960	74.1	1321 13	Q20833	Manipulated glypho
6	956.8	73.8	1692 13	Q22705	Glyphosate oxidore
7	925.6	71.4	1689 13	Q20832	Glyphosate oxidore
8	897	69.2	8012 20	X57305	Sugar beet T-DNA c
9	897	69.2	8798 20	X57308	Sugar beet T-DNA c
10	39.8	3.1	32207 20	V73805	KSHV LUR DNA (nucl
11	39.8	3.1	137507 19	V19941	KSHV long unique c
12	37.4	2.9	397 20	X89891	Spinocerebellar at

c 13	35.6	2.7	6558	21	Z45602	cdna sequence of a
c 14	35.2	2.7	6794	21	Z45597	cdna sequence of h
c 15	35	2.7	2004	17	T13952	Maize-Optimized VI
c 16	35	2.7	2004	18	T73997	DNA Optimised-B.
c 17	35	2.7	2004	19	V16170	Maize encoding an 80
c 18	35	2.7	2010	15	Q74683	Bacillus cereus ve
c 19	35	2.7	2576	17	T13945	Maize-Optimized VI
c 20	35	2.7	2576	18	T74006	Maize Optimised-B.
c 21	35	2.7	2576	19	V16181	Maize Optimised DN
c 22	35	2.7	2655	15	Q74682	Bacillus cereus ve
c 23	35	2.7	2655	17	T13951	Maize-Optimized VI
c 24	35	2.7	2655	17	T13954	Maize Optimised VI
c 25	35	2.7	2655	18	T73996	Maize Optimised-B.
c 26	35	2.7	2655	18	T74001	Maize Optimised-Ba
c 27	35	2.7	2655	19	V16169	DNA encoding a 100
c 28	35	2.7	2655	19	V16174	Maize Optimised DN
c 29	35	2.7	4031	17	T13947	Maize-Optimized VI
c 30	35	2.7	4031	18	T74010	Maize Optimised-B.
c 31	35	2.7	4031	19	V16189	Maize Optimised DN
c 32	35	2.7	10266	17	T33007	Mouse SHY-related
c 33	34.6	2.7	543	13	Q23092	Antigen tc-7a gene
c 34	34.4	2.7	1291	20	X87940	Mycobacterium tube
c 35	34.4	2.7	2852	19	V64558	M. tuberculosis im
c 36	34.4	2.7	2852	19	V44449	M. tuberculosis im
c 37	34.4	2.7	2852	20	Z19359	Mycobacterium tube
c 38	34.4	2.7	2852	20	Z19147	M. tuberculosis an
c 39	34.4	2.7	4888	20	X13244	M. tuberculosis re
c 40	34.2	2.6	9551	20	Z22301	Enterococcus faeca
c 41	34.2	2.6	54548	21	Z45596	cdna encoding a hu
c 42	34.2	2.6	138169	21	A34791	DNA sequence of th
c 43	34.2	2.6	141589	21	A35005	Human adenosine re
c 44	34.2	2.6	141589	21	A35030	Human adenosine re
c 45	34	2.6	1001	16	Q80734	Phosphatidylethano

ALIGNMENTS

RESULT 1

Q20835

ID Q20835 standard; DNA; 1296 BP.

XX Q20835;

XX 01-MAY-1992 (first entry)

XX Synthetic glyphosate oxidoreductase gene.

XX Recombinant; GOR; resistance; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT CDS 1..1296

FT /\*tag= a

XX

XX WO9200377-A.

XX

XX 09-JAN-1992.

XX

XX 24-JUN-1991; 91WO-US04514.

XX

XX 24-JUN-1991; 91US-0717370.

XX 25-JUN-1990; 90US-054236.

XX

XX (MONS ) MONSANTO CO.

XX

XX Kishore GM, Barry GF;

XX WPI: 1992-041559/05.

XX P-PSDB; R20642.

XX

XX Gene encoding glyphosate oxido-reductase enzyme - used to

PT transform plants to produce plants tolerant to glyphosate  
XX herbicide

Claim 1: Page 1032; 142pp; English.

The sequence is that of the gene encoding a glyphosate oxidoreductase (GOR) enzyme, the gene sequence was synthesised so that it could be redesigned to eliminate as much as possible the following sequences or sequence features (while avoiding the introduction of unnecessary restriction sites), stretches of G's and C's of 5 or more; A + T rich regions (predominantly) that could function as polyadenylation sites or potential RNA destabilisation regions, and codons not frequently found in plant genes. The G + C% for the synthetic gene is 51% and the potential to form short, high energy, hair-pin structures is reduced. However it still encodes the wild type GOR enzyme. It is used to transform plants such that they express the enzyme sufficiently to enhance the glyphosate tolerance of the plant. Transformed plants resistant to glyphosate can be obtained so that weeds can be selectively controlled in fields containing crops.

See also Q20832-Q20841 and Q22705.

Query Match 100.0%; Score 1296; DB 13; Length 1296;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGCGTGAGAACACAGAGAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTTCGACT	60
DB	1	atggctgagaaacacagagaggttggtatcgctggagctggaatcggttggtttgcact	60
QY	61	GCATTGATGCTTCAACGCTCGTGGATTCAAGGTTACCTTGATTGATCCAAACCCACCAAGT	120
DB	61	gcttgatgcttcaacgctcggtgattcaaggttaccttgatgatccaaacccaccaggt	120
QY	121	GAGGTGCTTTTCGGTAACGCTGGTGTGCTTCAACGGTTCCTCCGTTGTTCCTCAATGTCC	180
DB	121	gaaggtgcttcttcggtaacgctggttgcttcaacgggttcctccggttgctcaatgtcc	180
QY	181	ATGCCAGGAACCTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCAATGGGTCCATTTGCC	240
DB	181	atgccaggaaacttgactagcgttccaaagtggcttcttgacccaatgggtccatgtcc	240
QY	241	ATCCGTTTCAAGTACTTCCAAACCATCATGCTTGGTTGATTGCTTCTTGGTTCGTGGA	300
DB	241	atccgtttcaagtaacttccaaaccatcatgcttgggttgaattgcttcttggctgga	300
QY	301	AGACCAAAACAGGTGAGGAGCAAGCTAAGGCACCTCCGTAACCTCATCAAGTCCACTGTG	360
DB	301	agaccaaaacaggtgagagagcaagctaaaggcactccgtaacctcatcaagtccactgt	360
QY	361	CCTTTGATCAAGTCCTTGGCTGAGGAGGCTGATGCTAGCCACACTTATCCGTCACGAGGT	420
DB	361	cccttgatcaagcccttggctgagggagctgatagcagccaccttatccgtccagaagt	420
QY	421	CACCTTACCGTGTAACGCTGGAGAAAGAGACTTCGCCAAGGACCGTGGAGGTTGGGAACCT	480
DB	421	caccttaacggtgtaacgctggagaaagagacttcgccaaaggacccgtgaggttggaactt	480
QY	481	CGTCGCTCAACGGTGTTCGTACTAAATCCTCAGCGCTGATGCATTCGCTGATTTTCGAT	540
DB	481	cgtcgtctcaacgggttctgtaactctctcaaaactcctcagcgctgattgctgatttcgat	540
QY	541	CCTAAGTGTCTCAGCCCTTTACCAAGGAATCCTTATCGAAGAGAACGTCACACCATC	600
DB	541	cctaaattgtctcagccctttaccaaagggaatcctcatcgaagagaaacggtccaccatc	600
QY	601	AACCCACAAGGTCGTGACTCTCTTTGTTGCTGCTTTCATCGCTAACGCTGGAGAGTTC	660
DB	601	aaccaccaaggtctgactctctcttcttctgctgcttctcgttctcgtcaacggtgagagttc	660
QY	661	GTGCTGCTGCTGCTTATCGGATTCGAGACTGAAGGTGCTGCTCAAGGGTATCACCAAC	720

DB	661	gtgtctgctgctgttattcggaattcgagactgaaggtcggtctctcaagggttatccaccac	720
QY	721	ACCAACGGTGTCTTGTGTTGATGACAGCTGTTGTTGCAGCTGGTGACACTCCNAGTCT	780
DB	721	accaaaggtgtctctctgctgttgatgcagctgttgttgcagctggtgcacactccaagtct	780
QY	781	CTTGTCTAACTCCCTTGGTGATGACATCCCATTTGGATACCGAAGCTGGATACCCATCGTG	840
DB	781	cttgtctaactcccttgggtgatgacatcccatgtgataccgaacgttgataccacatcgtg	840
QY	841	ATGCCAACCCAGAGCTGCTGCACGTTATTCGAATACCGATGCTTCTGGAAGTTTCATC	900
DB	841	atgcgcaacccagaagctgctccacgtattccaactaccgatgcttctggaaagttcatc	900
QY	901	GCTACTCTTATGAGATGGGCTTCTCGTGTGGTGGAAACCGTGTGAGTTCGCTGCTCACT	960
DB	901	gctactcctatggagatgggtctctcggttgcgtggaaacggttgaagtcgctggtctcact	960
QY	961	GCTGCTCTTAACCTGGAAGCGTGTCTACGTTCTCTACACTCACGCTCGTAAAGTTGCTTTCCA	1020
DB	961	gctgctccttaactggaaagcgtgctcaagttctctacactcaacgctgtaagttgcttcca	1020
QY	1021	GCTCTGCTCTCTGCCAGTTCTGAAGAACGTTACTTCCAAAGTGGATGGGTTTCCGTCCAAAGC	1080
DB	1021	gctctgctcctgcccagttctgaagaacgttactccaagtggtggttccgtcccaagc	1080
QY	1081	ATCCGAGATTCCTTCCAGTGATTGGTGGTCTACCCGTTACTCCAGACGTTATCTAGGCT	1140
DB	1081	atcccgatctccctccagtgattggtgctgctacccgctactccacagcttatctacgct	1140
QY	1141	TTCCGCTCACGCTCACCTTCGGTATGACTTGGTGGTCCCAATGACCGCAACCCCTGCTTCGAG	1200
DB	1141	ttcgggtcaaggtcaactcggatagactggtgctccaaatgacccgaacccctcgttcttgag	1200
QY	1201	CTCCTCGCAGGTGAGAGACCTCTATCGACATCTCTCCATTCGCAACCAACCGTTTCGGT	1260
DB	1201	ctcctcgaggtgagaagacctctatcgacatctctccattcgcaacaaacggttttcggt	1260
QY	1261	ATTGGTAAAGTCCAAAGCAAACTGGTCTGTCATCCCTAA	1296
DB	1261	attggtaagtccaaagcaaaactggtcctgcatcctaa	1296
RESULT 2			
ID	X57309	standard; DNA; 8418 BP.	
XX	X57309;		
XX			
DT	26-JUL-1999	(first entry)	
XX			
DE	Sugar beet T-DNA containing cp4/epsps #2.		
XX			
KW	Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plant;		
KW	5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide;		
XX	tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.		
OS	Beta vulgaris.		
PN	WO922322-A1.		
XX			
PD	14-MAY-1999.		
XX			
PF	29-OCT-1998; 98WO-EP06859.		
XX			
PR	31-OCT-1997; 97US-0112003.		
XX			
PA	(NOVS ) NOVARTIS AG.		
PA	(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.		
PI	Mannerloef M, Steen P, Tenning PP;		
XX			



PT glyphosate, avoids constitutive expression and minimises development  
XX of herbicide tolerant weeds  
PS  
XX Example 3; Fig 7; 59pp; English.  
CC A chemically inducible plant gene expression cassette which comprises an  
CC inducible promoter linked to a gene (I) that confers resistance to a  
CC herbicide, is claimed. (I) imparts resistance to N-phosphonomethyl-  
CC glycine (glyphosate) or its salts, but may also be a gene for resistance  
CC to, e.g. chloracetanilides, glufosinate, sulphonyl ureas, imidazolonolones  
CC etc. The inducible promoter (e.g. alcA, alcR, alcA or other alcR-induced  
CC gene promoter) is operatively linked to an alcR regulator sequence.  
CC Induced expression of (I) avoids the risk that constitutive expression  
CC may interfere with plant development; allows volunteer plants to be  
CC controlled by herbicide applied without inducer and minimises the chance  
CC that herbicide-resistant strains of weeds will arise. The expression  
CC cassette is strictly controlled and suitable for general use in plants  
CC (both mono- and dicotyledons). The alcA/alcR gene switch was exemplified  
CC with genes conferring resistance to glyphosate. The switch was used to  
CC drive inducible expression of glyphosate oxidase (GOX) in plants.  
CC Switchable GOX was expressed alone or in conjunction with constitutive  
CC expression of 5-enol-pyruvylshikimate 3-phosphate (EPSPS) CP4. Constructs  
CC were optimised for expression in mono- and dicotyledonous crop species.  
CC The present sequence comprises a fusion of the GOX gene fused to the  
CC chloroplast transit sequence 1 from Arabidopsis RUBISCO (CPT1). This  
CC sequence was ligated into pMJB1 (see T85666) and used in construction of  
CC dicot vectors.  
XX  
SQ Sequence 1631 BP; 342 A; 454 C; 381 G; 454 T; 0 other;

Query Match 93.0%; Score 1205.2; DB 18; Length 1631;  
Best Local Similarity 95.3%; Pred. No. 0;  
Matches 1283; Conservative 0; Mismatches 13; Indels 50; Gaps 2;  
QY 1 ATGGCTGAGAACACACAGAGGTTGGTATCGCTGGAGCTGGATCGTTGGTTCGACT 60  
DB 274 atggctgagaaacacacagaggttggtatcgctggagctggagatcggtggttgcact 333  
QY 61 GCTTTGATGCTTCAACGCTCGTGATTCACAGTTACCTTGATTCACAAACCCACAGGT 120  
DB 334 gctttgatgcttcaacgctggtgatcaaggttaccttgattgatccaaacccacaggt 393  
QY 121 GAAGTGCTCTTTTCGGTAACGCTGGTGTGCTTCAACGGTTCTCCGTTGTTCGAATGTC 180  
DB 394 gaagtgctctcttcggttaacgctggttgcttcaacggttctcccggttggttccaatgctc 453  
QY 181 ATGCCAGGAACCTTGACTAGCTGTTCCAAAGTGCGTCTTGACC----- 223  
DB 454 atgccaggaacacttgactagctgttccaaagtggcttctggtatcctctgtgtaattcaagc 513  
QY 224 -----CAATGGGTCATTTGTCATTCCTGTCATTCAGTCTTCCAAACCATCATGCTTG 275  
DB 514 ttacggatccaaatgggttccatgctccatccggtttcaactacttccaaacacatgctgtg 573  
QY 276 GTTGATTCGTTCTTCTGCTGGAGACCAACAAAGGTGAAGGAGCAAGCTAAGGCAC 335  
DB 574 gttgattgcttcttctgctgctggaagacccaaggtggaaggaaggaaggaaggaaggaag 633  
QY 336 CCGTAACCTCATCAAGTCCACCTGCTTTGATCAAGTCTTGGCTGAGGAGGCTGATGC 395  
DB 634 cctgaacccatcaatgcttccactgtgcttggatcgaagtccttggtgaggaaggtgatgc 693  
QY 396 TAGCCACCTTATCCGTCAGCAAGGTCACCTTACCGTGACCGTGGAGAGCAGACATTCGC 455  
DB 694 tagccaccttatccgtcaagaaggtcaacttacccgtgtagccgtggaaggaaggaacttcgc 753  
QY 456 CAAGGACCGTGGAGGTGGGAACCTCGTCTCAACGGTGTTCGTACTCAAAATCCTCAG 515  
DB 754 caaggaccgtggaggttgggaactctgctcctcaacggtggttcgtactcaaatcctcag 813  
QY 516 CGCTGATGATTCGGTGATTTCCATCCTTACTTGTCTCAGCCCTTTACCAAGGAAATCCT 575

DB 814 cgtgatgcatgtgctgatttcgatcctaaactgtctcagcgcctttaccagggaatcct 873  
QY 576 TATCGAAGAGAACGGTCAACACCATCAACCCACAGGCTCTCGTGACTCTCTGTTTTCGTCG 635  
DB 874 tatcgaagagaacggtcacaccatcaaccacaaggtctcgtgactctcttgtttcgtcg 933  
QY 636 TTTTCATCGTCAACGGTGGAGAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 695  
DB 934 ttctcatcgctaaacggtggagagttcgtgctgctgctgctgctgctgctgctgctgctgctg 993  
QY 596 TCGTGTCTCTCAAGGGTATCAACACCAACCAACGGGTGCTTCTGCTGCTGCTGCTGCTGCTG 745  
DB 994 tctgctctcaaggttatcaccaccacacacggtggttcttctgctgctgctgctgctgctg 1053  
QY 746 -----CAGCTGTTGTTGCTGACGCTGGTGCACACTCCAACTCTCTTGTCTTAAC 790  
DB 1054 gtgaattcaagcttactgcagcttctgctgagctggtgcacactccaaagctccttgctaa 1113  
QY 791 CCCTTGTGTGATGATCCCATTTGGATACCGAAGCTGGATACCCACATCGTGTGATCGCCAA 850  
DB 1114 ccttgggtgatgacatcccatggatgataccgaagctggatgataccacatcgatcgcaacc 1173  
QY 851 CAGAAGCTGCTCCACGATTTCCAACTACCGATGCTTCTGGAAAGTTTCATCGCTACTCCCTA 910  
DB 1174 cagaagctgctccacgttatcccaactaccgagctcttctggaaagttcactgctactccta 1233  
QY 911 TGGAGATGGGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 970  
DB 1234 tggagatgggtctctctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 1293  
QY 971 ACTGGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1030  
DB 1294 actggaagcgtgctcactgcttctcactgctgctgctgctgctgctgctgctgctgctgct 1353  
QY 1031 CTGCCAGTTCTGGAAGACGTTACTTCCAAGTGGATGGGTTTCCGTTCCAAGCATCCACGAT 1090  
DB 1354 ctgccagttctggaagacgttactccaagtggatgggtttccgtccaagcatccagatt 1413  
QY 1091 CCCTTCCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1150  
DB 1414 ccttccagtgatgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 1473  
QY 1151 GTCACCTCGGTATGACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1210  
DB 1474 gtcaactcggtatgactggtggtggtggtggtggtggtggtggtggtggtggtggtggtg 1533  
QY 1211 GTGAGAAGACCTATATCGACATCTTCCATTCGACCAACCGTTTCCGTTTGGTGAAGT 1270  
DB 1534 gtgagaagacctatacgacatctctccattcgcacaaacccgtttcgggtattggtaagt 1593  
QY 1271 CCAAGCAAACTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1296  
DB 1594 ccaagcaaacctggctcctgctgctcctaa 1619  
RESULT 4  
Q20834  
ID Q20834 standard; DNA; 1321 BP.  
XX  
AC Q20834;  
XX  
DT 01-MAY-1992 (first entry)  
XX  
DE Modified glyphosate oxidoreductase gene.  
XX  
KW Recombinant; GOR; resistance; ss.  
XX  
OS Bacterial isolate LBAA.  
XX  
FH Key Location/Qualifiers  
FT 9..1304  
FT CDS /tag= a  
FT /notes= 'encodes wild type glyphosate oxidoreductase'



KW Recombinant; GOR; resistance; ss.  
OS Bacterial isolate LBAA.  
FH Key Location/Qualifiers  
FT CDS 9..1304  
FT /\*tag= a  
FT /note= "encodes wild type glyphosate oxidoreductase"  
XX  
XX WO9200377-A.  
XX  
XX  
XX PD 09-JAN-1992.  
XX PF 24-JUN-1991; 91WO-US04514.  
XX PR 24-JUN-1991; 91US-0717370.  
XX PR 25-JUN-1990; 90US-0543236.  
XX PA (MONS ) MONSANTO CO.  
XX Kishore GM, Barry GF;  
XX PI WPI: 1992-041559/05.  
XX DR P-PSDB; R20642.  
XX  
XX Gene encoding glyphosate oxido-reductase enzyme - used to  
XX transform plants to produce plants tolerant to glyphosate  
XX herbicide  
XX  
XX Claim 1: Fig 3; 142pp; English.  
XX  
XX The sequence is that of the gene encoding a glyphosate oxidoreductase  
XX (GOR) enzyme which has been manipulated such that it is suitable for  
XX introduction into and expression in plant transformation vectors, but  
XX it still encodes the wild type GOR enzyme. It was obtd. from bacterial  
XX isolate LBAA. It is used to transform plants such that they express  
XX the enzyme sufficiently to enhance the glyphosate tolerance of the  
XX plant. Transformed plants resistant to glyphosate can be obtd. so  
XX that weeds can be selectively controlled in fields contg. crops.  
XX See also Q20832-Q20841 and Q22705.  
XX  
XX Sequence 1321 BP; 292 A; 373 C; 369 G; 287 T; 0 other;  
SQ  
  
Query Match 74.1%; Score 960; DB 13; Length 1321;  
Best Local Similarity 83.8%; Pred. No. 1.2e-285;  
Matches 1086; Conservative 0; Mismatches 210; Indels 0; Gaps 0;  
  
QY 1 ATGGCTGAGAACCAACAGAGGTTGGTATCGCTGGAGCTGGAAATCGTTGGTTCACAT 60  
DB 9 atggctgagaaacacaaagtaggcatcgctggagcgggaatcgcgcgatgacg 68  
  
QY 61 GCTTTGATGCTTCAAGCTGCTGGATTCAAGGTTACCTTGATTCATCCAAACCCACAGGT 120  
DB 69 ggcgtgatgcttcagcgcgcggagatcaaaagtcacattgatgacccgaacctctggc 128  
  
QY 121 GAAGTGCTTCTTCGGTAACCGTGGTTCGTTCAACGGTTCTCCGTTGTTCCAAATGTC 180  
DB 129 gaagtgcacatcgcttgggaatccgagatgcttcaacggctcatcgctcctctatgtcc 188  
  
QY 181 ATGCCAGGAACCTGACTAGCTTCCAAAGTGGCTTCCTTGACCCCAATGGGTCCATGTC 240  
DB 189 atgccgggaacttgacgagcgtgcgaagtggctccttgacccgatggggcgtgtgca 248  
  
QY 241 ATCCGTTTTCAGCTACTTCCAAACCATCATCTGGTTGATTCGTTTCTGCTGCTGCA 300  
DB 249 atccggttcagctattttccaaaccatcatgacctggtgatccgtcttctgttagccgga 308  
  
QY 301 AGACCAAAACAGGTGAAGGACCAAGCTTAAGGACCTCCGTAACCTCATCAAGTCCACTGTG 360  
DB 309 agaccaaacaagtgagaggagcagcggaagcactccgcaaatctcatcaagtcacggtg 368  
  
QY 361 CCTTTGATCAAGCTCTTGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGT 420

DB 369 ccgctgatcaagtcattggcggagagggctgtagcgagccatctgaltccgccatgaaggt 428  
QY 421 CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAAGGACCGCTGGAGGTTGGGAATY 480  
DB 429 catctgaccgtatctgctggaagcagacttcgcaagaccgagcgttgggaactg 488  
QY 481 CGTCGTCTCAACGGTGTTCGTACTCAATCCTCAGCGCTGATGCATTCGCTGATTCGAT 540  
DB 489 cggcgtctcaacgggtgttcgcagcagatctctcagcgcgagtcgctgctgggatttcgat 548  
QY 541 CCTAATCTGTCTACGCCCTTTACCAAGGGAATCCTTATCAAGAGAACGCTCACACCATC 600  
DB 549 ccgaacttgtcgatcgctttaccgaaggcatctctatagaagagcaacggttcacagatt 608  
QY 601 AACCCACAAGGCTCTCGTACTCTCTTGTTCGTGCTTTCATCCCTAACGGTGGAGAGTTC 660  
DB 609 aatccgcaaggcgtctgacctcttcttgcgcttcttgcgcaacggtggcgaattt 668  
QY 661 GTGCTGCTGCTGTTATCGGATTTCGAGACTGAAGGTCTGCTCTCAAGGTTATCACACC 720  
DB 669 gtatctgcgcgtgtcatcgctttgagactgaaggtagggcgttaaaaggcatatacaacc 728  
QY 721 ACCAACGGTGTTCGTGCTGTTGATGACGCTGTTGTTGACGCTGGTGCACACATCCAAAGTCT 780  
DB 729 aggaacggcgttcttgcgcttgatgacgctgttgcgcagcggcgacacactcgaaatca 788  
QY 781 CTTGCTTAACCTCCCTTGGTGATGACATCCCAATGGATACCGAAGCTGGATACCATCTCGTG 840  
DB 789 ctgtctaattcgctagcgatgacatctccgcgtcgatcaccgaacgtggatatactcgtc 848  
QY 841 ATCGCCAAACCCAGAACGCTGCTCCACGTAATTCACCACTACCGATGCTTCTGGAAAGTTCATC 900  
DB 849 atcgcgaatccggaaacgcgtccacgacttcgcagacgcgctgcaggaataatcattc 908  
QY 901 GCTACTCTTATGGAGATGGGTCTTCGTGTTGCTGGAACCGTTGAGTTCGCTGGTCTCACT 960  
DB 909 gcgacacctatgaaatggggttcgctggtggcgggtacggttgagttcgctggggtcaca 968  
QY 961 GCTGCTCTTAACCTGGAAGCGTCTGCTACGTTCTCTACACTCACGCTGCTAAGTTGCTTCCA 1020  
DB 969 gcgcgtctctaaactggaaacgctgcgcgtatgctctatcagcagcgtcgaaactcttcca 1028  
QY 1021 GCTCTCGCTCTGCCAGTTCTGAAGAACGTTACTTCCAACTGGATGGTGGTTCCGCTCCAAGC 1080  
DB 1029 ggcctcgccctgcgcgttctggaagacgatattcccaaatggatggggttcgcggccgagc 1088  
QY 1081 ATCCAGATTCCTTCCAGTGTGCTGCTGCTACTCCGCTACTCCAGACGTTATCTACGCT 1140  
DB 1089 atcccggtatcgctccctcgatggcgggcaacccgcgacacccgacgtactatgct 1148  
QY 1141 TTTCCGTTACCGGTCACTCGGTATGACTGGTTCCTCAATGACCGCAACCTCTGTTTCTGAG 1200  
DB 1149 ttcggccacggtcatctcgcgcgtacagaggggcgcgcatgaccgcgaacgctcgtcagag 1208  
QY 1201 CTCTCTGCGAGGTGAGAAGACCTCTATCGACATCTCTTCCATTCGACCAACCGTTTCGCT 1260  
DB 1209 ctctctgcgagcgcaaaagacctcaatcgacatttcgctctgcacccaaacgcgttctgct 1268  
QY 1261 ATTGGTAAGTCCCAAGCAAACTGGTCTGCTGATCTCTAA 1296  
DB 1269 attggcaaatccaaagcaaacgggtccggcaagttaa 1304

RESULT 6  
Q22705  
ID Q22705 standard; DNA; 1692 BP.  
XX  
AC Q22705;  
XX  
DT 01-MAY-1992 (first entry)  
XX  
DE Glyphosate oxidoreductase gene.





Db 1380 attgcaaatccaaagcaacgggtccgcaagtaa 1415

RESULT 7

ID Q20832 standard; DNA; 1689 BP.

XX Q20832;

AC 01-MAY-1992 (first entry)

XX Glyphosate oxidoreductase gene.

XX Recombinant; GOR; resistance; ss.

XX Bacterial isolate LBAA.

XX Key Location/Qualifiers

FT CDS 120..1412

FT /tag= a

FT /note= "glyphosate oxidoreductase coding region"

FT misc\_feature 349..350

FT /tag= b

FT /note= "in the alternative sequence G is present here"

FT /tag= c

FT /note= "in the alternative sequence T is present here"

FT misc\_feature 389..390

FT /tag= d

FT /note= "in the alternative sequence C is present here"

XX WO9200377-A.

XX 09-JAN-1992.

XX 24-JUN-1991; 91WO-US04514.

XX 24-JUN-1991; 91US-0717370.

PR 25-JUN-1990; 90US-0543236.

XX (MONS ) MONSANTO CO.

XX Kishore GM, Barry GF;

XX WPI; 1992-041559/05.

DR P-PSDB; R20642.

XX Gene encoding glyphosate oxido-reductase enzyme - used to

PT transform plants to produce plants tolerant to glyphosate

PT herbicide

XX Claim 1; Page 93; 142pp; English.

PS The sequence is that of a gene encoding a glyphosate oxidoreductase  
CC (GOR) enzyme. It was obtd. from bacterial isolate LBAA. It is used  
CC to transform plants such that they express the enzyme sufficiently  
CC to enhance the glyphosate tolerance of the plant. Transformed plants  
CC resistant to glyphosate can be obtd. so that weeds can be selectively  
CC controlled in fields contg. crops. This sequence (SEQ ID No.3 in the  
CC specification) contains apparent discrepancies (see feature table)  
CC with a supposedly identical sequence (fig 2), since it is unclear  
CC from the specification which of these is correct, both sequences have  
CC been indexed. See also Q20833-Q20841 and Q22705 - the alternative  
CC sequence for the GOR gene.

XX Sequence 1689 BP; 381 A; 477 C; 470 G; 360 T; 1 other;

XX Query Match 71.4%; Score 925.6; DB 13; Length 1689;

XX Best Local Similarity 83.6%; Pred. No. 5,4e-275;

XX Matches 1084; Conservative

3; Gaps 3;

1 ATGGCTGAGAACCAAGAGGTGCTATCGCTGGAGCTGGAAATCGTTGGTGTTCGACT 60

Db 120 atgtctgagaaccacaaaaagtaggcatacgctggagcoggaatacgctggcgctatgcaacg 179

QY 61 GCTTTGATGCTTCAAGTCGTGATTCACAGGTTACCTTGATTCATCCAAACCCACCAGGT 120

Db 180 gcgctgatcttcagcgccgcgagattcaaaagtcaaccttgattgacccgaagcctctctggc 239

QY 121 GAAGGTGCTTCTTTTCGGTAACGCTGGTTGCTTCAACGGTTCCYCCGTTGTTTCCAATGTGCC 180

Db 240 gaaggtgcatcgcttggaatgccgatgcttcaacggctcatccgctcgctccatgctcc 299

QY 181 ATCCAGGAAACTTGACTAGCGTTCCAAAGTGGCTTCTTTCGACCCAAATGGGTCCATGTGCC 240

Db 300 atcgcggaacttgacgagctgcccgaagtggctctcttgacccgatggg-cggtgctca 358

QY 241 ATCCGTTTTCAGCTACTTTCACCAACCATCATGCTTGGTTGATTCGTTCTTCTTGGTTCGTTGGA 300

Db 359 atccgggttcagcta-tttccaaacctcatgccc-tggttgattcgctctcttgtagccgga 416

QY 301 AGACCAAAAGGTGAAGGAGCAAGCTAAGGCACTCCGTAACCTCATCAAGTCCACTGTG 360

Db 417 agaccaaaaggtagaagcagcgaagcactccgcaatctcatcaagtccacgggtg 476

QY 361 CTTTTCATCAAGTCTTGGCTGAGGAGGTGATGCTTAGCCACCTTATCCGTCACGAAAGT 420

Db 477 cctctgatcaagtcatctggcgagggagctgagtgcgagccatctgatccgccatgaaggt 536

QY 421 CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAAGGACCGTGGAGGTTCGGAACTT 480

Db 537 catctgacctgatatctgtggagagcagacttcgcaagaccgagcgaggttgggaactg 596

QY 481 CGTCGTCTCAACGCTGTGCTACTCAAACTCTCAGCGCTGATGCAITTCGCTGATTCGAT 540

Db 597 cggcgctcaacggtgttcgacgcagatcctcagcgcgcatgcttgcggaattcogat 656

QY 541 CTTAATTTGCTCACGCCCTTTACCAAGGGAATCTTTATCGAAGAGAACCGGTTCACACCATC 600

Db 657 cggaaactgtcgatgctgttaccgaaggcattctctatagaagagagacggtccacagatt 716

QY 601 AACCCACAAGGTCTCGTGACTCTCTTGTTCGTCTTTCATCGTTCATCGTTCAGGTGGAGATT 660

Db 717 aatcccgcaaggcgctcgtaacctctgttccggcgcttttatcgcgcaacggtggcgaaact 776

QY 661 GTGTCCTCGTGTATTCGGATTCGAGACTGAAGGTCTGCTCTCAAGGATATCACCAAC 720

Db 777 gtaatcgcggtgctatcgatcggtttgagactgaaggtagggcgtctaaaggcattacaacc 836

QY 721 ACCAACGGTGTCTTCTGCTGTTGATGACGCTGTTGTTGCGAGCTGGTGCACACTCCAAGTCT 780

Db 837 acgaacggcgttctggcggttgatgacgaggttgctgcagcgccgagcgcacactcgaataca 896

QY 781 CTTGCTTAACCTCCCTTGTGTGATGACATCCCATTCGATACCGNAGCTGATACCAATCGTG 840

Db 897 ctgtgcaatcgctagggcgatgacatcccgctcgatcccgcaacgtggatcatatcgtc 956

QY 841 ATGCCCAACCCAGAGCTGCTCCACGTAATTCACCACTACCGATGCTTCTGGAAGTTTCATC 900

Db 957 atcggaatccggaagccgctccacgcatccgacgacgagctgctcaggaataatcag 1016

QY 901 GCTACTCTTATGGAGATGGGTCTGCTGTTGCTGTTGCGAACCCTTGAGTTCGCTGGTCTTCACT 960

Db 1017 ggcacacctatggaatgggcttcgctgctggcggtgacgggtgagttcgctggggtccaca 1076

QY 961 GCTGCTCTTAACCTGGNAGCTGCTCAGCTTCTCTACACTCACGCTCGTAAGTTGCTTCCA 1020

Db 1077 ggcgctcctaactggaaacgctgcgcatgtgctcta taccgacgctcgaaacctcttcca 1136

QY 1021 GCTCTCGCTCCCTCCAGTTCTCTGAAGAACGTTACTTCAAGTGGATGGTGTTCCTCTCCAAGC 1080

Db 1137 gccctcgccctgcgagttctcgaagaacacatattccaaatggatgggggttccggccgagc 1196

QY 1081 ATCCCCAGATTCCCTTCCAGTGATTTGCTGCTGCTTACCCGTTACTTCCAGACGTTATCTACGCT 1140

Db 1197 atccccgattcgctccccggtgattggcggggcaaccgggacacccggagcgttaattctatgct 1256  
Qy 1141 TTCGGTCACGGTCACCTCGGTATGACTGGTGCTCCAATGACCGCAACCCCTCGTTTCTGAG 1200  
Db 1257 ttccggccatggtcatctcggcatgacagggcgccgaltgaccgcaacgctcgtctcagag 1316  
Qy 1201 CTCTCCGAGGTGAGAGACCTCTATCGACATCTCTCCATTTCGACCAACCAACCTTCGGT 1260  
Db 1317 ctctcgcagggcgaagaccctcaatcgacatttcgccttcgcaccaaaccgctttggt 1376  
Qy 1261 ATTGGTAAGTCCAAAGCAAACTGGTCTCGCATCCCTAA 1296  
Db 1377 attcgaaatccaagcaaacgggtccggcaagtttaa 1412  
  
RESULT 8  
X57305  
ID X57305 standard; DNA; 8012 BP.  
XX  
AC X57305;  
XX  
DT 26-JUL-1999 (first entry)  
XX  
DE Sugar beet T-DNA containing cp4/epsps fragment.  
XX  
KW Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plant;  
KW 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide;  
KW tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.  
XX  
OS Beta vulgaris.  
XX  
PN W09923232-A1.  
XX  
PD 14-MAY-1999.  
XX  
PP 29-OCT-1998; 98WO-EP06859.  
XX  
PR 31-OCT-1997; 97US-0112003.  
XX  
PA (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
XX  
PI Mannerloef M, Steen P, Tenning PP;  
XX  
DR WPI; 1998-313347/26.  
XX  
PT Glyphosate resistant transgenic sugar beet plants  
XX  
PS Claim 8; Page 24-29; 55pp; English.  
XX  
CC This invention describes a novel sugar beet plant, including its  
CC descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase  
CC (cp4/epsps) enzyme activity which is obtainable by Agrobacterium  
CC mediated transformation with a gene allowing expression of cp4/epsps  
CC in plants, where the plant lacks both right and left T-DNA border  
CC sequences. The transgenic sugar beet plants of the invention are capable  
CC of tolerating herbicide treatment with glyphosate (also known as  
CC N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.  
XX  
SQ Sequence 8012 BP; 2096 A; 1855 C; 1879 G; 2182 T; 0 other;  
  
Query Match 69.2%; Score 897; DB 20; Length 8012;  
Best Local Similarity 100.0%; Pred. No. 7.7e-266;  
Matches 897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 ATCGCTGAGAACCAAGAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTTCGACT 60  
Db 7116 atgsgctgagaaccacaagaagggttggtatcgctgagctggaatcgttggtgttgcact 7175  
Qy 61 GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTGATTGATCCAAACCCACGAGGT 120  
Db 7176 gctttgatgtctcaacgctcgtggtattcaagggttaccttgattgatccaaacccacagggt 7235

Qy 121 GAAGTGCTTCTTTTCGGTAAACGCTGGTTTGGCTTCAACGGTTCTCTCGTTGTTCCTCAATGTCC 180  
Db 7236 gaagggtctcttcggtaacgctggttgcttcaacggttctctcgttggttccaaatgccc 7295  
Qy 181 ATGCCAGGAACACTTCAGCTAGCGTTCCAAAGTGGCTTCTTTGACCCCAATGGGTCCATTGTCC 240  
Db 7296 atgcaggaacttgactagcgttccaaagtggctctcttgacccaatgggttccattgtccc 7355  
Qy 241 ATCCGTTTCAGCTACTTTTCCAAACCATCATGCTTGGTTGATTTCGTTTCTTGGTCTCTGGA 300  
Db 7356 atccgtttcagctacttccaaacctaatgctctggttgattcgttctctgcttctgga 7415  
Qy 301 AGACCAACAAGGTGAGGAGCAAGCTTAAGGCATTCCTTAACCTCATCAAGTCCACTGTG 360  
Db 7416 agacaaacaagggtgaaggagcaagtaagcactccgtaacctcatcaagtcacactgtg 7475  
Qy 361 CCTTTGATCAAGTCTTTCGGCTGAGGAGGCTGATGCTAGCCACCTTTATCCGTCACCAAGGT 420  
Db 7476 cctttgatcaagtccttggtgagaggctgatgtagccaccttatccggtcacaagggt 7535  
Qy 421 CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAAGGACCGTGGAGGTTGGGAACCT 480  
Db 7536 caccttacggtgtaccgttgagagaagcagaacttcgccaaggacctgagggttgggaactt 7595  
Qy 481 CGTGTCTCAACGGTGTTCGGTACTCAAAATCTCAGCGCTGATGCAATTCGGTGATTTCCGAT 540  
Db 7596 cgtcgtctcaacgggtgttctcgtaactcaaatcctcagcgtgaltgcatlgcgtgattctgat 7655  
Qy 541 CCTAACTTGTCTCAGCGCTTTACCAAGGGAATCCTTATTCGAAGAACCGGTACACCATC 600  
Db 7656 cctaaacttgtctcagcgtcttaccaaagggaatccttatacgaaagaacgggtccacccatc 7715  
Qy 601 AACCCACAAGGTCTCGTGACTCTCTTGTTCGTTCGTTTCATCGCTTAACGGTGGAGAGTTC 660  
Db 7716 aaccacaagggtctcgtgaactctctgttctcgtctgattcgtctcaacgggttggaagttc 7775  
Qy 661 GTGTCTGCTGTGTATTCGATTCGAGACTGAAGTCTGCTCTCAAGGGTATACACCACC 720  
Db 7776 gtgtcgtcgtgttattatcggaatcgagactgaaggctgctctcacaagggtatcaccacc 7835  
Qy 721 ACCAAGCGTTCCTTTCGCTGTTGATGCCACTGTTGTTGAGCTGGTGCACACTCCAGTCT 780  
Db 7836 accaagcggttctctgctgtgtgatgctgctgtgtgagctgtgtgtgagctgggtgacactccaagtct 7895  
Qy 781 CTTCGTAACCTCCCTGGTGGATGACATCCCATTCGATACCGAACGTTGGATACCCATCGTG 840  
Db 7896 ctgctaactccctggtgtgatgacatcccatggataccgaaacgtggataccacacatcgtg 7955  
Qy 841 ATCGCCAAACCCAGAGCTGCTCCACGTTATTCCAACTACCGATGCTTCTGGAAAGTTC 897  
Db 7956 atcgccaaccagaagctgctccacgtatcccaactaccgatgctcttcggaaagtcc 8012  
  
RESULT 9  
X57308  
ID X57308 standard; DNA; 8798 BP.  
XX  
AC X57308;  
XX  
DT 26-JUL-1999 (first entry)  
XX  
DE Sugar beet T-DNA containing cp4/epsps.  
XX  
KW Sugar beet; transformation; T-DNA; Insertion; cp4/epsps; plant;  
KW 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide;  
KW tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.  
XX  
OS Beta vulgaris.  
XX  
PN W09923232-A1.  
XX  
PD 14-MAY-1999.

XX 29-OCT-1998; 98WO-EP06859.  
XX 31-OCT-1997; 97US-0112003.  
XX (NOVS ) NOVARTIS AG.  
XX (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
XX Mannerloef M, Steen P, Tenning PP;  
XX WPI; 1999-313347/26.  
XX  
XX Glyphosate resistant transgenic sugar beet plants  
XX  
XX Claim 11; Page 31-36; 55pp; English.  
XX  
XX This invention describes a novel sugar beet plant, including its  
XX descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase  
XX (cp4/epsps) enzyme activity which is obtainable by Agrobacterium  
XX mediated transformation with a gene allowing expression of cp4/epsps  
XX in plants, where the plant lacks both right and left T-DNA border  
XX sequences. The transgenic sugar beet plants of the invention are capable  
XX of tolerating herbicide treatment with glyphosate (also known as  
XX N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.  
XX  
XX Sequence 8798 BP; 2346 A; 1999 C; 2032 G; 2421 T; 0 other;  
SQ

Query Match 69.2%; Score 897; DB 20; Length 8798;  
Best Local Similarity 100.0%; Pred. No. 8.1e-266;  
Matches 897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTGAGAACCAAGAAGGTGGTATCGCTGGAGCTGGAAATCGTTGGTTGCACT 60  
|||||  
Db 7205 atggctgagaaaccacagaaggttggtatcgctggagctggaatccttggtgtttcac 7264

QY 61 GCTTTGATGCTTCAACGTCGCTGATTCAAGTTACCTTGATGATCCAAACCCACCAAGT 120  
|||||  
Db 7265 gctttgatgcttcaacgctcggtgattcaaggttaccttgatgatccaaacccaccaggt 7324

QY 121 GAAGTGCTTCTTTCGGTAACGCTGCTGCTTCAACGGTTCCTCCGTTGTTCAATGTCC 180  
|||||  
Db 7325 gaaggcgctcttcctcggttaacgctggtgcttcaacggttcctccgctgtttccaa 7384

QY 181 ATGCCAGGAACTTGACTACGCTTCCAAAGTGGCTTCTTGACCCAAATGGGTCCATTGTCC 240  
|||||  
Db 7385 atgccaggaacttgactagctgtccaaagtggcttcttgacccaatgggtccattgtcc 7444

QY 241 ATCCGTTTCAGCTACCTTCCAAACCATCATGCTTGGTTGATTCGTTTCTGTTGCTGGA 300  
|||||  
Db 7445 atccggtttcagctactttccaaacccatcagcttggtgattgattcgttctgtgtgga 7504

QY 301 AGACCAAAACAAAGTGAAGGAGCAAGCTAAGGCACTCCGTAACCTCATCAAGTCCACTGTG 360  
|||||  
Db 7505 agaccaaaacaagtggaagagcaagctaaaggcaactccgtaacctcatcaagtcacctg 7564

QY 361 CCTTTGATCAAGTCTTGGCTGAGGAGGCTGATGCTAGGCACCTTATCCGTACACGAAGT 420  
|||||  
Db 7565 cctttgatcaagtcccttggtgaggaagctgactagcagcattatccgtcacgaaggt 7624

QY 421 CACCTTACCGTGTACCGTGGAGAGCAGACTTCCGCCAAGACCGGTGGAGTGGGAACATT 480  
|||||  
Db 7625 caccctaccgtgtaccgtggagaagcagacttcgcaaggaacgctggaggttgggaacct 7684

QY 481 CGTCGCTCAACGGTGTTCGTACTCAATCCCTCAGGCGTGATTCGTCGTTGATTCGAT 540  
|||||  
Db 7685 cgtcgctcaacaggggtgtcgttactcaaaacctcagcgcgcgaagcgtgattccgat 7744

QY 541 CCTAACTTCTCAGCCCTTTACCAAGGGAATCCTTTATCGAAGAGAACGGTGCACACCATC 600  
|||||  
Db 7745 cctaaactgtctcagccctttaccaagggaaaccttlatcgaagagaacggtcacaccalc 7804

QY 601 AACCCACAAGGTCCTGACTCTCTTGTTCGTGTTTCATCGCTAACCGTGGAGAGTTTC 660

Db 7805 |||||  
QY 661 GTGTCTGCTGCTGTTATCGGATTTCGAGACTGAAGGTGCTGCTCTCAAGGCGTATCACCACC 720  
|||||  
Db 7865 gtgctcgtcgtgcttattcggattcggagactggaaggtcgtgctctcaagggatataccacc 7924  
|||||  
QY 721 ACCAACGGTGTCTTCTGCTGTTGATGACAGCTGTTGTTGTCAGCTGCTGCACACTCCAACTCT 780  
|||||  
Db 7925 accaagcgtgttctctgctgttgatgacgctgttgctgacgtggtgcacactccaaagtct 7984  
|||||  
QY 781 CTTCCTAACTCCCTTGGTGTGATGACATCCCATTCGATACCCAACTCGATACCCACATCGT 840  
|||||  
Db 7985 cttgctaactcccttggtgatgacatcccatgtgataccgaacgtggtataccaccatcgt 8044  
|||||  
QY 841 ATCGCAACCCAGAACGCTGCTGCACGCTATTCCTCAACTACCGATCTTCTGGAAGTTC 897  
|||||  
Db 8045 atcgcaaacccagaagcgtgctcacgtattcccaactacacgactgtctctggaagttc 8101  
|||||

RESULT 10  
V73805  
ID V73805 standard; DNA; 32207 BP.  
XX  
AC V73805;  
XX  
DT 25-FEB-1999 (first entry)  
XX  
DE KSHV LUR DNA (nucleotides 105,301-137,507).  
XX  
KW Kaposi's sarcoma; acquired immune deficiency syndrome; AIDS; DHFR; Bcl-2;  
KW dihydrofolate reductase; LUR; long unique region; vaccine; prophylaxis;  
KW diagnosis; treatment; HHV8; capsid protein IV; tegument protein IV;  
KW glycoprotein; kaposin; cyclin D; immediate early protein; IEP; OX-2;  
KW v-adi; G-protein coupled receptor; FGARAT; ds.  
XX  
OS Kaposi's sarcoma-associated herpesvirus.  
XX  
PN US5849564-A.  
XX  
PD 15-DEC-1998.  
XX  
PF 29-NOV-1996; 96US-0770379.  
XX  
PR 29-NOV-1996; 96US-0770379.  
XX  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
PI Bohenzky RA, Chang Y, Edelman IS, Moore PS, Russo JJ;  
XX  
DR WPI; 1999-069741/06.  
XX  
PT Kaposi's sarcoma-associated herpes virus nucleic acid - encodes  
PT dihydrofolate reductase and is useful for treatment, prophylaxis  
PT or diagnosis of Kaposi's sarcoma  
XX  
PS Disclosure; Column 155-182; 109pp; English.  
XX  
XX This sequence is a fragment of the Kaposi's sarcoma-associated  
CC herpesvirus (KSHV) LUR (long unique region). This fragment contains  
CC coding regions for ORF65 which encodes capsid protein IV, ORF66, ORF67  
CC which encodes tegument protein IV, ORF68 which encodes a glycoprotein,  
CC ORF69, K12 which encodes kaposin, K13, ORF72 which encodes cyclin D,  
CC ORF73 which encodes immediate early protein (IEP), K14 which encodes  
CC OX-2 (v-adi), ORF74 which encodes G-protein coupled receptor, ORF75  
CC which encodes tegument protein/FGARAT, K15. KSHV is a new human  
CC Herpesvirus (HHV8) believed to cause Kaposi's sarcoma (KS) which is the  
CC most common form of neoplasm occurring in persons with acquired immune  
CC deficiency syndrome (AIDS). The DHFR protein is useful for vaccination,  
CC prophylaxis, diagnosis and treatment of a subject with Kaposi's sarcoma  
CC and for detecting expression of a DNA virus associated with Kaposi's  
CC sarcoma in a cell.  
XX

```
SQ Sequence 32207 BP; 7229 A; 9156 C; 8713 G; 7109 T; 0 other;

Query Match      3.1%; Score 39.8; DB 20; Length 32207;
Best Local Similarity 47.7%; Pred. No. 0.14;
Matches 116; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

Qy 727 GGTGTTCTTGCTGTGATGCAGCTGTTGTCAGCTGTGTGCACACTCCAAAGTCTCTTGTCT 786
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 19842 gctgctcatcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 19901

Qy 787 AACTCCCTTGCTGATGACATCCATGGATACCCGAACGTGGATACCATCGTGTATCGCC 846
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 19902 catcctgctgctgctcaccctgctgctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 19961

Qy 847 AACCAGAAAGTGTCTCCACGATTTCCAACTACCCGATGCTTCTGGAAAGTTTCACTACT 906
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 19962 catcctgctgctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 20021

Qy 907 CCTATGGAGATGGGCTTCGCTGCTGCTGGAAACCGTTGAGTTCGCTGCTCAGTGTGCT 966
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 20022 catcctgctgctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 20081

Qy 967 CCT 969
      |||
Db 20082 cat 20084

RESULT 11
V19941
ID V19941 standard; DNA; 137507 BP.
XX
AC V19941;
XX
DT 03-AUG-1998 (first entry)
XX
DE KSHV long unique coding region and terminal repeat.
XX
KW KSHV; HHV8; human herpes virus 8; macrophage inflammatory protein II;
KW interleukin-6; IL-6; interferon regulatory factor; rheumatoid arthritis;
KW complement-binding protein; glycoprotein; capsid protein IV; infection;
KW immediate early protein; Kaposi's sarcoma; protective vaccine; lymphoma;
KW lymphoproliferative disease; leukaemia; splenomegaly; mycosis fungoides;
KW HIV immune status; anti-inflammatory agent; therapy; ds.
XX
OS Kaposi's sarcoma-associated herpes virus.
XX
FH Key Location/Qualifiers
FT CDS 1142..2794
FT FT /*tag= a
FT FT /product= complement-binding protein
FT FT 8699..11236
FT FT /*tag= b
FT FT /product= glycoprotein B
FT FT complement (17261..17875)
FT FT /*tag= c
FT FT /product= interleukin 6
FT FT complement (21548..21832)
FT FT /*tag= d
FT FT /product= macrophage inflammatory protein II
FT FT complement (27137..27424)
FT FT /*tag= e
FT FT /product= interferon regulatory factor 1
FT FT 28661..29741
FT FT /*tag= f
FT FT /product= protein T1.1
FT FT complement (58976..60175)
FT FT /*tag= g
FT FT /product= glycoprotein M
FT FT complement (69412..69915)
FT FT /*tag= h
FT FT /product= glycoprotein L
FT FT complement (88410..88910)
FT FT

/*tag= i
/product= interferon regulatory factor 2
89600..90541
/*tag= j
/product= interferon regulatory factor 3
90173..90643
/*tag= k
/product= glycoprotein X
complement (93636..94127)
/*tag= l
/product= interferon regulatory factor 4
complement (111931..112443)
/*tag= m
/product= capsid protein IV
complement (123808..127296)
/*tag= n
/product= immediate early protein

W09804576-A1.
05-FEB-1998.
22-JUL-1997; 97WO-US13346.
29-NOV-1996; 96US-0757669.
25-JUL-1996; 96US-0686243.
25-JUL-1996; 96US-0686349.
25-JUL-1996; 96US-0686350.
25-JUL-1996; 96US-0687253.
25-JUL-1996; 96US-0688814.
05-SEP-1996; 96US-0708678.
10-OCT-1996; 96US-0728323.
13-NOV-1996; 96US-0747887.
13-NOV-1996; 96US-0748640.
(UYCO ) UNIV COLUMBIA NEW YORK.
Bohenzky RA, Chang Y, Edelman IS, Moore PS, Russo JJ;
WPT; 1998-130615/12.
New nucleic acid encoding Kaposi's sarcoma associated herpes virus
proteins - useful for, e.g. detecting levels of HHV8 in, and
preparation of vaccines for treatment of, HIV patients
Example 2; Page 135-203; 230pp; English.
This sequence represents the long unique region and terminal repeat of
the Kaposi's sarcoma-associated herpes virus (KSHV). KSHV is also known
as human herpes virus 8 (HHV8). This sequence contains the DNAs of the
invention which encode KSHV polypeptides selected from: (a) viral
macrophage inflammatory protein (MIP) II; (b) viral interleukin-6 (IL-6);
(c) viral IRF 1; (d) complement-binding protein; glycoproteins B, M or L;
(d) capsid protein IV encoded by ORF65; and (e) immediate early protein
encoded by ORF73. Labelled probes for the nucleic acid, proteins encoded
by it, and antibodies (Ab) specific for the proteins are useful for
detecting HHV8, specifically for diagnosis of Kaposi's sarcoma, in body
fluids or tissue samples. HHV8 infections can be treated with antisense
or triplex forming molecules or agents that bind specifically to the
protein. Ab may be used for prophylaxis or treatment of HHV8 infection,
while the protein can be used in protective vaccines. Ab may also be used
to differentiate between lymphomas, and HHV8 may be implicated in many
other lymphoproliferative diseases such as lymphomas, leukaemia,
splenomegaly and mycosis fungoides. Cells and animals containing the
nucleic acid are useful for drug screening. HHV8-derived peptides can be
used as targets for antiviral drugs, e.g. dihydrofolate reductase gene
can be inhibited with methotrexate. These can also be used to determine
the immune status of a patient infected with HIV. HHV8 derived protein
viral MIP III may be used as an anti-inflammatory agent for,
e.g. treating rheumatoid arthritis. This sequence is stated as containing
81 open reading frames.
Sequence 137507 BP; 32579 A; 37795 C; 35758 G; 31375 T; 0 other;
```

[illegible]

CC gene. The human OPA gene is derived from the PCTG4 region of chromosome  
CC Xq13. Polymorphisms in this region are associated with mental  
CC retardation, autism, depression, bipolar affective disorder or  
CC hypothyroidism. One 12 bp insertion polymorphism occurs within the  
CC coding region of the human OPA gene, and introduces a 4 amino acid  
CC insertion in a putative OPA domain. This domain has been shown to be  
CC involved in tissue specific expression. Another polymorphism consists  
CC of a pentanucleotide repeat approximately 7 kb upstream of the 12 bp  
CC polymorphism. Another polymorphism consists of a dinucleotide repeat  
CC approximately 4.5 kb downstream of the 12 bp polymorphism. The  
CC specification describes a method for screening for polymorphisms in a  
CC PCTG4 nucleic acid sequence obtained from a subject. The PCTG4 related  
CC sequences within the q13 region of the X chromosome have polymorphisms  
CC associated with neuropsychiatric disorders. The methods can be used  
CC to screen for the presence of a heritably linked form of mental  
CC retardation, autism, depression, bipolar affective disorder or  
CC hypothyroidism.  
XX  
SQ Sequence 6558 BP; 1637 A; 1801 C; 1644 G; 1475 T; 1 other;

Query Match 2.7%; Score 35.6; DB 21; Length 6558;  
Best Local Similarity 45.2%; Pred. No. 1.3;  
Matches 131; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

QY 665 CTGCTCGTGTATCGGACTCGAGACTGAAGTTCGTCCTCAAGGGTATCACCAACCA 724  
DB 6396 CTGGCGCTGGAACCTGGGCTGGGCTGGGCTGGGCTGGGCTGGCTGCTGCTG 6337

QY 725 ACGTGTTCTTCTGCTTATGATCAGCTGTGTTGTCAGCTGGTGCACACATCCAAAGTCTCTTG 784  
DB 6336 CTGCTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6277

QY 785 CTAACCTCCCTTGGTGATGACATCCCATTTGGATACCGAAGCTGGATACACATCGTGATCG 844  
DB 6276 CTGCTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6217

QY 845 CCAACCCAGAAAGCTGCTCCAGTATTCACAACTACCGATGCTTCTCGAAAGTTCATCGCTA 904  
DB 6216 CTGTCGGATATGGTACTGCTGTTGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6157

QY 905 CTCCTATCGAGATGGCTTCTGCTGTTGCTGGNACCGTTGAGTTCCCTGGT 954  
DB 6156 CTGCTGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6107

RESULT 14  
245597/C  
ID 245597 standard; cDNA; 6794 BP.  
XX  
AC 245597;  
XX  
DT 06-APR-2000 (first entry)  
XX  
DE cDNA sequence of human OPA gene.  
XX  
KW Human; PCTG4 region; X chromosome; q13 region; polymorphism;  
KW mental retardation; autism; depression; bipolar affective disorder;  
KW hypothyroidism; OPA gene; neuropsychiatric disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9955915-A2.  
XX  
PD 04-NOV-1999.  
XX  
PF 29-APR-1999; 99WO-US09365.  
XX  
PR 29-APR-1998; 98US-0083465.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA (IOWA ) UNIV IOWA RES FOUND.  
XX

PI Philibert RA, Ginns EI;  
XX  
DR WPI; 2000-126357/11.  
XX  
PT Identification of polymorphisms in the PCTG4 region of Xq13 for  
PT diagnosing mental retardation or autism -  
XX  
Example 7; Page 68-71; 100pp; English.  
XX  
The present sequence represents the cDNA sequence of the human OPA  
CC gene, which is derived from the human PCTG4 region of chromosome Xq13.  
CC Polymorphisms in this region are associated with mental retardation,  
CC autism, depression, bipolar affective disorder or hypothyroidism.  
CC One 12 bp insertion polymorphism occurs within the coding region of  
CC the human OPA gene, and introduces a 4 amino acid insertion in a  
CC putative OPA domain. This domain has been shown to be involved in tissue  
CC specific expression. Another polymorphism consists of a pentanucleotide  
CC repeat approximately 7 kb upstream of the 12 bp polymorphism. Another  
CC polymorphisms consists of a dinucleotide repeat approximately 4.5 kb  
CC downstream of the 12 bp polymorphism. The specification describes a  
CC method for screening for polymorphisms in a PCTG4 nucleic acid sequence  
CC obtained from a subject. The PCTG4 related sequences within the q13  
CC region of the X chromosome have polymorphisms associated with  
CC neuropsychiatric disorders. The methods can be used to screen for the  
CC presence of a heritably linked form of mental retardation, autism,  
CC depression, bipolar affective disorder or hypothyroidism.  
XX  
SQ Sequence 6794 BP; 1624 A; 1938 C; 1754 G; 1478 T; 0 other;

Query Match 2.7%; Score 35.2; DB 21; Length 6794;  
Best Local Similarity 54.7%; Pred. No. 1.7;  
Matches 70; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 643 CTAACGGTGGAGAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 702  
DB 6289 GCTGTCGCCGAGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6230

QY 703 CTCACGGGTATCACCCACCACCAACGGTGTCTTGTGCTGATGCAGCTGTTGTCAGCT 762  
DB 6229 GCTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6170

QY 763 GGTGCACA 770  
DB 6169 GCTGCTCA 6162

RESULT 15  
T13952/C  
ID T13952 standard; DNA; 2004 BP.  
XX  
AC T13952;  
XX  
DT 15-AUG-1996 (first entry)  
XX  
DE Maize-optimized VIP1A(a) gene.  
XX  
KW Pesticide; insecticide; biological control agent; Lepidoptera;  
KW Coleoptera; transgenic plant; maize; Zea mays; Insect resistance;  
KW VIPI; Bacillus cereus; western corn rootworm;  
KW Diabrotica vergifera vergifera; ss.  
XX  
OS Synthetic.  
XX  
PN WO9610083-A1.  
XX  
PD 04-APR-1996.  
XX  
PF 27-SEP-1995; 95WO-EP03826.  
XX  
PR 05-JUN-1995; 95US-0463483.  
PR 28-SEP-1994; 94US-0314594.  
XX





GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 03:18:19 ; Search time 157.96 Seconds  
(without alignments)  
1240.873 Million cell updates/sec

Title: US-08-484-274-8  
Perfect score: 1296  
Sequence: 1 ATGGCTGAGAACACAGAA.....AAACTGGTCTCGATCCTCTAA 1296

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 262060 seqs, 75620496 residues

Total number of hits satisfying chosen parameters: 524120

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA.\*  
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2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/5C\_COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/5D\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/6\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/PTCUS\_COMB.seq.\*  
7: /cgn2\_6/ptodata/2/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1296	100.0	1296	1	US-08-391-339-8
2	1296	100.0	1296	2	US-08-484-274A-8
3	1288	99.4	1296	1	US-08-391-339-17
4	1288	99.4	1296	2	US-08-484-274A-17
5	1011.2	78.0	1296	1	US-08-391-339-7
6	1011.2	78.0	1296	2	US-08-484-274A-7
7	961.6	74.2	1296	1	US-08-391-339-6
8	961.6	74.2	1296	2	US-08-484-274A-6
9	960	74.1	1692	2	US-08-484-274A-3
10	928.8	71.7	1293	1	US-08-391-339-4
11	928.8	71.7	1293	2	US-08-484-274A-4
12	928.8	71.7	1689	1	US-08-391-339-3
13	58.8	4.5	62	1	US-08-391-339-27
14	58.8	4.5	62	2	US-08-484-274A-27
15	58.4	4.5	69	1	US-08-391-339-30
16	58.4	4.5	69	2	US-08-484-274A-30
17	56.2	4.3	69	1	US-08-391-339-33
18	56.2	4.3	69	2	US-08-484-274A-33
19	53.6	4.1	68	1	US-08-391-339-32
20	53.6	4.1	68	2	US-08-484-274A-32
21	53	4.1	61	1	US-08-391-339-31
22	53	4.1	61	2	US-08-484-274A-31
23	52.8	4.1	65	1	US-08-391-339-28
24	52.8	4.1	65	2	US-08-484-274A-28
25	49.8	3.8	7218	1	US-08-232-463-14
26	39.8	3.1	3489	4	US-08-728-323A-1

c 26

27	39.8	3.1	32207	3	US-08-770-379-20	Sequence 20, Appl
c 28	35	2.7	2004	2	US-08-471-033-18	Sequence 18, Appl
c 29	35	2.7	2004	3	US-08-471-044-18	Sequence 18, Appl
c 30	35	2.7	2004	3	US-08-463-483A-18	Sequence 18, Appl
c 31	35	2.7	2004	3	US-08-471-046A-18	Sequence 18, Appl
c 32	35	2.7	2004	3	US-08-470-566B-18	Sequence 18, Appl
c 33	35	2.7	2004	4	US-08-469-334-18	Sequence 18, Appl
c 34	35	2.7	2004	5	US-09-300-529-18	Sequence 18, Appl
c 35	35	2.7	2576	2	US-08-471-033-35	Sequence 35, Appl
c 36	35	2.7	2576	3	US-08-471-044-35	Sequence 35, Appl
c 37	35	2.7	2576	3	US-08-463-483A-35	Sequence 35, Appl
c 38	35	2.7	2576	3	US-08-471-046A-35	Sequence 35, Appl
c 39	35	2.7	2576	3	US-08-470-566B-35	Sequence 35, Appl
c 40	35	2.7	2576	4	US-08-469-334-35	Sequence 35, Appl
c 41	35	2.7	2576	5	US-09-300-529-35	Sequence 35, Appl
c 42	35	2.7	2655	2	US-08-471-033-17	Sequence 17, Appl
c 43	35	2.7	2655	2	US-08-471-033-26	Sequence 26, Appl
c 44	35	2.7	2655	3	US-08-471-044-17	Sequence 17, Appl
c 45	35	2.7	2655	3	US-08-471-044-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1  
US-08-391-339-8  
; Sequence 8, Application US/08391339  
; Patent No. 5463175  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dennis R. Hoerner, Jr.,  
; ADDRESSEE: Monsanto Co. Bldg  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391,339  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/156,968  
; FILING DATE:  
; APPLICATION NUMBER: US/07/717,370  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner, Dennis R., Jr.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10533)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1296 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (synthetic)  
US-08-391-339-8

Query Match 100.0%; Score 1296; DB 1; Length 1296;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Db	1	ATGGCTGAGAACACACAGAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTGGTTCGACT	60
QY	61	GCATTGATGCTTCAACGCTCGTGATTCAGGTTACCTTACCTTGAATTCATCCAAACCCACCAAGT	120
Db	61	GCATTGATGCTTCAACGCTCGTGATTCAGGTTACCTTGAATTCATCCAAACCCACCAAGT	120
QY	121	GAAGGTGCTTCTTTCGGTACGCTGGTTCCTCAACGGTTCCTCCGTTGTTCCTCAATGTC	180
Db	121	GAAGGTGCTTCTTTCGGTACGCTGGTTCCTCAACGGTTCCTCCGTTGTTCCTCAATGTC	180
QY	181	ATGCCAGGAACCTTGACTAGCTGTTCCAAAGTGGCTTCTTGACCCAAATGGGTCCTATGTC	240
Db	181	ATGCCAGGAACCTTGACTAGCTGTTCCAAAGTGGCTTCTTGACCCAAATGGGTCCTATGTC	240
QY	241	ATCCGTTTACGCTACCTTCCAAACCATCATCCCTTGGTGTGATTCCTTTCCTTTCGTTGGA	300
Db	241	ATCCGTTTACGCTACCTTCCAAACCATCATCCCTTGGTGTGATTCCTTTCCTTTCGTTGGA	300
QY	301	AGACCAACAAAGTGAAGGAGCAAGCTAAGGCACCTCGTAACTCATCAAGTCCACTGTG	360
Db	301	AGACCAACAAAGTGAAGGAGCAAGCTAAGGCACCTCGTAACTCATCAAGTCCACTGTG	360
QY	361	CCTTTGATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGT	420
Db	361	CCTTTGATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGT	420
QY	421	CACCTTACCGTGTACCGTGGAGAGCAGACTTCCGCAAGAACCGTGGAGGTTGGGAAC	480
Db	421	CACCTTACCGTGTACCGTGGAGAGCAGACTTCCGCAAGAACCGTGGAGGTTGGGAAC	480
QY	481	CGTCGCTCAACGCTGTCCTACTCAATCTCAGCGCTGATGCATTCGCTGATTCGAT	540
Db	481	CGTCGCTCAACGCTGTCCTACTCAATCTCAGCGCTGATGCATTCGCTGATTCGAT	540
QY	541	CCTAACTGTCTCACGCTTTACCAAGGAATCCTTATCGAAGAACCGTGCACCATC	600
Db	541	CCTAACTGTCTCACGCTTTACCAAGGAATCCTTATCGAAGAACCGTGCACCATC	600
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Db	601	AACCCACAAAGTCTGTGACTCTCTTGTTCGTCGTTTCATCGCTAACGCTGGAGAGTTC	660
QY	661	GTGCTGCTGCTGTATCGGATTCGAGACTGAAGTGGTCTCTCAAGGATATCACACC	720
Db	661	GTGCTGCTGCTGTATCGGATTCGAGACTGAAGTGGTCTCTCAAGGATATCACACC	720
QY	721	ACCAAGGTTCTTCTGCTGTGATGAGCTGTGTTGTCAGCTGGTGACACTCCAAGTCT	780
Db	721	ACCAAGGTTCTTCTGCTGTGATGAGCTGTGTTGTCAGCTGGTGACACTCCAAGTCT	780
QY	781	CTTGCTAACTCCCTTGGTGATGACATCCCATATGGATACCGAAACGTTGATACCAATCGTG	840
Db	781	CTTGCTAACTCCCTTGGTGATGACATCCCATATGGATACCGAAACGTTGATACCAATCGTG	840
QY	841	ATCGCCAAACCCAGAGCTGCTCCACCTATTCCAACTACCGATGCTTCTGGAAGTTCATC	900
Db	841	ATCGCCAAACCCAGAGCTGCTCCACCTATTCCAACTACCGATGCTTCTGGAAGTTCATC	900
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Db	901	GCTACTCCTATGAGATGGGCTTTCGTTGCTGGAACCGTTGAGTTCGCTGGTCTCACT	960
QY	961	GCTGCTCCTAACTGGAAGGCTGCTACGTTCTACACTCACGCTCGTAAGTTGCTTCCA	1020
Db	961	GCTGCTCCTAACTGGAAGGCTGCTACGTTCTACACTCACGCTCGTAAGTTGCTTCCA	1020
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Db	1021	GCCTCTCGCTCCTGCCAGTTCTGAAGAACGTTACTCCAAAGTGGATGGTTTCCTGCCAAGC	1080

QY	1081	ATCCAGATTCCCTTCCAGTCAITTTGGTGTCTACCGTACTCCAGAGCTTATCTACGCT	1140
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QY	1141	TTCGGTCCAGGTCACCTCCGGTATGACTGGTGTCTCAATGACCGCAACCCCTGTTCTGAG	1200
Db	1141	TTCGGTCCAGGTCACCTCCGGTATGACTGGTGTCTCAATGACCGCAACCCCTGTTCTGAG	1200
QY	1201	CTCCTCCAGGTGAGAGAGCTCTATGACATCTCTCCATTCGACCAACCCGTTTCGGT	1260
Db	1201	CTCCTCCAGGTGAGAGAGCTCTATGACATCTCTCCATTCGACCAACCCGTTTCGGT	1260
QY	1261	ATTGGTAAGTCCAAAGCAAACTGGTCCCTGCATCTAA	1296
Db	1261	ATTGGTAAGTCCAAAGCAAACTGGTCCCTGCATCTAA	1296
RESULT 2			
US-08-484-274A-8			
; Sequence 8, Application us/08484274A			
; Patent No. 5776760			
; GENERAL INFORMATION:			
; APPLICANT: Kishore, Ganesh M.			
; TITLE OF INVENTION: Glyphosate Tolerant Plants			
; NUMBER OF SEQUENCES: 33			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Arnold, White & Durkee			
; STREET: P.O. Box 4433			
; CITY: Houston			
; STATE: Texas			
; COUNTRY: USA			
; ZIP: 77210-4433			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/484,274A			
; FILING DATE: 07 June 1996			
; CLASSIFICATION: 435			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Patterson, Melinda L.			
; REGISTRATION NUMBER: 33,062			
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (713)789-2679			
; INFORMATION FOR SEQ ID NO: 8:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 1296 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: double			
; TOPOLOGY: linear			
; MOLECULE TYPE: DNA (synthetic)			
US-08-484-274A-8			

Query Match 100.0%; Score 1296; DB 2; Length 1296;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	ATGGCTGAGAACACAGAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTGGTTCGACT	60
Db	1	ATGGCTGAGAACACAGAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTGGTTCGACT	60
QY	61	GCATTGATGCTTCAACGCTCGTGGATTCAGGTTTACCTTGAATTCATCCAAACCCACCAAGT	120
Db	61	GCATTGATGCTTCAACGCTCGTGGATTCAGGTTTACCTTGAATTCATCCAAACCCACCAAGT	120
QY	121	GAAGGTGCTTCTTTCGGTAAACGCTGGTTCCTCAACGGTTCCTCCGTTGTTCCAAATGTC	180
Db	121	GAAGGTGCTTCTTTCGGTAAACGCTGGTTCCTCAACGGTTCCTCCGTTGTTCCAAATGTC	180



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QY 301 AGACCAACAAGGTGAAGGAGCAAGCTTAAGGCACCTCGTAACTCATCAAGTCCACTGTG 360  
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QY 361 CCTTTGATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGT 420  
Db 361 CCTTTGATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGT 420  
QY 421 CACCTTACCCTGTACCGTGTGAGAGGACTTCGCCAAGGACCGTGGAGGTGGGAACCTT 480  
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QY 481 CGTCGTCTCAACGGTCTTCCTACTCAAACTCTCAGCGCTGATGCAATTCGCTGATTTTCGAT 540  
Db 481 CGTCGTCTCAACGGTCTTCCTACTCAAACTCTCAGCGCTGATGCAATTCGCTGATTTTCGAT 540  
QY 541 CTTAACTTGTCTCAGCGCTTTACCAAGGGAATCCTTATCGAAGAGAACCGGTACACCATC 600  
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QY 601 AACCCACAAGGTCTCGTGACTCTCTTGTTCGTCTGTTTATCGTACGCTAACGGTGGAGGTTT 660  
Db 601 AACCCACAAGGTCTCGTGACTCTCTTGTTCGTCTGTTTATCGTACGCTAACGGTGGAGGTTT 660  
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QY 721 ACCAAGGTTGTTCTGCTGTTGATGAGCTGTTGTTGCGAGCTGGTGCACACTCCAAGTCT 780  
Db 721 ACCAAGGTTGTTCTGCTGTTGATGAGCTGTTGTTGCGAGCTGGTGCACACTCCAAGTCT 780  
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Db 781 CTTGCTTAACCTCCCTTGGTGATGACATCCCAATGGATACCGAAGCTGGATACCAACATCGTG 840  
QY 841 ATCGCAACCCAGAAAGCTGCTCCACGTTATTCCAACTACCGATGCTTCTGGAAGATTCATC 900  
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Db 1021 GCTCTCGCTCCTGCCAGTCTCTGAAGAACGTTACTTCCAAGTGGATGGGTTTCGTCCTCAAGC 1080  
QY 1081 ATCCAGATATCCCTTCCAGTGATTCGTCTGCTTACCGGTACTCCAGACGTTATCTACGCT 1140  
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Db 1261 ATTTGGTAAAGTCCAAAGCAAACTGGTCTCTGCACTCACTAA 1296  
RESULT 4  
US-08-484-274A-17  
: Sequence 17, Application US/08484274A  
: Patent No. 5776760  
: GENERAL INFORMATION:  
: APPLICANT: Kishore, Ganesh M.  
: APPLICANT: Barry, Gerard F.  
: TITLE OF INVENTION: Glyphosate Tolerant Plants  
: NUMBER OF SEQUENCES: 33  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Arnold, White & Durkee  
: STREET: P.O. Box 4433  
: CITY: Houston  
: STATE: Texas  
: COUNTRY: USA  
: ZIP: 77210-4433  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/484,274A  
: FILING DATE: 07 June 1996  
: CLASSIFICATION: 435  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Patterson, Melinda L.  
: REGISTRATION NUMBER: 33,062  
: REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (713)789-2679  
: INFORMATION FOR SEQ ID NO: 17:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 1296 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: double  
: TOPOLOGY: linear  
: MOLECULE TYPE: DNA (recombinant)  
: FEATURE:  
: NAME/KEY: CDS  
: LOCATION: 1..1296  
US-08-484-274A-17  
Query Match 99.4%; Score 1288; DB 2; Length 1296;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1291; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
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QY 121 GAAGGTGCTTCTTTTCGGTAACGCTGGTTCGTTCAACGGTTCCTCCGTTGTTTCCAATGTC 180  
|||||  
Db 121 GAAGGTGCTTCTTTTCGGTAACGCTGGTTCGTTCAACGGTTCCTCCGTTGTTTCCAATGTC 180  
|||||  
QY 181 ATCCCAAGGAACCTTGACTAGCGTTCCAAAGTGGCTTCTTGACCAATGGGTCCATTTGTC 240  
|||||  
Db 181 ATCCCAAGGAACCTTGACTAGCGTTCCAAAGTGGCTTCTTGACCAATGGGTCCATTTGTC 240  
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QY 241 ATCCGTTTTCAGCTACTTTCACCAACCATCATGCTTGGTGTGATTCGTTTCTTGTGCTGGA 300  
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Db 241 ATCCGTTTTCAGCTACTTTCACCAACCATCATGCTTGGTGTGATTCGTTTCTTGTGCTGGA 300  
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QY 301 AGACCAACAAGGTGAAGGAGCAAGCTTAAGGCACCTCGTAACTCATCAAGTCCACTGTG 360  
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|||||

Db 301 AGACCAAAAGGTGAAGGAGCAAGCTAAGGCATCTCCGTAACCTCATCAAGTCCACTGTG 360  
Qy 361 CTTTGTATCAAGTCTTGGCTGAGAGGCTGATGCTAGCCACCTTATCCGTCAACGAAGT 420  
Db 361 CTTTGTATCAAGTCTTGGCTGAGAGGCTGATGCTAGCCACCTTATCCGTCAACGAAGT 420  
Qy 421 CACCTTACCGGTGACCGTGGAGAGCAGACATTCGCCAAGGACCGTGGAGGTGGGAACCTT 480  
Db 421 CACCTTACCGGTGACCGTGGAGAGCAGACATTCGCCAAGGACCGTGGAGGTGGGAACCTT 480  
Qy 481 CTTCTCTCAACGGTGTTCGTACTCAAACTCCTACGCGTGTATTCGCTGATTTCCGAT 540  
Db 481 CTTCTCTCAACGGTGTTCGTACTCAAACTCCTACGCGTGTATTCGCTGATTTCCGAT 540  
Qy 541 CTTAACTTCTCAGCGCTTTACCAAGGGAATTCCTTATCGAAGAGACGGTCAACCATC 600  
Db 541 CTTAACTTCTCAGCGCTTTACCAAGGGAATTCCTTATCGAAGAGACGGTCAACCATC 600  
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Db 1201 CTCTCCGAGGTGAGAAGACCTCTATCCACATCTCTCCATTCGCAACCAACCGTTTCGGT 1260  
Qy 1261 ATTGGTAAGTCCAAGCAAACTGGTCTGCATCTCTAA 1296  
Db 1261 ATTGGTAAGTCCAAGCAAACTGGTCTGCATCTCTAA 1296

RESULT 5  
US-08-391-339-7  
; Sequence 7, Application US/08391339  
; Patent No. 5463175  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.

; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dennis R. Hoerner, Jr.,  
; ADDRESSEE: Monsanto Co. B4F,  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391,339  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/156,968  
; FILING DATE:  
; APPLICATION NUMBER: US/07/717,370  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner, Dennis R., Jr.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10533)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1296 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (recombinant)  
US-08-391-339-7

Query Match 78.0%; Score 1011.2; DB 1; Length 1296;  
Best Local Similarity 86.3%; Pred. No. 0;  
Matches 1118; Conservative 0; Mismatches 178; Indels 0; Gaps 0;  
Qy 1 ATGGCTGAGAACCAAGAAGGTTCGTATCGCTGAGGCTGGAATCGTTGGTCTTTGCAC 60  
Db 1 ATGGCTGAGAACCAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCAC 60  
Qy 61 GCTTTGATGCTTCAACGCTGCTGGAATTCAAAGTCACCTTGATTGACCCGAAACCTCT 120  
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Qy 1261 ATTGGTAAGTCCAGCAAGCAACTGCTCTCCATCTCTAA 1296
Db 1261 ATTGGCAATCCAGCAAGCAAGCGGTCCGCAAGTTAA 1296
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RESULT 6

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US-08-484-274A-7
; Sequence 7, Application US/08484274A
; Patent No. 5776760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
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; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/484,274A
; APPLICATION NUMBER: 07 June 1996
; FILING DATE: 435
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: patterson, melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBF130 38-21(13560)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)789-2679
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (recombinant)
; US-08-484-274A-7
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Query Match 78.0%; Score 1011.2; DB 2; Length 1296;
Best Local Similarity 86.3%; Pred. No. 0;
Matches 1118; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

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Db 1 ATGGCTCAGACACCAAGAGGTTCGCTATCGCTCGAGCTGGAATCGTTGGTGGTTCGACT 60

Qy 61 GCTTTGATGCTTCAACGTCGTTGGAATTCGAAGGTTCACCTTGATTCGAACCCACCCAGGT 120
Db 61 GCTTTGATGCTTCAACGTCGTTGGAATTCGAAGGTTCACCTTGATTCGAACCCACCCAGGT 120

Qy 121 GAAGGTGCTTCTTCGGTGAAGCTGGTTCGCTTCAACGGTTCCTCGTGGTTCGAATGTC 180
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Qy 181 ATGCCAGAAACTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCCAATGGGTCCATTTGCC 240
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Db 481 CGGCGTCTCAACGGTGTTCGACCGCATCCTCTCTGATGCTGTTCGCGTGATTTTCGAT 540

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Db 721 ACTAACGGTGTCTGCTGTTGATGCGAGCTGTTGTTGACAGTGGTGGACACATCTAAATCA 780  
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Db 781 CTTCCTTAATTCGGTAGCGATGACATCCCGCTCGATACCCAGACGTGGATATCATATGTC 840  
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Db 1261 ATTGGCAAAATCCAAAGCAACGGGTCGCGCAAGTTAA 1296

RESULT 7  
US-08-391-339-6  
; Sequence 6, Application US/08391339  
; Patent No. 5463175  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dennis R. Hoerner, Jr.,  
; ADDRESSEE: Monsanto Co. BB4F  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/391.339

; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/156.968  
; FILING DATE:  
; APPLICATION NUMBER: US/07/171.370  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner, Dennis R., Jr.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10533)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1296 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (recombinant)  
; US-08-391-339-6  
  
Query Match 74.2%; Score 961.6; DB 1; Length 1296;  
Best Local Similarity 83.9%; Pred. No. 0;  
Matches 1087; Conservative 0; Mismatches 209; Indels 0; Gaps 0;  
  
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Qy 301 AGACCAACAAGGTGAAGGAGCAAGCTAAGGCACTCCGTAACCTCATCAAGTCCCACTGTG 360  
Db 301 AGACCAACAAGGTGAAGGAGCAAGCTAAGGCACTCCGTAACCTCATCAAGTCCCACTGTG 360  
Qy 361 CCTTTGATCAAGTCTTGGCTGAGGAGCTGATGCTAGCCACCTTATCCGTCACCAAGGT 420  
Db 361 CCTTTGATCAAGTCTTGGCTGAGGAGCTGATGCTAGCCACCTTATCCGTCACCAAGGT 420  
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Db 421 CATCTGACCGTATATCGTGGAGAGCAGACTTCCGCAAGGACCGTGGAGGTTGGGAATTT 480  
Qy 481 CGTGTCTCAACGGTGTTCGTAACCTCAATCTCAGCGCTGATGCTATTCGTTGATTTCCGAT 540  
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Qy 541 CCTAACTTGTCTCAGCGCTTTTACCAAGGAATCTTATCGAAGAGCAACGGTCCACACCATC 600  
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Qy 601 AACCCAAAGGTCGCTGACTCTCTTCTGCTCGTTTCATCGCTACGGTGGAGAGTTC 660  
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721	Db		
721	Db	ACGAACGGGTCTTGCGCGCTTGATCAGCGGTGTGCGAGCGCGGCACACTCGAAATCA	780
781	Qy	CTTGTCTAACTCCCTTGGTGATGACATCCGATTCGATACCGAAGCTGGATACCAACATCGTG	840
781	Db		
781	Db	CTTGTCTAAATTTCGTAGCGGATGACATCCCGCTTCGATACCGAAGCTGGATATCATATCGTC	840
841	Qy	ATCGCAACCCAGAAAGCTGCTCCAGCTATTCCAACTACCGATGCTCTGGAAAGTTTCATC	900
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901	Db		
901	Db	GCAGACACCTATGSAATGGGGCTTCGCGTGGCGGTACGGTTGAGTTGCGTGGGCTCACA	960
961	Qy	GCTGTCTTAATGAGAGGGTGCTCAGCTTCTCTATCACTCAGGCTCGTAAGTTGCTTCCA	1020
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1081	Qy	ATCCCAGATTCCCTTCCAGTAGTTGGTCTGCTACCCGCTACTCCAGACGTTATCTACGCT	1140
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1141	Qy	TTCGGCTCAGGGTCACCTTCGGTATGACTGGTGCTCCAATGACCGCAACCCCTGTTCTTGAG	1200
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1201	Qy	CTCCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTCGCAACCAACCCGTTTCGGT	1260
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1261	Qy	ATTGGTAGTTCGAAGCAAACTGGTCTCGATCTCTAA	1296
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## RESULT 8

US-08-484-274A-6  
; Sequence 6, Application US/08484274A  
; Patent No. 5776760  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,274A  
; FILING DATE: 07 June 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Patterson, Melinda L.  
; REGISTRATION NUMBER: 33,062  
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A  
; TELECOMMUNICATION INFORMATION:



Db 841 ATCCGAATCGGAAGCGCTCCACGCATTCGAGACCGCATGCTCAGGAAAAATTCATC 900  
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Db 1201 CTCTCGCAGCGAAGACCTCAATCGACATTTGCGCCCTTCGCAACCAACCGCTTTGGT 1260  
Qy 1261 ATTGCTAAGTCCAGCAAACTGGTCTGCTGCATCCCTAA 1296  
Db 1261 ATTGGCAATCCAGCAAAACGGTCCGGCAAGTTAA 1296

RESULT 9

US-08-484-274A-3  
; Sequence 3, Application US/08484274A  
; Patent No. 5776760  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glyphosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P. O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,274A  
; FILING DATE: 07 June 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Patterson, Melinda L.  
; REGISTRATION NUMBER: 33,062  
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (713)789-2679  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1692 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-484-274A-3

Query Match 74.18; Score 960; DB 2; Length 1692;

Best Local Similarity 83.8%; Pred. No. 0;  
Matches 1086; Conservative 0; Mismatches 210; Indels 0; Gaps 0;  
Qy 1 ATGCTGAGAACACAAAGGTTGGTATCGCTGGAGCTGGAATCGTGTGGTGTGGTACT 60  
Db 120 ATGCTGAGAACACAAAGGTTAGGATCGCTGGAGCCGGAATCGTGGCGGTATGCACG 179  
Qy 61 GCTTTGATGCTTCAACGCTCGTGGATTCAAGGTTACCTTGATTGATCCAAACCCACAGGT 120  
Db 180 GCGTGTATGCTTTCAGCGCCCGGGAATCAAGTCACTTTGATTTGACCCGAAACCTTCTTGG 239  
Qy 121 GAAGGTGCTTCTTTCGGTAACGCTGGTTCCTCAACGGTTCTCGCTGTGTGTTCCTCAATGTCC 180  
Db 240 GAAGGTGCTATGTTGGGATGCGCGGATGCTTCAACGGCTCATCCGCTGCTCCTATGTCC 299  
Qy 181 ATGCCAGGAAACTTTGACTAGCTTTCCAAAGTGGCTTTCTTGACCCAAATGGGTCCAATGTCC 240  
Db 300 ATGCCGGGAAACTTTGACGAGCGTCCGAAGTGGCTTCTTGACCCGATGGGCGCTTGTGCA 359  
Qy 241 ATCCGTTTCAGCTACTTTCCAAACCATCATGCTTTGGTGTGATTCTTCTTGTGCTGGA 300  
Db 360 ATCCGTTTCAGCTATTTTCCAAACCATCATGCCCTGGTTGATTCGCTTTCTGTAGCCGGA 419  
Qy 301 AGACCAAAAGGTGAGGAGCAAGCTAAGGCACTCCGTAACCTCATCAAGTCCCACTGTG 360  
Db 420 AGACCAAAAGGTGAGGAGCAAGGAGCGGAAAGCACTCCGCAATCTCATCAAGTCCCAAGGTG 479  
Qy 361 CTTTGTATCAAGTCTTTCGGTGGAGGCTGATGCTTAGCCACCTTATCCGTCAGCAAGGT 420  
Db 480 CTTGTATCAAGTCTTTCGGGAGGAGGCTGATGCGAGSCCATCTGATCCGCCATGAAGGT 539  
Qy 421 CACCTTACCCTGTACCGTGGAGAGACAGACTTCCGCAAGGACCGTGGAGGTGGGAACCTT 480  
Db 540 CATCTGACCGTATATCGTGGAGAGACAGACTTCGCAAGAGCCGCGAGGTGGGAACGTG 599  
Qy 481 CGTGTCTCAACGGTGTTCGTACTCAAAATCCTCAGCGCTGATGATTCGCTGATTCGCTGATTCGAT 540  
Db 600 CGGCTCTCAACGGTGTTCGCAAGGAGATCCTCAGCGCGGATGCGTTCGCGGATTTCCGT 659  
Qy 541 CTTAACTTGTCTCAGCGCTTTACCAAGGGAATCTTATCGAAGAGAACCGGTCAACACCTC 600  
Db 660 CCGAACTTGTGCGATGCGTTTACCAAGGGCATCTTATAGAAGAGAACCGGTCAACAGATT 719  
Qy 601 AACCACCAAGGTCTCGTCACTCTCTTGTTCGTGTTTCATCGCTTAACGGTGGAGAGTTC 660  
Db 720 AATCCGCAAGGGCTCGTGACCTCTTGTTCGCGGCTTTTATCGCGAACCGGTGGCGAATTC 779  
Qy 661 GTGCTGCTCGTGTATCGGATTCGAGACTGAAGGTCTGCTCTCAAGGTATACACCACC 720  
Db 780 GTATCTGCGCGTGTATCGGCTTTGAGACTGAAGGTAGGGCGCTTAAAGGCATTAACAACC 839  
Qy 721 ACCAAGCGTGTTCCTTGTGTTGATGCAAGTGTGTTGCAAGCTGGTGCACACTTCCAAAGTCT 780  
Db 840 ACGAAGCGGCTTCTGGCGGTTGATGCAAGGTTGTGCGAGCGCGCGGCACTCGAANAACA 899  
Qy 781 CTTGCTAACTCCCTTGGTGTGATGACATCCCATTTGATACCGAAGCTGGATACACATCGTG 840  
Db 900 CTTGCTAACTCCCTTGGTGTGATGACATCCCATTTGATACCGAAGCTGGATACATATCGTC 959  
Qy 841 ATCGCAACCCAGAGCTGCTCCAGTATTCCAACTACCGATGCTTCTGGAAGGTTTCATC 900  
Db 960 ATCGGAATCCGGAAGCGCTCCAGCATTCGAGACCGATTCGAGACCGATGCTCAGGAAATTCATC 1019  
Qy 901 GCTACTCTATGGAGATGGGCTTTCGTTGCTTGAACCGTTGAGTTCGCTGGTCTCACT 960  
Db 1020 GCGACACCTATGGAAATGGGGCTTCGCGTGGCGGTTAGTTCGCTGGGCTCACA 1079  
Qy 961 GCTGCTCTAACTGGAAGCGTGTGCTACAGTTCCTTACACTCAGGCTCGTAAGTTGCTTCCA 1020  
Db 1080 GCGGCTCTTAACGTGGAACCGTGGCATGTGCTCTATAGCGACGCTCGCAAAACCTTCTGCA 1139  
Qy 1021 GCTCTGCTCTGCGAGTTCGAGAACGTTACTTCCAAGTGGTTCGCTCAAGC 1080

Db 1140 GCCCTCCGCGCTCGGAGTCTGAAGAACGATATTCAAAATGGATGGGGTTCCGGCCGAGC 1199  
QY 1081 ATCCAGATTCCCTTCAGTGATTGGTCGTACCGGTACTCCAGACGTTATCTACGCT 1140  
Db 1200 ATCCGGATTTCGCTCCCGTGATTGCGGGGAACCCGGACACCCGACGTAATCTATGCT 1259  
QY 1141 TTCCGTCACGGTACCTTCGCTATGACTGGTGTCCCAATGACCCCAACCCCTTCGTTCTGAG 1200  
Db 1260 TTCCGGCATGGTCTATCTCGGCATGACAGGGGCGCGATGACCGCAACGCTCGTCTCAGAG 1319  
QY 1201 CTCCTCGCAGGTGAGAGACCTCTATCGACATCTCTCCATTCGCAACCAACCGTTTCGCT 1260  
Db 1320 CTCCTCGCAGGGGAAAAGACCTCAATCGACATTTTCGCCCTTCGCAACCAACCGCTTGGT 1379  
QY 1261 ATTGGTAAGTCCAAAGCAATGCTGCTCGCATCCATA 1296  
Db 1380 ATTGGCAATCCAAAGCANAGGGTCCGGCAAGTTAA 1415

RESULT 10

US-08-391-339-4  
: Sequence 4, Application US/08391339  
: Patent No. 5463175  
: GENERAL INFORMATION:  
: APPLICANT: Kishore, Ganesh M.  
: APPLICANT: Barry, Gerard F.  
: TITLE OF INVENTION: Glyphosate Tolerant Plants  
: NUMBER OF SEQUENCES: 33  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Dennis R. Hoerner, Jr.,  
: ADDRESSEE: Monsanto Co. B4F  
: STREET: 700 Chesterfield Village Parkway  
: CITY: St. Louis  
: STATE: Missouri  
: COUNTRY: USA  
: ZIP: 63198  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/391,339  
: FILING DATE:  
: CLASSIFICATION: 800  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US/08/156,968  
: FILING DATE:  
: APPLICATION NUMBER: US/07/717,370  
: FILING DATE:  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Hoerner, Dennis R., Jr.  
: REGISTRATION NUMBER: 30,914  
: REFERENCE/DOCKET NUMBER: 38-21(10533)  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (314)537-6099  
: INFORMATION FOR SEQ ID NO: 4:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 1293 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: double  
: TOPOLOGY: linear  
: MOLECULE TYPE: DNA (genomic)  
: FEATURE:  
: NAME/KEY: CDS  
: LOCATION: 1..1293

US-08-391-339-4  
Query Match 71.7%; Score 928.8; DB 1; Length 1293;  
Best Local Similarity 83.8%; Pred. No. 0;  
Matches 1086; Conservative 0; Mismatches 207; Indels 3; Gaps 3;

QY 1 ATGCGCTGAGAACACAAAGAGTTGGTTATCGCTGGAGCTGCAATCGTTGGTGTTCGACT 60  
Db 1 ATGCTGAGAACACAAAGTAGGCATCGCTGGAGCCGGAATCGTCGGCGTATGCACG 60  
QY 61 GCTTTGATGCTTCAACGCTCGTGATTCGAAGGTTACCTTGATTGATTCAAACCCACAGGT 120  
Db 61 GCCTGTGATGCTTCAAGCCCGCGGATTCAAAAGTCACTTGTATGATGACCCGAAACCCCTCTCGC 120  
QY 121 GAAGGTGCTTCTTTCGGTAAACGCTGGTTGCTTCAACGGTTCCCTCCGTTGTTCCAAATGCTC 180  
Db 121 GAAGGTGCTATGTTGGGAATGCGGATGCTTCAACGGCTCATCCGTCGTCCTTATGCTC 180  
QY 181 ATCCAGGAAACTTGACTAGCGTTTCCAAAGTGGCTTCTTGACCCCAATGGGTGCTCATTTGCTC 240  
Db 181 ATCCGGGAAACTTGAGAGCGTGGCGAAGTGCTCTTTCACCCGATGGG - CGGTTGTCA 239  
QY 241 ATCCGTTTTCAGCTACTTTCACCAACCATCATGCTTGGTTGATTGATTGTTCTTCTTGTCTGCTGA 300  
Db 240 ATCCGGTTTCACTA -TTTCCCAACCATCATGCC -TGGTTGATTGCTTCTTGTGTAGCCGA 297  
QY 301 AGACCAAAACAAAGTGAAGGAGCAAGCTAAGGCACCTCCGTAACCTCATCAAGTCCACTGTG 360  
Db 298 AGACCAAAACAAAGTGAAGGAGCAGGCGAAGACACTCCGCAATCTCATCAAGTCCACGGTG 357  
QY 361 CCTTTGATCAAGTCTTGGCTGAGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGT 420  
Db 358 CCTCTGATCAAGTCAATTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGT 417  
QY 421 CACCTTACCGTGTACCGTGGAGAGACGACTTCCCAAGGACCGTGGAGGTTGGGAACCT 480  
Db 418 CATCTGACCGTATATCGTGGAGAAGCAGACTTCCCAAGGACCGCGAGGTTGGGAACCTG 477  
QY 481 CGTCGCTCAACGCTGTTCGTACTCAAACTCTCAGCGCTGATGATTCGTTGCTGATTTCGAT 540  
Db 478 CGCGGTCTCAACGCTGTTCGCACGCGAGATCCTCAGCGCCGATGCGTTGCGGGGATTCGAT 537  
QY 541 CTTAACTTGTCTCACGCCCTTTACCAAGGGAATCCTTATCGAAGAGAACGCTGCACACATC 600  
Db 538 CCGAACTTGTGCGATGCGTTTACCAAGGCGCTTCTTATAGAAGAACGCTGCACACGAT 597  
QY 601 AACCCACAGGCTCTCGTACTCTTCTGTTTCGTTTCATCTCCTACGCTGAGAGATTC 660  
Db 598 AATCCGCAAGGGCTCGTGACCCCTCTTGTTCGGCGCTTTTATCGCGAACGCTGCGGAATTC 657  
QY 661 GTGCTGCTGCTGTTATCGGATTTCGAGACTGAAGGCTGCTCTCAAGGGTATTCACAC 720  
Db 658 GTATCTGCGCGTGTCTATCGCTTTGAGACTGAAGGTAGGCGCTTAAAGGCAATACNACC 717  
QY 721 ACCAACGGTGTCTTGTGTTGATGAGCTGTTGTTGCAAGCTGGTGCACACTCCAAAGTCT 780  
Db 718 ACGAAGCGGCTTCTGCGCGTTGATGACGCGGTTGTGCGAGCGGCACACTCGMAATCA 777  
QY 781 CTTGCTAACTCCCTTGGTGATGACATCCCATTCGATACCGAACGTTGGATACCATCCGTG 840  
Db 778 CTTGCTAACTTCGCTAGGCGATGACATCCCGCTCGATACCGAACGTTGGATATCATATCGTC 837  
QY 841 ATCCCAACCCAGAAAGCTGCTCCACGTTATTCCAACTACCGATGCTTCTGGAAGTTTCATC 900  
Db 838 ATCCGCAATCCGGAAGCGCTCCACGATTCGCGACGCGCATGCGTCAAGGAATTCATC 897  
QY 901 GCTACTCTTATGAGATGGGTCTTTCGTTGCTGGAAACCGTTGAGTTGCTGCTGCTCACT 960  
Db 898 GCGACACCTATGGAATGGGGCTTCGCGTGGCGGGTACGGTTGAGTTGCTGCTGGGCTCACA 957  
QY 961 GCTGCTCTAACTGGAAGCGTGTCTCAGTTCTCTACACTCACGCTCGTAGTTGCTTCCA 1020  
Db 958 GCGGCTCTTAACTGGAAGCGTGGCGATGCTCTATACGCAACGCTCGAAACATCTTCTTCCA 1017  
QY 1021 GCTCTCGCTCCTGCCAGTTCTGAAGAACGTTTACTTCAAGTGGATGGTTTTCCTGCTCAAGC 1080  
Db 1018 GCCTCGCGCTGCGAGTCTGGAAGAACGATATTCCAATGGATGGGTTCCGCGCGAGC 1077  
QY 1081 ATCCCAAGTTCCCTTCCAGTGATTGGTGTGCTACCGCTACTCCAGACGTTATCTACGCT 1140

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Db 1078 ATCCGGGATTCGCTCCCGGATGATGGCGGGCAACCCGGACACCCGACGTAATCTATGCT 1137
Qy 1141 TTCGGTCACGCTACCTCGGTATGACTGGTGTCTCAATGACCGCAACCCCTCGTTTCTGAG 1200
Db 1138 TTCGGCCATGGTCATCTCGGCATGACAGGGCGCGGATGACCGCAACGCTCGTCTCAGAG 1197
Qy 1201 CTCTCCGAGGTGAGAGACCTCTATGACATCTCTCAATTCGACCAACCCGTTTCGGT 1260
Db 1198 CTCTCCGAGCGGAAAGAGCTCAATGACATTTGCGCCCTTCGCAACCAACCGCTTTGGT 1257
Qy 1261 ATTGGTAAGTCCAAAGCAAACTGGTCTGCACTCTAA 1296
Db 1258 ATTGGCAATCCAAAGCAAAACCGGTTCGCGCAAGTTAA 1293

RESULT 11
US-08-484-274A-4
: Sequence 4, Application US/08484274A
: Patent No. 5776760
: GENERAL INFORMATION:
: APPLICANT: Kishore, Ganesh M.
: APPLICANT: Barry, Gerard F.
: TITLE OF INVENTION: Glyphosate Tolerant Plants
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/484,274A
: FILING DATE: 07 June 1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Patterson, Melinda L.
: REGISTRATION NUMBER: 33,062
: REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (713)789-2679
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1293 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1293
: US-08-484-274A-4

Query Match 71.7%; Score 928.8; DB 2; Length 1293;
Best local Similarity 83.8%; Pred. No. 0;
Matches 1086; Conservative 0; Mismatches 207; Indels 3; Gaps 3;

Qy 1 ATGGCTGAGAACCAAGAAGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTTCGCACT 60
Db 1 ATGTCTGAGAACCAAAAAAGTAGGAGATCGCTGGAGCCGGGAATCGTCGGCGTATGCACG 60
Qy 61 GCTTTGATGCTTCAACGTCGTTGATTCAGAGTTACCTTTGATTGATCCAAACCCACCAAGGT 120
Db 61 GCGCTGATGCTTTCAGCGCCGGATTCAAAGTCACCTTTGATTGATGACCCGACCCCTCCTGGC 120
Qy 121 GAAGTGCTTCTTCGGTAAACGCTGGTGTTCCTCAACGGTTCCTCCGTTGTTCCAAATGTCC 180
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Db 121 GAAGTGCTCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGTCCCTATGTCC 180
Qy 181 ATGCCAGAAACTATGACTAGCTTCCAAAGTGGCTTCTTGACCCAATGGGTGCCATTTGCC 240
Db 181 ATGCCGGGAAACTATGACGAGCGTCCGAAGTGGCTCCTTTGACCCGATGGG-CCGTTGTCA 239
Qy 241 ATCCGTTTTCAGCTACTTTTCCAAACCATCATGCCTTGGTGTGATTCGTTTCTGTTCCTGGA 300
Db 240 ATCCGGTTTCAGCTA-TTTTCCAAACCATCATGCC-TGGTTGATTTCGCTTCTGTTAGCCGA 297
Qy 301 AGACCAAAACAAAGGTGAAGGAGCAAGCTTAAGGCATCTCCGTAACTTCATCAAGTCCACATGTG 360
Db 298 AGACCAAAACAAAGGTGAAGGAGCAAGCGGCAAAACACTTCGCGCAATCTCATCAAGTCCACGCTG 357
Qy 361 CCTTTGATCAAGTCTCTTGGCTGAGGAGGCTGATGCTTAGCCACCTTATTCCTCCGTCACGAAGGT 420
Db 358 CCTCTGATCAAGTCAATTTGGCGGAGGAGGCTGATCCGAGCCATCTGATCCGCCCATGAAGGT 417
Qy 421 CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAAGGACCGTGGAGGTTTGGGAATTT 480
Db 418 CATCTGACCGTATATCTGTGGAGAGCAGACTTCGCCAAGGACCGCGGAGGTTTGGGAATG 477
Qy 481 CCTCGTCTCAACGGTCTTCGTACTCAAAATCCTTCAGCGCTGATGCAATTCGCTGATTTCCGAT 540
Db 478 CGCGCTCTCAACGGTGTTCGCAACGAGATCCTCAGCGCCGATGCGTTTCGGGGATTTCCGAT 537
Qy 541 CCTAACTTGTCTCAGCGCTTTACCAAGGAATCCTTATCGAAGAGAGAGCGTCAACACCATC 600
Db 538 CCGAATCTGTCCGATGCGTTTACCAAGGGCAATCTTATAGAAAGAGAGCGTCAACAGATTT 597
Qy 601 AACCCACAAGGTCTCGTACCTCTTGTGTCTGCTGTTTCATCGCTAACGGTGGAGAGTTTC 660
Db 598 AATCCGCAAGGGCTCGTGACCCCTCTTGTTCGGCGTTCCTATCGCGAAGCGTGGCGAATTC 657
Qy 561 GTGCTCTCGTGTATTCGGATTCGAGACTGAAGTGTGCTCTCAAGGGTATCACCAC 720
Db 658 GTATCTCGCGTGTGTCATCGCGCTTTGAGACTGAAGTGAAGGCGCTTAAAGGCATTTACAACC 717
Qy 721 ACCAAGGTGTCTTGTGCTGTGATGTCAGCTGTTGTCAGCTGTCACACTCCCAAGTCT 780
Db 718 ACGAAGCGGCTTCGCGCGTGTGATGTCAGCGGTTCGTCAGCGCGCGGCACACTCCAAATCA 777
Qy 781 CTTCCTAACTCCCTTGGTGTGATGACATCCCATTTGGATACCGCAACGTGGATACCACATCGT 840
Db 778 CTTCCTAACTCGTAGCGGATGACATCCCGCTCGATACCGCAACGTGGATATCATATCGTC 837
Qy 841 ATCCCAACCCAGAGCTGCTCCAGCTATTTCCAACTACCGATGCTTCTGGAAGTTCATC 900
Db 838 ATCCGGAATCCGGAAGCGCTCCACGCAATTCGCGACGACCGATGCGTTCAGGAAAAATTCATC 897
Qy 901 GCTACTCTATGGAGATGGGTCTTCGTGTTGCTGGAACCGTTGAGTTCGCTGCTCACT 960
Db 898 GCGACACTATGGAATGGGCTTCGCGTGGCGGTACGGTTGAGTTCGCTGCGCTCACA 957
Qy 961 GCTGCTCTAACTGGAAGCGTGTCTCAGCTTCTCTACACTCAGCTCGCTAAGTTCCTTCCA 1020
Db 958 GCGCTCTCTAACTGGAAGCGTGTCTCAGCTTCTATACGCAACGCTCGGAAACTTCTTCCA 1017
Qy 1021 GCTCTCCGCTCTGCCAGTTCTGAAGAAAGCTTACTTCCAAAGTGGATGGGTTTCCGTCCAAGC 1080
Db 1018 GCGCTCCGCTCTGGAGTTCTGAAGAAACGATATTTCCAAATGGATGGGTTCGCGCCGAGC 1077
Qy 1081 ATCCAGATTCCTTCAGTGTATTGGTGTCTACCGCTACTCCAGAGCTTATCTAGCT 1140
Db 1078 ATCCCGGATTCGCTTCGCGGTGATTTGGCGGGCAACCCGGACACCCGACGTAATCTATGCT 1137
Qy 1141 TTCGGTCACGCTCACCTCGGTATGACTGGTGTCTCAATAGCCGCAACCCCTCGTTTCTGAG 1200
Db 1138 TTCGGCCATGGTCTATCTCGGCATGACAGGGGCGCGGATGACCGCAACGCTGCTCTCAGAG 1197
Qy 1201 CTCTCCGAGGTGAGAGAGACCTCTATGACATCTCTCCATTCGCAACCAACCGTTTCGGT 1260
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## RESULT 13

US-08-391-339-27  
: Sequence 27, Application US/08391339  
: Patent No. 5463175  
: GENERAL INFORMATION:  
: APPLICANT: Kishore, Ganesh M.  
: APPLICANT: Barry, Gerard F.  
: TITLE OF INVENTION: Glyphosate Tolerant Plants  
: NUMBER OF SEQUENCES: 33  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Dennis R. Hoerner, Jr.,  
: ADDRESSEE: Monsanto Co., BB4F  
: STREET: 700 Chesterfield Village Parkway  
: CITY: St. Louis  
: STATE: Missouri  
: COUNTRY: USA  
: ZIP: 63198  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/391,339  
: FILING DATE:  
: CLASSIFICATION: 800  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US/08/156,968  
: FILING DATE:  
: APPLICATION NUMBER: US/07/17,370  
: FILING DATE:  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Hoerner, Dennis R., Jr.  
: REGISTRATION NUMBER: 30,914  
: REFERENCE/DOCKET NUMBER: 38-21(10533)  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (314)537-6099  
: INFORMATION FOR SEQ ID NO: 27:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 62 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: DNA (synthetic)  
US-08-391-339-27

Query Match 4.5%; Score 58.8; DB 1; Length 62;  
Best Local Similarity 96.8%; Pred. No. 1.6e-10;  
Matches 60; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 30 CGCTGGAGCTGGAATCGTTGGTGTTCGACATGCTTTGATGCTTCAACGTCGTGGATTCAA 89  
|||||  
Db 1 CCCTGGAGCTCGAATCGTTGGTGTATGATGCTTCAACGTCGTGGATTCAA 60  
Qy 90 GG 91  
|  
Db 61 AG 62

## RESULT 14

US-08-484-274A-27  
: Sequence 27, Application US/08484274A  
: Patent No. 5776760  
: GENERAL INFORMATION:  
: APPLICANT: Kishore, Ganesh M.  
: APPLICANT: Barry, Gerard F.  
: TITLE OF INVENTION: Glyphosate Tolerant Plants  
: NUMBER OF SEQUENCES: 33  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Arnold, White & Durkee  
: STREET: P.O. Box 4433

CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210-4433  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,274A  
FILING DATE: 07 June 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Patterson, Melinda L.  
REGISTRATION NUMBER: 33,062  
REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (713)789-2679  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 62 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (synthetic)  
US-08-484-274A-27

Query Match 4.5%; Score 58.8; DB 2; Length 62;  
Best Local Similarity 96.8%; Pred. No. 1.6e-10;  
Matches 60; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 30 CGCTGGAGCTGGAATCGTTGGTGTTCGACATGCTTTGATGCTTCAACGTCGTGGATTCAA 89  
|||||  
Db 1 CCCTGGAGCTCGAATCGTTGGTGTATGATGCTTCAACGTCGTGGATTCAA 60  
Qy 90 GG 91  
|  
Db 61 AG 62

## RESULT 15

US-08-391-339-30  
: Sequence 30, Application US/08391339  
: Patent No. 5463175  
: GENERAL INFORMATION:  
: APPLICANT: Kishore, Ganesh M.  
: APPLICANT: Barry, Gerard F.  
: TITLE OF INVENTION: Glyphosate Tolerant Plants  
: NUMBER OF SEQUENCES: 33  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Dennis R. Hoerner, Jr.,  
: ADDRESSEE: Monsanto Co., BB4F  
: STREET: 700 Chesterfield Village Parkway  
: CITY: St. Louis  
: STATE: Missouri  
: COUNTRY: USA  
: ZIP: 63198  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/391,339  
: FILING DATE:  
: CLASSIFICATION: 800  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US/08/156,968  
: FILING DATE:  
: APPLICATION NUMBER: US/07/17,370  
: FILING DATE:

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; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 69 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
US-08-391-339-30

Query Match 4.5%; Score 58.4; DB 1; Length 69;
Best Local Similarity 91.2%; Pred. No. 2.3e-10;
Matches 62; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 715 ACCACCACCAACGGTGTCTTGGTGTGATGCAGCTGTTGTCAGCTGGTGACACTCC 774
Db 2 ACAACCACTAACGGTGTCTTGGTGTGATGCAGCTGTTGTCAGCTGGTGACACTCT 61

QY 775 AGTCTCT 782
Db 62 AAATCACT 69
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Search completed: January 1, 2001, 03:18:40  
Job time: 29344 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 01:12:53 ; Search time 3327.86 Seconds  
(without alignments)  
2407.829 Million cell updates/sec

Title: US-08-484-274-8  
Perfect score: 1296  
Sequence: 1 ATGGGTGAGACCAACAGAA.....AAACTGGTCTCGATCCTTAA 1296

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues 14379728  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*  
1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_est3.\*  
4: gb\_est4.\*  
5: gb\_est5.\*  
6: gb\_est6.\*  
7: gb\_est7.\*  
8: gb\_est8.\*  
9: gb\_est9.\*  
10: gb\_est10.\*  
11: gb\_est11.\*  
12: gb\_est12.\*  
13: gb\_est13.\*  
14: gb\_est14.\*  
15: gb\_est15.\*  
16: gb\_est16.\*  
17: gb\_est17.\*  
18: gb\_est18.\*  
19: gb\_est19.\*  
20: gb\_est20.\*  
21: gb\_est21.\*  
22: gb\_est22.\*  
23: gb\_est23.\*  
24: gb\_est24.\*  
25: gb\_est25.\*  
26: gb\_est26.\*  
27: gb\_est27.\*  
28: gb\_est28.\*  
29: gb\_est29.\*  
30: gb\_est30.\*  
31: gb\_est31.\*  
32: gb\_est32.\*  
33: gb\_est33.\*  
34: gb\_est34.\*  
35: gb\_est35.\*  
36: gb\_est36.\*  
37: gb\_est37.\*  
38: gb\_est38.\*  
39: gb\_est39.\*  
40: gb\_est40.\*  
41: em\_estba.\*  
42: em\_estfun.\*  
43: em\_esthum1.\*

44: em\_esthum2.\*  
45: em\_esthum3.\*  
46: em\_esthum4.\*  
47: em\_esthum5.\*  
48: em\_esthum6.\*  
49: em\_esthum7.\*  
50: em\_esthum8.\*  
51: em\_esthum9.\*  
52: em\_esthum10.\*  
53: em\_esthum11.\*  
54: em\_esthum12.\*  
55: em\_esthum13.\*  
56: em\_esthum14.\*  
57: em\_esthum15.\*  
58: em\_esthum16.\*  
59: em\_esthum17.\*  
60: em\_esthum18.\*  
61: em\_esthum19.\*  
62: em\_esthum20.\*  
63: em\_estin1.\*  
64: em\_estin2.\*  
65: em\_estin3.\*  
66: em\_estin4.\*  
67: em\_estom.\*  
68: em\_estov1.\*  
69: em\_estov2.\*  
70: em\_estpl1.\*  
71: em\_estpl2.\*  
72: em\_estpl3.\*  
73: em\_estpl4.\*  
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75: em\_estro1.\*  
76: em\_estro2.\*  
77: em\_estro3.\*  
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83: em\_estro9.\*  
84: em\_estro10.\*  
85: em\_estro11.\*  
86: em\_estro12.\*  
87: em\_estro13.\*  
88: gb\_gss1.\*  
89: gb\_gss2.\*  
90: gb\_gss3.\*  
91: gb\_gss4.\*  
92: em\_gss1.\*  
93: em\_gss2.\*  
94: em\_gss3.\*  
95: em\_gss4.\*  
96: gb\_gss5.\*  
97: gb\_gss6.\*  
98: gb\_gss7.\*  
99: gb\_gss8.\*  
100: gb\_gss9.\*  
101: em\_gss5.\*  
102: em\_gss6.\*  
103: em\_gss7.\*  
104: em\_gss8.\*  
105: em\_gss9.\*  
106: em\_gss10.\*  
107: em\_gss11.\*  
108: gb\_gss10.\*  
109: gb\_gss11.\*  
110: em\_gss12.\*  
111: gb\_gss12.\*  
112: gb\_gss13.\*  
113: gb\_gss14.\*  
114: gb\_gss15.\*  
115: gb\_gss16.\*  
116: gb\_gss17.\*

117: gb\_gss18:\*  
118: gb\_gss13:\*  
119: em\_gss13:\*  
120: gb\_gss20:\*  
121: gb\_gss21:\*  
122: gb\_gss22:\*  
123: gb\_gss23:\*  
124: gb\_gss24:\*  
125: em\_gss14:\*  
126: em\_gss15:\*  
127: em\_gss16:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46.8	3.6	482	5	AA664125 ac06c04.s
2	44.6	3.4	526	32	BE019568 ba83f05.y
3	44.6	3.4	970	123	CNS03H6V
4	44.4	3.4	805	123	AL243904 Tetraodon
5	42.6	3.3	619	124	AL304427 Tetraodon
6	40.6	3.1	619	124	Z90754 F.rubripes
7	40.4	3.1	1003	123	AL004959 F.rubripes
8	40.4	3.1	1101	121	AL303092 Tetraodon
9	40.4	3.1	752	7	AL063860 Drosophila
10	40.4	3.1	906	122	AA940845 LB23113.5
11	39.8	3.1	946	8	AL199074 Tetraodon
12	39.4	3.0	1101	121	AI069309 mgae0006c
13	39.3	3.0	300	16	AL107204 Drosophila
14	39.3	3.0	567	124	AV182303 AV182303
15	38.8	3.0	612	10	Z90761 F.rubripes
16	38.8	3.0	1076	124	AI402856 GH22177.5
17	37.8	2.9	412	2	AL38180 Tetraodon
18	37.4	2.9	587	23	AA250789 zs06a01.s
19	37.2	2.9	533	8	AW615911 EST325409
20	37.2	2.9	533	5	AI012527 EST206978
21	37.2	2.9	644	5	AA670515 SMOV3MCAM
22	37.2	2.9	651	8	AA618853 SMOV3MCAL
23	37.2	2.9	786	96	AI113539 GH09871.5
24	36.8	2.8	408	5	AQ361731 mgx00004D
25	36.8	2.8	467	23	AA695185 GM02371.5
26	36.8	2.8	563	115	AW651210 EST329664
27	36.6	2.8	434	124	A2122827 RPCI-23-1
28	36.4	2.8	576	6	AL160534 Leishmani
29	36.4	2.8	592	36	AA754683 vu20e10.r
30	36.2	2.8	172	39	C77876 C77876 Mous
31	36.2	2.8	401	10	R85066 yo42b12.r1
32	36.2	2.8	437	90	AI436816 SMOV3MCAM
33	36.2	2.8	475	22	AQ246813 HS_3009.A
34	36.2	2.8	680	10	AW443546 EST308476
35	36.2	2.8	816	34	AI388163 GH18971.5
36	36.2	2.8	1007	121	BE253678 601110742
37	36.2	2.8	1016	123	AL108276 Drosophila
38	36.2	2.8	280	88	AL287459 Tetraodon
39	36.2	2.8	418	11	AQ066682 HS_2195.B
40	36.2	2.8	427	50	AI551096 vx37a04.x
41	36.2	2.8	438	19	AW022884 df45e04.y
42	36.2	2.8	940	123	AV530124 AV530124
43	35.6	2.7	534	33	AL285089 Tetraodon
44	35.6	2.7	546	12	BE024912 894006H01
45	35.6	2.7	613	13	AI670172 605019D02
					AI879203 au55h01.y

ALIGNMENTS

RESULT 1  
AA664125

LOCUS  
DEFINITION  
AA664125 482 bp mRNA EST 12-NOV-1997  
ac06c04.s1 Stragatene lung (#937210) Homo sapiens cDNA clone  
IMAGE:855654 3' similar to contains element MSRI MSRI repetitive  
element ; mRNA sequence.  
ACCESSION  
AA664125 GI:2618116  
VERSION  
AA664125  
KEYWORDS  
EST.  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS  
1 (bases 1 to 482)  
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,  
Krizman,D., Kucaba,T., Lacy,M., Le.N., Lennon,G., Marra,M., Martin  
J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,  
White,Y., Wylie,T., Waterston,R. and Wilson,R.  
TITLE  
WashU-NCI human EST Project  
JOURNAL  
Unpublished (1997)  
COMMENT  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 425.  
FEATURES  
source  
1..482  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:855654"  
/clone\_lib="Stratagene lung (#937210)"  
/sex="male"  
/dev\_stage="72 years"  
/lab\_host="SOLR cells (kanamycin resistant)"  
/note="Organ: lung; Vector: pBluescript SK-; Site: 1: EcoRI  
; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo  
dT, normal lung. Average insert size: 1.0 kb; Uni-ZAP XR  
Vector: -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3'  
adaptor sequence: 5' CTCGAGTCTTTTCTTTTCTTTT 3'"  
BASE COUNT 51 a 113 c 176 g 142 t  
ORIGIN  
Query Match 3.6%; Score 46.8; DB 5; Length 482;  
Best Local Similarity 48.8%; Pred. No. 0.0052;  
Matches 126; Conservative 0; Mismatches 132; Indels 0; Gaps 0;  
QY 727 GGTGTTCTTCTGCTGATGAGCTGTTGTCAGCTGCTGCACACTCCAGCTCTTCTGCT 786  
||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||  
Db 213 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 272  
||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||  
QY 787 AACTCCCTTGGTGATGACATCCCACTTGGATACCGAGCTGGATACCATCGTGTATGCC 846  
||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||  
Db 273 GCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 332  
||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||  
QY 847 AACCCACAAGCTGCTCCACCTGATTTCCAACTACCCATGCTTCTGCAAGTTCATCGCTACT 906  
||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||  
Db 333 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 392  
||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||  
QY 907 CCTATGAGATGGCTTCTCGTGTTCGTTGCTGGAACCCCTTGGTTCGCTGCTGCTGCTGCT 966  
||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||  
Db 393 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 452  
||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||  
QY 967 CCTAACTGGAAGCGTGTCT 984  
||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||  
Db 453 GCTGCTAGCGCGCGCTGCT 470

RESULT 2  
BE019568/c





[illegible]



ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
REFERENCE 1 (bases 1 to 1101)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr  
- web : www.genoscope.cns.fr)  
COMMENT Determination of this BAC-end sequence was carried out as part of a  
collaboration with the Berkeley Drosophila Genome Project (BDGP).  
The BDGP is constructing a physical map of the Drosophila  
melanogaster genome using these BACs. For further information  
please see <http://www.fruitfly.org> The BDGP Drosophila  
melanogaster BAC library was prepared by Kazutoyo Osoegawa and  
Aaron Mammosier in Pieter de Jong's laboratory in the Department of  
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
NY. The library is named RPCI-98 and was constructed by partial  
EcoRI digestion of Drosophila DNA provided by the BDGP from the  
isogenic strain y2; cn bw sp, the same strain used for the BDGP's  
p1 and EST libraries. A more detailed description of the library  
and how to order individual BAC clones, the entire library, or  
filters for hybridization from the BACPAC Resource Center can be  
found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES  
source  
Location/Qualifiers  
1..1101  
/organism="Drosophila melanogaster"  
/db\_xref="taxon:7227"  
/clone\_lib="RPCI-98"  
/dev\_stage="BACRO7E07"  
/note="end : TET3"

BASE COUNT 276 a 306 c 227 g 232 t 60 others  
ORIGIN

Query Match 3.1%; Score 40.4; DB 121; Length 1101;  
Best Local Similarity 45.5%; Pred. No. 0.55;  
Matches 143; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

QY 708 GGGTATCACCAACACCGTGTCTTGTGTGATGCAGCTGTTCAGCTGCTGC 767  
|||||  
Db 631 GGCTGGAACTCGCACTGCTGTGCTGGAGCTGTGATGGTGTGCTGTGATGG 572  
QY 768 ACATCCCAAGTCTTCTTAACCTCCCTTGGTGATGACATCCCATTCGACCAACCTGG 827  
|||||  
Db 571 AACGGCAATCTCTGCTGATCTGATCTGTCATCTGTGTCAGACAGTAGCGGCTTCATCTTGCCTC 512  
QY 828 ATACCACATGCTGATGCCAACCCAGAGCTGCTCCAGCTATTCCAACTACCGATGCTTC 887  
|||||  
Db 511 GTAGCTGGCTGATAAGGATACGCCCGCAACGTTCTGCAATTTCCGGCAGCACACTGGCTGCGGC 452  
QY 888 TGGAAATTCATCCCTACTCTATGGAGATGGGTCTTTCGTGCTGGAACCGTTGAGTT 947  
|||||  
Db 451 TGGAACTGCTGAAGTTGCTGCTGCTGCTGTGCTGTGCTGTGCTGTGCTGCTGCTG 392  
QY 948 CGCTGGTCTCACTGCTGCTCCTTAACCTGGAAGCGGTGCTCAGCTTCTCTACACTCAGCTCG 1007  
|||||  
Db 391 TGGTGATGCTGCTGATTCAACTGGCCGGCGCTCGGCATCATATGCCCAATAGTTATCATCG 332  
QY 1008 TAAGTTGCTCCAG 1021  
|||||  
Db 331 CCAATGGGTGCCCTG 318

RESULT 9  
AA940845/c  
LOCUS  
DEFINITION  
LD23113.5prime LD Drosophila melanogaster embryo pOT2 Drosophila  
melanogaster cDNA clone LD23113 5prime similar to M23221: fs(1)h  
F8gn0004656 PID:g157453 SWISS-PROT:P13709, mRNA sequence.  
ACCESSION  
VERSION  
AA940845  
AA940845.1 GI:3100758

25-NOV-1998  
EST  
melanogaster embryo pOT2 Drosophila

KEYWORDS EST.  
SOURCE fruit fly.  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
REFERENCE 1 (bases 1 to 752)  
AUTHORS Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C., Brokstein  
P., Lewis, S. and Rubin, G. M.  
TITLE BDGP/HMI Drosophila EST Project  
JOURNAL Unpublished (1997)  
COMMENT Contact: Harvey, D.  
G. M. Rubin-Molecular and Cell Biology  
University of California Berkeley  
539 LSA, Berkeley, CA 94720-3200, USA  
Fax: 510 643 9947  
Email: <http://www.fruitfly.org/EST>, [est@fruitfly.berkeley.edu](mailto:est@fruitfly.berkeley.edu)  
Plate: 231 row: B column: 1  
High quality sequence stop: 639.  
Location/Qualifiers  
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/organism="Drosophila melanogaster"  
/db\_xref="taxon:7227"  
/clone\_lib="LD23113"  
/sex="male and female"  
/dev\_stage="0 to 24 hours mixed stage embryonic"  
/lab\_host="XL1 Blue"  
/note="Organ: embryo; Vector: pOT2; Site\_1: EcoRI; Site\_2:  
XhoI; Sized fractionated cDNAs were directly ligated into  
pOT2."

BASE COUNT 234 a 231 c 177 g 108 t 2 others  
ORIGIN

Query Match 3.1%; Score 40; DB 7; Length 752;  
Best Local Similarity 51.1%; Pred. No. 0.64;  
Matches 91; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 641 TCGCTAACGGTGGAGAGTCTGCTGCTGTTATCGGATTCGACACTGAAGCTGCTG 700  
|||||  
Db 486 TTGCTGCTGTGGAGATGTTGCTGCTGCTGTGTTGTTGNTGCGGCTGCGACACTGCTG 427  
QY 701 CTCTCAAGGTATCACCAACCAACCGTGTCTTGTGTTGATGACAGCTGTGTTGTCAG 760  
|||||  
Db 426 CTGGTTAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 367  
QY 761 CTGGTGCACACTCCAACTCTTGTGCTAACTCCCTTGTGCTGATGACATCCCATGGATAC 818  
|||||  
Db 366 CTGGTGCCTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 309

RESULT 10  
CNS021LL  
LOCUS  
DEFINITION  
CNS021LL 906 bp DNA GSS 13-MAY-2000  
Tetraodon nigroviridis genome survey sequence T7 end of clone  
141F22 of library G from Tetraodon nigroviridis, genomic survey  
sequence.  
AL199074  
ACCESSION AL199074.1 GI:7837225  
VERSION  
GSS: genome survey sequence.  
KEYWORDS  
SOURCE  
ORGANISM  
Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Eurypterygii; Ctenosquamata; Acanthomorpha; Eucanthomorpha;  
Holacanthopterygii; Acanthopterygii; Percomorpha;  
Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.  
REFERENCE 1 (bases 1 to 906)  
AUTHORS Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,  
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and  
Weissenbach, J.  
TITLE Characterization and repeat analysis of the compact genome of the





Query Match	3.0%;	Score 38.8;	DB 10;	Length 612;
Best Local Similarity	51.1%;	Pred. No. 1.3;		

Tue Jan 2 15:21:47 2001

us-08-484-274-8.rst